Homework on optimization algorithms.

P8160 Advanced Statistical Computing

Problem 1:

Design an optmization algorithm to find the minimum of the continuously differentiable function

$$f(x) = -e^{-x}\sin(x)$$

on the closed interval $[0, 1.5]$. Write out your algorithm and implement it into **R**.

Answer: your answer starts here. . .

To find the minimum of a continuously function,we first make some changes to the function let

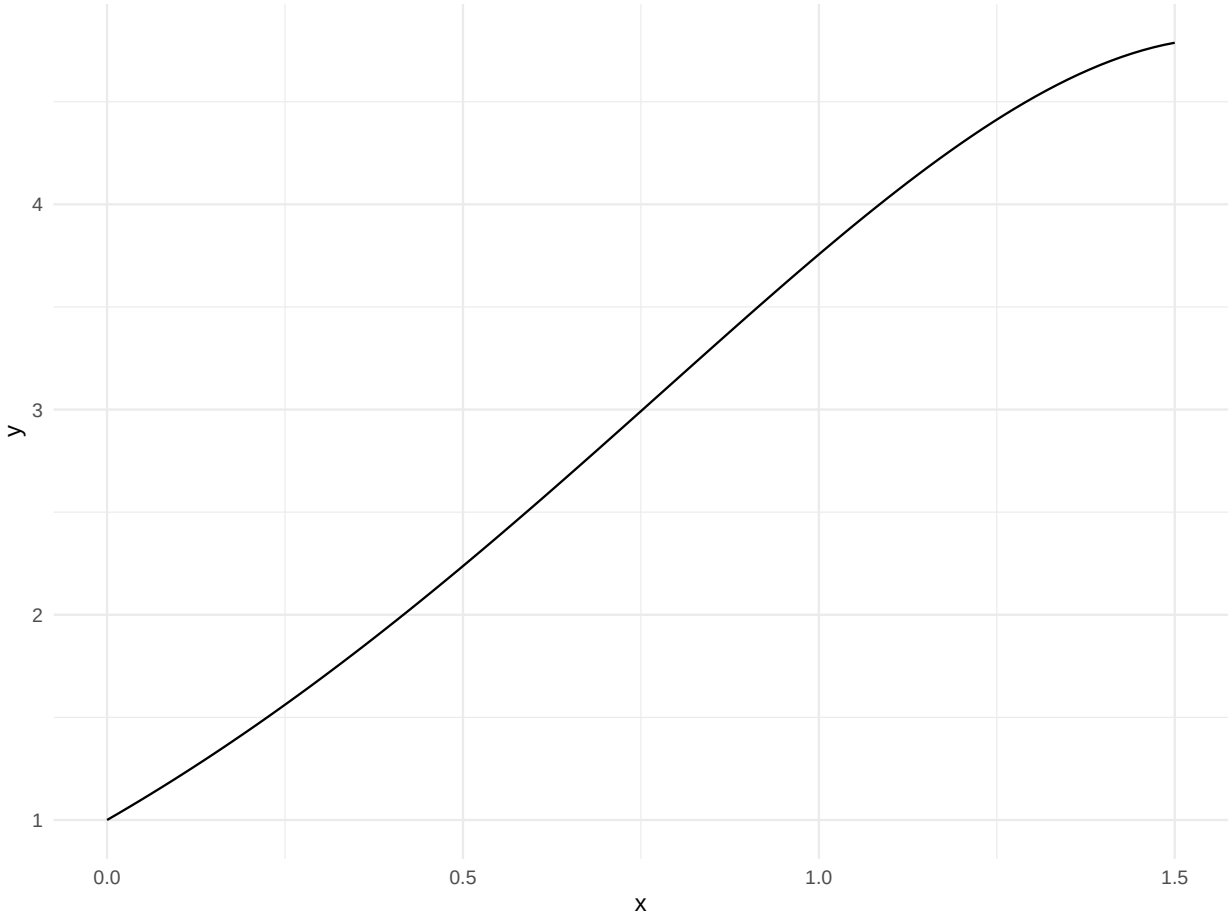
$$g(x) = e^{x}\sin(x)$$

and instead find the maximum of g(x).

The gradient of $g(x)$ is :

$$\nabla g(x) = e^{x}(\sin(x) + \cos(x))$$

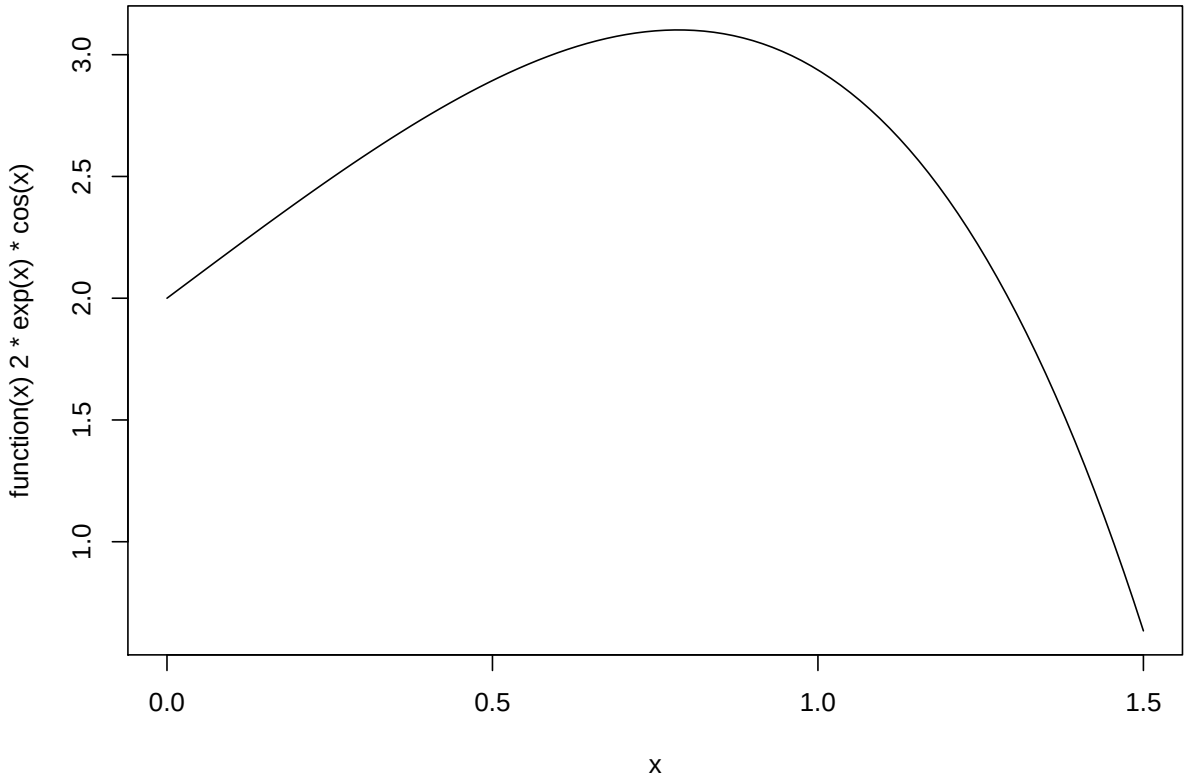
```
ggplot(tibble(x = seq(0,1.5,length = 10)),aes(x))+
  geom_function(fun = function(x) exp(x)*(sin(x)+cos(x)))
```



and the Hessian is:

$$\nabla^2 g(x) = 2e^x \cos(x)$$

```
plot(function(x) 2*exp(x)*cos(x),xlim = c(0,1.5))
```



the hessian is greater than 0 everywhere in [0,1.5], so we can't use Newton method.

```
goose_egg =
  function(
    fun,
    left = NULL,
    right = NULL,
    range = NULL,
    ratio = 0.618,
    tol = 10e-4,
    ...
  ){
    if (!any(left,right)){
      left = range[1]
      right = range[2]
    }

    mid_1 = left + ratio*(right - left)

    f_mid_1 = fun(mid_1)

    mid_2 = mid_1 + ratio*(right-mid_1)

    f_mid_2 = fun(mid_2)
```

```
    f_left = fun(left)

    f_right = fun(right)

    i = 1

    while (abs(f_left - f_right)>tol && i<1000){
      i = i + 1
      if (f_mid_1 < f_mid_2) {
        f_left = f_mid_1
        left = mid_1
      } else {
        f_right = f_mid_2
        right = mid_2
      }
      mid_1 = left + ratio * (right - left)
      f_mid_1 = fun(mid_1)
      mid_2 = mid_1 + ratio * (right - mid_1)
      f_mid_2 = fun(mid_2)
    }
    return(mean(mid_1,mid_2))
  }
```

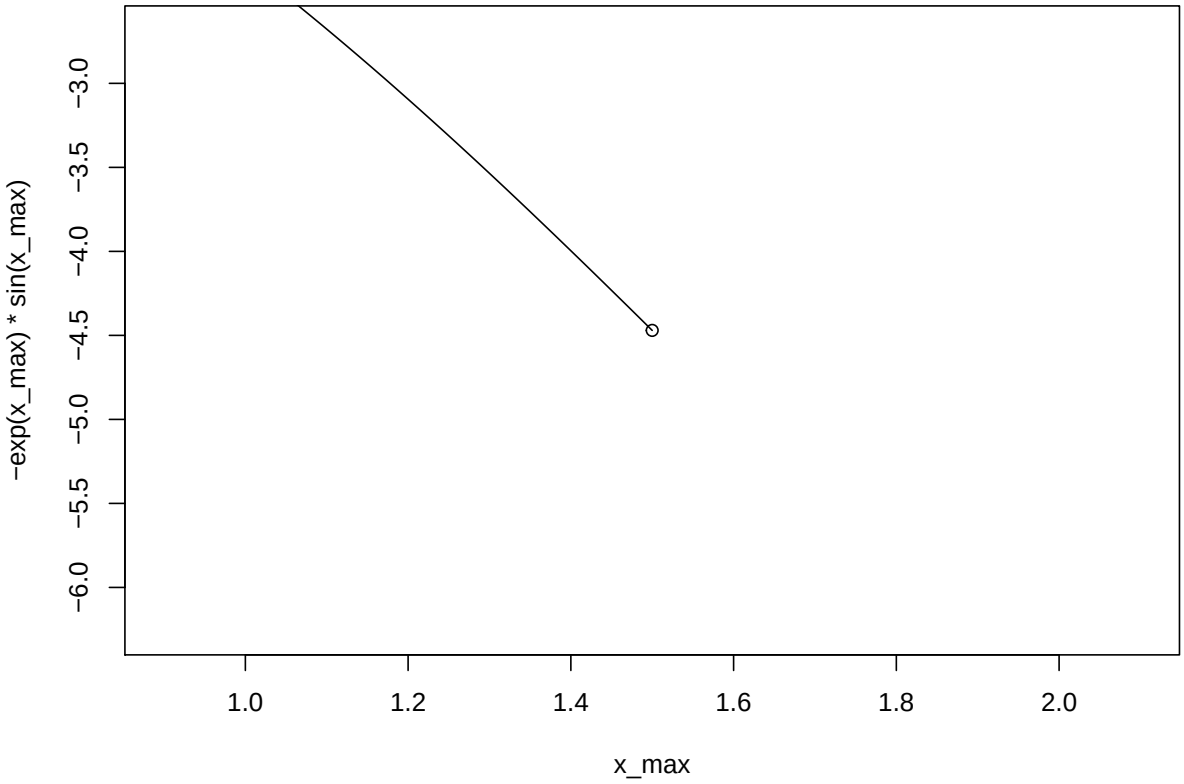
```
x_max = goose_egg(function(x) exp(x)*sin(x),range = c(0,1.5))

print(x_max)
```

```
## [1] 1.5
```

```
plot(x_max,-exp(x_max)*sin(x_max))

plot(function(x) {-exp(x)*sin(x)}, xlim = c(0,1.5), add = T)
```



Problem 2:

The Poisson distribution, written as

$$P(Y = y) = \frac{\lambda^y e^{-\lambda}}{y!}$$

for $\lambda > 0$, is often used to model "count'' data — e.g., the number of events in a given time period.

A Poisson regression model states that

$$Y_i \sim \text{Poisson}(\lambda_i),$$

where

$$\log \lambda_i = \alpha + \beta x_i$$

for some explanatory variable x_i. The question is how to estimate α and β given a set of independent data $(x_1, Y_1), (x_2, Y_2), \ldots, (x_n, Y_n)$.

1. Generate a random sample (x_i, Y_i) with $n = 500$ from the Possion regression model above. You can choose the true parameters (α, β) and the distribution of X.
2. Write out the likelihood of your simulated data, and its Gradient and Hessian functions.
3. Develop a modify Newton-Raphson algorithm that allows the step-halving and re-direction steps to ensure ascent directions and monotone-increasing properties.
4. Write down your algorithm and implement it in R to estimate α and β from your simulated data.

Answer: your answer starts here...

2.1

```
print("hello world")
```

```
X = rbind(rep(1,500),rnorm(500))
Beta = runif(2)
lambda = exp(t(X)%*%Beta)
Y = map(lambda,~rpois(1,.x)) %>% unlist()
dat = list(y = Y, x=X)
ans = glm(Y~0+t(X),family = poisson())
```

2.2

- The log-likelihood of Poisson distribution is

$$l(Y;\lambda) = \sum\{y * log(\lambda) - \lambda - log(y!)\}$$

OR

$$l(Y;\alpha,\beta) = \sum\{y * (\alpha + x\beta) - exp(\alpha + x\beta) - log(y!)\}$$

- The Score funtion is

$$\nabla(Y;\alpha,\beta) = \frac{\partial}{\partial\lambda} l(Y;\lambda) = (\sum\{y - exp(\alpha + x\beta)\}, \sum\{y * x - x * exp(\alpha + x\beta)\})$$

- The hessian is

$$\nabla^2(Y;\lambda) = \frac{\partial^2}{\partial\lambda^2} l(Y;\lambda)$$

$$= \begin{pmatrix} \sum -exp(\alpha + x\beta) & \sum -x * exp(\alpha + x\beta) \\ \sum -x * exp(\alpha + x\beta) & \sum -x^2 * exp(\alpha + x\beta) \end{pmatrix}$$

which is negative defined everywhere.

```
Poisson =
  function(Y,X,
           theta_vec) {
    lambda = exp(t(X) %*% theta_vec)
    loglink = sum(Y * log(lambda) - lambda - log(factorial(Y)))

    fisher = var(Y * log(lambda) - lambda - log(factorial(Y)))

    gradient = c(sum(Y - lambda), sum(Y * X[2,] - X[2,] * lambda))

    hessian = matrix(c(
      sum(-lambda),
      sum(-X[2,] * lambda),
      sum(-X[2,] * lambda),
      sum((-X[2,] ^ 2) * lambda)
    ), ncol = 2)
```

```
    return(list(
      loglink = loglink,
      fisher = fisher,
      gradient = gradient,
      hessian = hessian
    ))
  }

Poisson(Y,X,c(7,2))
```

```
## $loglink
## [1] -3974589
##
## $fisher
##          [,1]
## [1,] 8.21e+08
##
## $gradient
## [1] -3980250 -7302954
##
## $hessian
##          [,1]     [,2]
## [1,] -3981198 -7.3e+06
## [2,] -7303206 -1.6e+07
```

2.3

the Newton method updating is:

$$\nabla g(x_{k+1}) = \nabla g(x_k) + \eta * \nabla^2 g(x_k)(x_{k+1} - x_k)$$

where η is the step size that ensure $\nabla g(x_{k+1}) > \nabla g(x_k)$

```
#Develop a modify Newton-Raphson algorithm that allows the
#step-halving and
#re-direction steps
#to ensure ascent directions and monotone-increasing properties.

newton_update =
  function(fun,
           previous_theta,
           y,x,
           step_size = 1,
           optimizer = F,
           backtracking = T,
           tol = 1e-8) {
    #take previous gradient and a updated hessian, return update gradient with
    #backtracking
    #if (abs(fun(y,x,previous_theta)$loglink) == Inf) stop("Check your log-likelihood")
    trial = 0

    gradient = fun(y,x,previous_theta)$gradient
```

```
    if (is.function(optimizer)) {
      hessian = optimizer(y,x, fun,) # get H
    } else{
      if (is.numeric(optimizer)) {
        H = optimizer # use H
      } else{
        hessian = fun(y,x, previous_theta)$hessian
        H = solve(hessian)
        while (all(eigen(H)$values > 0)) {# eigen decomposition
          P = eigen(hessian)
          lambda = max(P$values)
          hessian =
            P$vectors %*% (diag(P$values) - (lambda + tol) * diag(length(P$values))) %*%
            solve(P$vectors)

          H = solve(hessian)
        }
      }
    }

    #updating
    cur_theta = previous_theta - step_size * H %*% gradient

    #backtracking
    while (backtracking & fun(y,x,cur_theta)$loglink < fun(y,x,previous_theta)$loglink & trial < 2000) {
      step_size = step_size / 2

      trial = trial + 1 # avoild dead loops

      cur_theta = previous_theta - step_size * H %*% gradient
    }

    return(cur_theta)
  }

newton_update(fun = Poisson,previous_theta = c(7,2), y=Y,x =X)
```

```
##      [,1]
## [1,]    6
## [2,]    2
```

```
naive_newton =
  function(fun,
           init_theta = 1,
           y,x,
           tol = 1e-8,
           maxtiter = 2000,
           optimizer = F,
           ...) {

    f = fun(y,x,init_theta)

    if (any(is.null(f$loglink),
```

```
            is.null(f$gradient),
            is.null(f$hessian))) {
      stop("fun input must return both gradient and hessian")
    }
    result = tibble()

    i = 0

    cur_theta = init_theta

    prevlog = -Inf # \nabla g(x_{k})

    while (any(abs(f$loglink)==Inf,abs(f$loglink - prevlog) > tol) && i < maxtiter) {
      i = i + 1
      prev_theta = cur_theta
      prevlog = f$loglink
      cur_theta = newton_update(fun, prev_theta,y,x)
      f = fun(y,x,cur_theta)
      result =
        rbind(result, tibble(
          iter = i,
          x_i = list(prev_theta),
          `g(x_i)` = prevlog
        ))
    }
    return(list(theta = cur_theta,result = result))
  }
```

```
Beta_hat = naive_newton(Poisson,init_theta = c(7,2),Y,X)$theta

tibble(
  term = c("alpha", "beta"),
  theta = Beta,
  theta_hat = Beta_hat
) %>%
  knitr::kable()
```

term	theta	theta_hat
alpha	0.585	0.606
beta	0.234	0.247

Problem 3:

The data *breast-cancer.csv* have 569 row and 33 columns. The first column **ID** lables individual breast tissue images; The second column **Diagnonsis** indentifies if the image is coming from cancer tissue or benign cases (M=malignant, B = benign). There are 357 benign and 212 malignant cases. The other 30 columns correspond to mean, standard deviation and the largest values (points on the tails) of the distributions of the following 10 features computed for the cellnuclei;

- radius (mean of distances from center to points on the perimeter)

- texture (standard deviation of gray-scale values)
- perimeter
- area
- smoothness (local variation in radius lengths)
- compactness (perimeter$\hat{2}$ / area - 1.0)
- concavity (severity of concave portions of the contour)
- concave points (number of concave portions of the contour)
- symmetry
- fractal dimension ("coastline approximation" - 1)

The goal is to build a predictive model based on logistic regression to facilitate cancer diagnosis;

1. Build a logistic model to classify the images into malignant/benign, and write down your likelihood function, its gradient and Hessian matrix.
2. Build a logistic-LASSO model to select features, and implement a path-wise coordinate-wise optimization algorithm to obtain a path of solutions with a sequence of descending λ's.
3. Write a report to summarize your findings.

3

3.1

the data is a binomial outcome response, which follows a Bernoulli distribution, Using logit link, which

$$log(\frac{p}{1-p}) = X^T\beta$$

s.t

$$p = \frac{exp(X\beta)}{1+exp(X\beta)}$$

the log-likelihood of Bernoulli is

$$l(Y;\beta) = \sum\{y * log(\frac{p}{1-p}) + log(1-p)\} = \sum\{y * X^T\beta - log(1+exp(X^T\beta))\}$$

The gradient is

$$\nabla l(Y;\beta) = (\frac{\partial}{\partial\beta_i}l(Y;\beta)) = (\sum(y * x_i - \frac{x_i exp(X^T\beta)}{1+exp(X^T\beta)})$$

and the hessian is

$$\nabla^2 l(Y;\beta) = (\sum -\frac{x_i * x_j * exp(X^T\beta)}{(1+exp(X^T\beta)^2)})$$

```
Bernoulli =
  function(y,x,
           theta_vec){
    if (length(theta_vec)!=ncol(x)) stop("length of theta_vec must match dim of x")
    if (is.factor(y)) y = y %>% as.numeric()-1
    Y = y
    X = x
    loglink = sum(Y * X%*%theta_vec - log(1+exp(X%*%theta_vec)))

    if (abs(loglink) == Inf){
     stop("Choose a better starting value")
    }

    fisher = var(Y * X%*%theta_vec - log(1+exp(X%*%theta_vec)))

    X = x*1e-0

    gradient = map(1:length(theta_vec),
                   ~ sum(Y * X[, .x] - X[, .x] * exp(X %*% theta_vec) /
                           (1 + exp(X %*% theta_vec)))) %>% unlist()

    hessian =
      expand.grid(i = seq(1,length(theta_vec)),
                  j = seq(1,length(theta_vec))) %>%
      summarise(beta = map2(i,j,~sum(-X[,.x]*X[,.y]*exp(X%*%theta_vec)/(1+exp(X%*%theta_vec))^2))) %>%
      unnest(beta) %>%
      pull(beta)

    hessian = matrix(hessian,ncol = length(theta_vec))

    return(
      list(loglink = loglink,
           fisher = fisher,
           gradient  = gradient*1e+0,
           hessian = hessian*1e+0)
    )
  }

 Bernoulli(Y,X,rep(0,10))
```

```
## $loglink
## [1] -394
##
## $fisher
##      [,1]
## [1,]    0
##
## $gradient
##  [1]    317.09    907.67   1707.73 -21099.85      5.60     -1.09     -8.82
##  [8]     -4.74     10.64      4.58
##
## $hessian
##           [,1]     [,2]     [,3]      [,4]      [,5]      [,6]      [,7]
```

```
##  [1,]   -30154   -39461  -196955  -1489947  -194.847 -2.23e+02   -205.45
##  [2,]   -39461   -55557  -257249  -1865996  -264.207 -2.94e+02   -258.39
##  [3,]  -196955  -257249 -1287036  -9765529 -1270.701 -1.47e+03  -1358.71
##  [4,] -1489947 -1865996 -9765529 -78593927 -9101.146 -1.10e+04 -11005.14
##  [5,]     -195     -264    -1271     -9101    -1.349 -1.50e+00     -1.30
##  [6,]     -223     -294    -1467    -11036    -1.500 -1.94e+00     -1.85
##  [7,]     -205     -258    -1359    -11005    -1.300 -1.85e+00     -2.02
##  [8,]     -114     -141     -754     -6154    -0.713 -9.68e-01     -1.02
##  [9,]     -366     -498    -2387    -17084    -2.514 -2.81e+00     -2.44
## [10,]     -125     -172     -815     -5750    -0.869 -9.62e-01     -0.82
##             [,8]      [,9]     [,10]
##  [1,]  -114.280   -366.09  -125.098
##  [2,]  -141.187   -498.30  -171.984
##  [3,]  -753.925  -2387.38  -815.186
##  [4,] -6153.567 -17083.93 -5750.212
##  [5,]    -0.713     -2.51    -0.869
##  [6,]    -0.968     -2.81    -0.962
##  [7,]    -1.023     -2.44    -0.820
##  [8,]    -0.554     -1.33    -0.443
##  [9,]    -1.331     -4.78    -1.632
## [10,]    -0.443     -1.63    -0.568
```

```
# Bernoulli(dat,ans$coefficients[-1] %>% as.vector())
```

3.2

```
soft_threshold =
  function(beta, lambda) {
    if (abs(beta)>lambda){
      if (beta >0) return(beta - lambda)
      return(beta +lambda)
    }
    return(0)
    }
```

```
bfun =
  function(y, x, theta_vec) {
    if (is.factor(y))
      y = y %>% as.numeric() - 1
    p_prev = exp(x %*% theta_vec) / (1 + exp(x %*% theta_vec)) #  row matrix

    w_prev = p_prev * (1 - p_prev) # row matrix

    z_prev = x %*% theta_vec + (y - p_prev) / w_prev # row * 1 matrix

    loglink = #sum(w_prev * (z_prev - x %*% theta_vec) ^ 2) / (2 * length(y))
      -sum(y * x%*%theta_vec - log(1+exp(x%*%theta_vec)))

    return(list(
      loglink = loglink,
      p = p_prev,
```

```
      w = w_prev,
      z = z_prev
    ))
  }

gfun = function(y,x,theta_vec){
  z = y
  w = rep(1/length(y),length(y))
  loglink = sum(w *(y - x %*% theta_vec) ^ 2) / 2
  return(
    list(z=z,w=w,loglink=loglink)
  )
}
```

```
Qlasso =
  function(y,
           x,
           family_fun,
           lambda = 0,
           theta_vec = NA,
           maxiter = 500,
           tol = 1e-6,
           intercept = T,
           ...) {
    # data preparation
    if (is.factor(y))
      y = y %>% as.numeric() - 1
    y = y
    x = scale(x)
    xsd = attr(x, "scaled:scale") %>% as.vector()
    if (intercept) {
      x = cbind(rep(1, length(y)), x) # add alpha
      xsd = append(1, xsd)
    }

    # Manually choosing starting value
    if (!is.na(theta_vec)) {
      if (length(theta_vec) != ncol(x))
        theta_vec = append(rep(0, ncol(x) - length(theta_vec)), theta_vec)
    } else
      theta_vec = rep(0, ncol(x))

    #update part
    iter = 0

    cur_result = family_fun(y, x, theta_vec)$loglink

    if (abs(cur_result) == Inf|is.na(cur_result))
      stop("Diverge at starting value")

    prev_result = -Inf

    while (abs(cur_result - prev_result) > tol
           && iter < maxiter) {
```

```
      iter = iter + 1

      prev_result = cur_result

      for (i in 1:length(theta_vec)) {
        #weight
        fun_prev = family_fun(y, x, theta_vec)
        z_prev = fun_prev$z # working response
        w_prev = fun_prev$w # weight

        #update
        cur_theta =
          sum((z_prev-x[,-i]%*%theta_vec[-i])*x[,i]*w_prev)

        #soft-threshod
        if (i > 1){
        cur_theta =
          soft_threshold(cur_theta,
                         lambda) / sum(w_prev * (x[, i] ^ 2))
        } else cur_theta = cur_theta/sum(w_prev * (x[, i] ^ 2))

        #update theta
        theta_vec[[i]] = cur_theta
      }

      cur_result = family_fun(y, x, theta_vec)$loglink + lambda*sum(abs(theta_vec))
    }
    return(list(
      coefficient = theta_vec/xsd,
      loglikelihood = cur_result))
  }
```

```
cv_Qlasso =
  function(y,x,family_fun,lambda=NA,number = 5,intercept = T){
    result = tibble()
    lambda = as.vector(lambda)
    if (all(is.na(lambda))) {
      Y = y
      if (is.factor(y)) Y = y %>% as.numeric()-1
      Y = as.vector(Y)
      max_lambda = length(Y)*max(colSums(diag(Y) %*% scale(x)))
      lambda = exp(seq(log(max_lambda),-10,length=20))
    }
    block_length = length(y)/number
    for (lam in lambda) {
      for (i in 1:number) {
        #create training partition
        test_index = (1 + (number-1)*block_length):(number*block_length)
        trainX = x[-test_index,]
        testX = x[test_index,]
        trainY = y[-test_index]
        testY = y[test_index]
```

```
        #train
        trainF = Qlasso(trainY,trainX,family_fun,lambda = lam,intercept = intercept)
        if (intercept) {prev_coef = trainF$coefficient[-1]
        }else {prev_coef = trainF$coefficient}
        #test
        testF = family_fun(testY,testX,prev_coef)
        result =
          result %>%
          rbind(expand.grid(coefficient = trainF$coefficient,
                            lambda = lam,
                            loglikelihood = testF$logli+ lam*sum(abs(trainF$coefficient))) %>%
                  cbind(tibble(term = (1:length(trainF$coefficient))-1) %>%
                          mutate_all(as.character))
                )
      }
    }
    # take the mean of everything
    result = result %>%
      group_by(lambda,term) %>%
      summarise(across(c(coefficient,loglikelihood),mean))%>%
      arrange((loglikelihood)) %>%
      nest(coef = c(coefficient,term))

    coef = result[1,] %>%
      unnest() %>%
      pull(coefficient)

    lambda = result[1,"lambda"] %>% as.numeric()

    loglikelihood = result[1,"loglikelihood"] %>% as.numeric()

    return(list(
      coefficient = coef,
      loglikelihood = loglikelihood,
      lambda = lambda,
      cvtable = result
    ))
  }
```

```
tibble(glm = glm(Y_g~X_g)$coefficient,
       glmnet_0lambda = coef(glmnet(X_g,Y_g,lambda = 0)) %>% as.vector(),
       Qlasso_0lambda = Qlasso(Y_g,X_g,gfun)$coefficient,
       Qlasso_01lambda = Qlasso(Y_g,X_g,gfun,5)$coefficient,
       glmnet_01lambda = coef(glmnet(X_g,Y_g,lambda = 5)) %>% as.vector()
       ) %>%
  knitr::kable(caption = "Function comparison at Gaussian Family")
```

Table 2: Function comparison at Gaussian Family

glm	glmnet_0lambda	Qlasso_0lambda	Qlasso_01lambda	glmnet_01lambda
-0.130	-0.130	-1.766	-1.77	-1.28
1.755	1.755	1.755	0.00	0.00
6.423	6.423	6.423	2.29	2.32

glm	glmnet_0lambda	Qlasso_0lambda	Qlasso_01lambda	glmnet_01lambda
4.119	4.119	4.119	0.00	0.00
9.380	9.380	9.380	5.32	5.35
0.414	0.414	0.414	0.00	0.00
0.672	0.672	0.672	0.00	0.00
7.815	7.815	7.815	4.06	4.08
4.113	4.113	4.113	0.00	0.00
7.397	7.397	7.397	1.76	1.79
4.018	4.018	4.018	0.00	0.00

```
tibble(glm = glm(Y~X,family = binomial())$coefficient,
       glmnet_0lambda = coef(glmnet(X,Y,"binomial",lambda = 0)) %>% as.vector(),
       Qlasso_0lambda = Qlasso(Y,X,bfun)$coefficient,
       Qlasso_01lambda = Qlasso(Y,X,bfun,5)$coefficient,
       glmnet_01lambda = coef(glmnet(X,Y,"binomial",lambda =1)) %>% as.vector()
       ) %>%
  knitr::kable(caption = "Function comparision at binomial family")
```

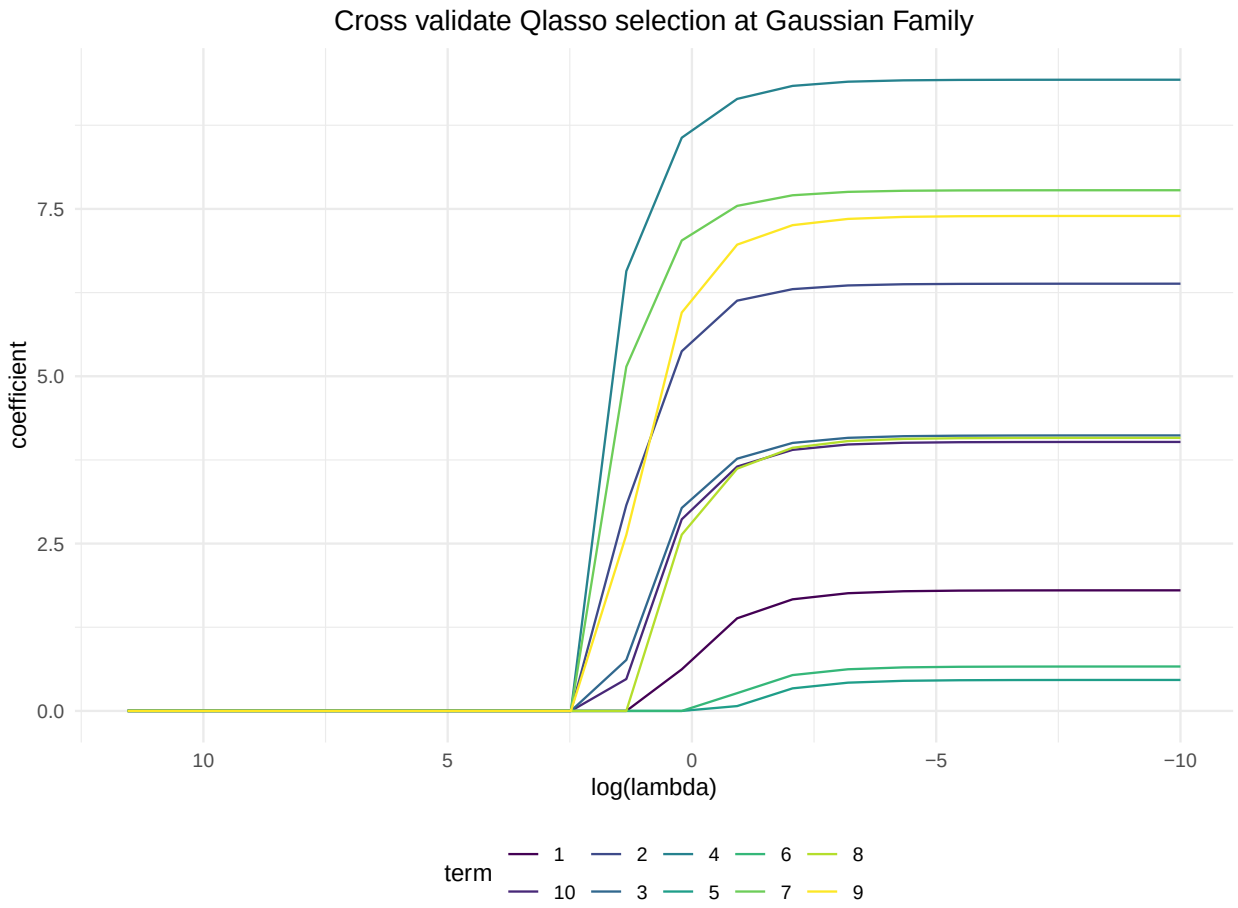
Table 3: Function comparision at binomial family

glm	glmnet_0lambda	Qlasso_0lambda	Qlasso_01lambda	glmnet_01lambda
7.360	8.317	-0.493	0.571	0.521
2.049	1.608	2.370	-0.325	0.000
-0.385	-0.384	-0.384	-0.235	0.000
0.072	0.120	0.021	0.000	0.000
-0.040	-0.038	-0.040	-0.002	0.000
-76.432	-75.580	-77.331	-14.262	0.000
1.462	0.452	3.047	0.000	0.000
-8.469	-8.730	-8.441	-0.418	0.000
-66.822	-66.866	-66.107	-63.745	0.000
-16.278	-16.226	-16.361	-6.526	0.000
68.337	67.619	66.635	0.000	0.000

From above tables we can see that the `Qlasso` function of mine works reasonably close to `glmnet` except for the intercept terms in the case of Gaussian family. However, the result of binomial family behave rather different with L1 penalties. The function produce similar result with lambda = 0 except for `intercept` and once adding lamdba, the effect of lambda is rather different to `glmnet`.

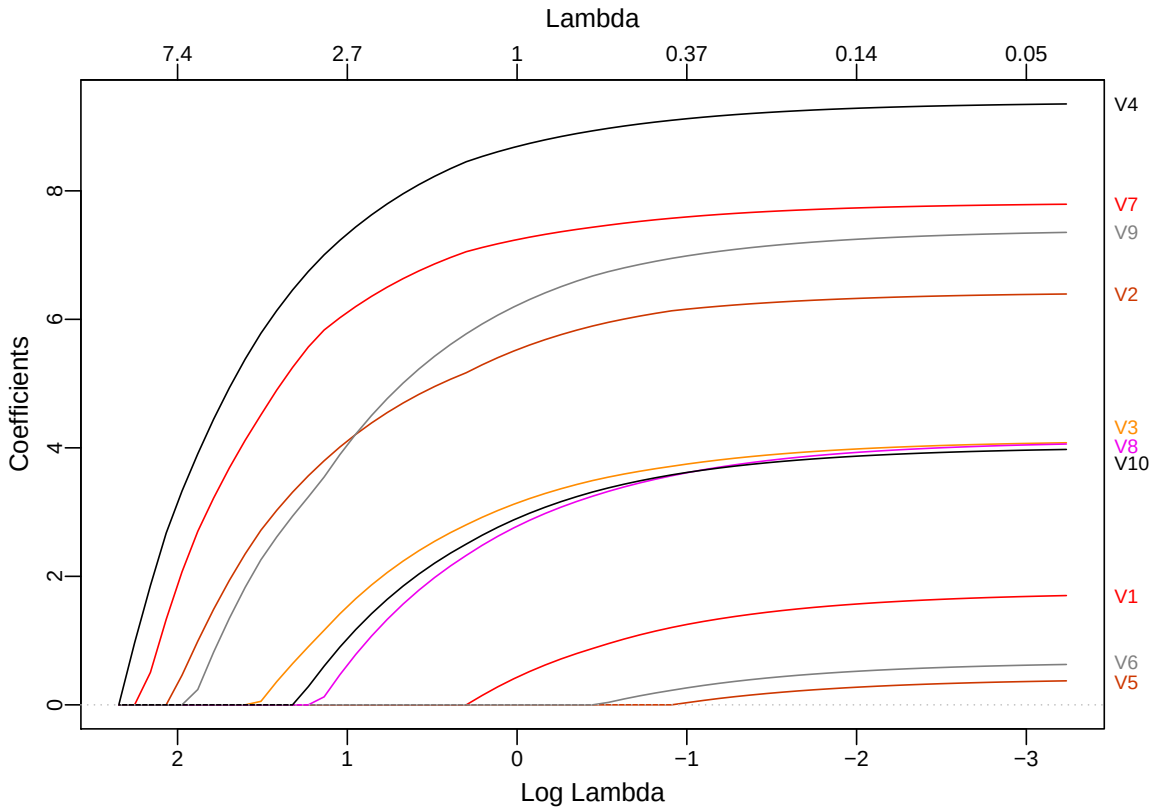
```
gaussian_Qlasso = cv_Qlasso(Y_g,X_g,gfun)

gaussian_Qlasso$cvtable %>%
  unnest(coef) %>%
  filter(term != 0) %>%
  ggplot(aes(x = log(lambda), y = coefficient, color = term)) +
  geom_line() +
  scale_x_reverse() +
  labs(title = "Cross validate Qlasso selection at Gaussian Family")
```




```
gaussian_glmnet = cv.glmnet(X_g,Y_g)

plotmo::plot_glmnet(gaussian_glmnet$glmnet.fit)
```




```
tibble(term = c("intercept",colnames(X_g %>% as_tibble())),
       Qlasso = gaussian_Qlasso$coef,
       glmnet = coef(gaussian_glmnet) %>% as.vector()) %>%
  knitr::kable(caption = "Gaussian family result")
```

Table 4: Gaussian family result

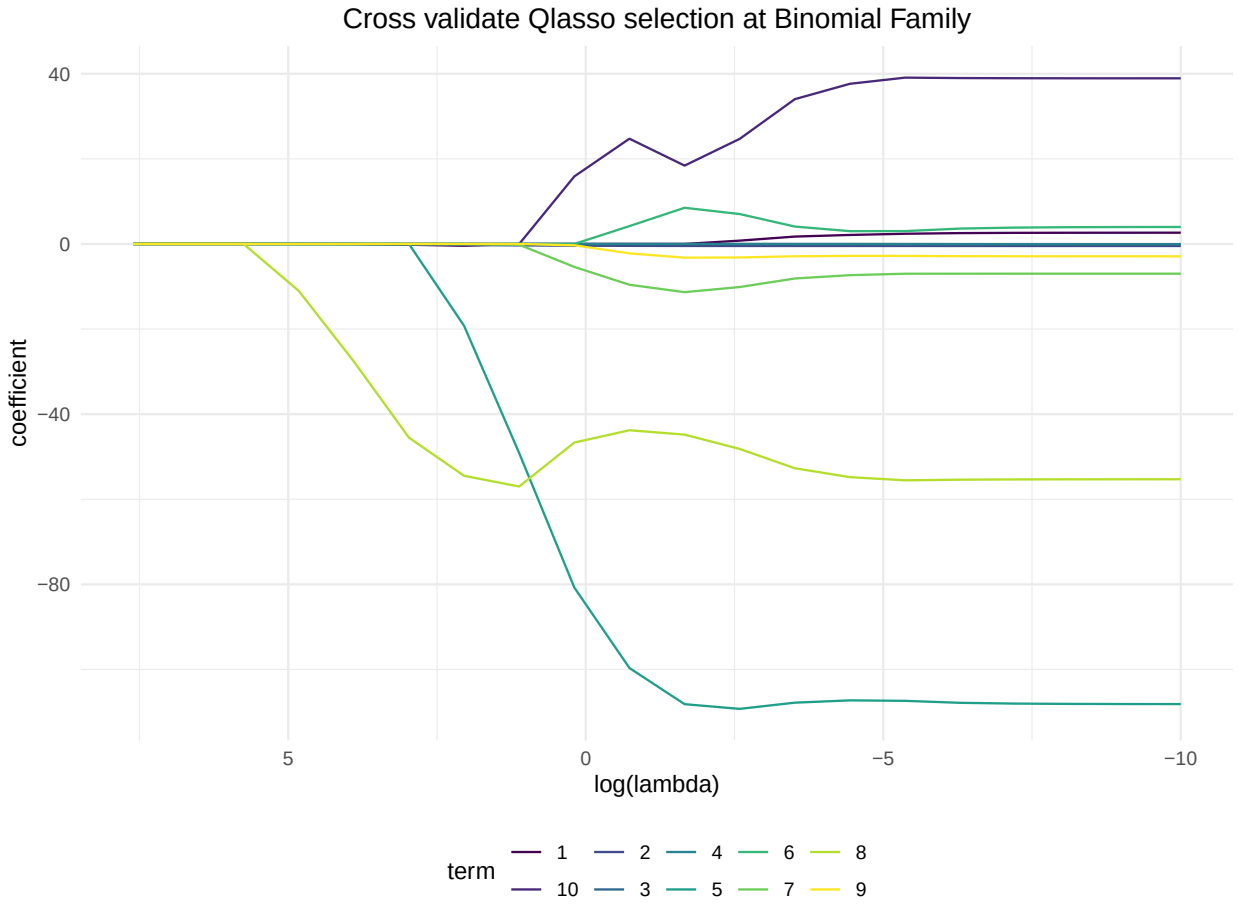
term	Qlasso	glmnet
intercept	-2.114	-0.157
V1	1.802	1.630
V2	4.019	6.358
V3	6.383	4.027
V4	4.116	9.316
V5	9.430	0.320
V6	0.463	0.571
V7	0.664	7.761
V8	7.779	3.989
V9	4.080	7.296
V10	7.395	3.919

Using cross validation we can see that for gaussian, the penalty in the same scale as the `glmnet`, but because

of the intercept is different, the optimum model chosen is different. same result(bug) can be observed in the binomial family, but rather deteriorate. The penalty although work similar to `glmnet` in terms of trends, but on a rather different scale. Also, the intercept produce by the function is not even the $log(\frac{\bar{Y}}{1-\bar{Y}})|X=0$, so the objective function failed to aid the function to choose the optimun model.

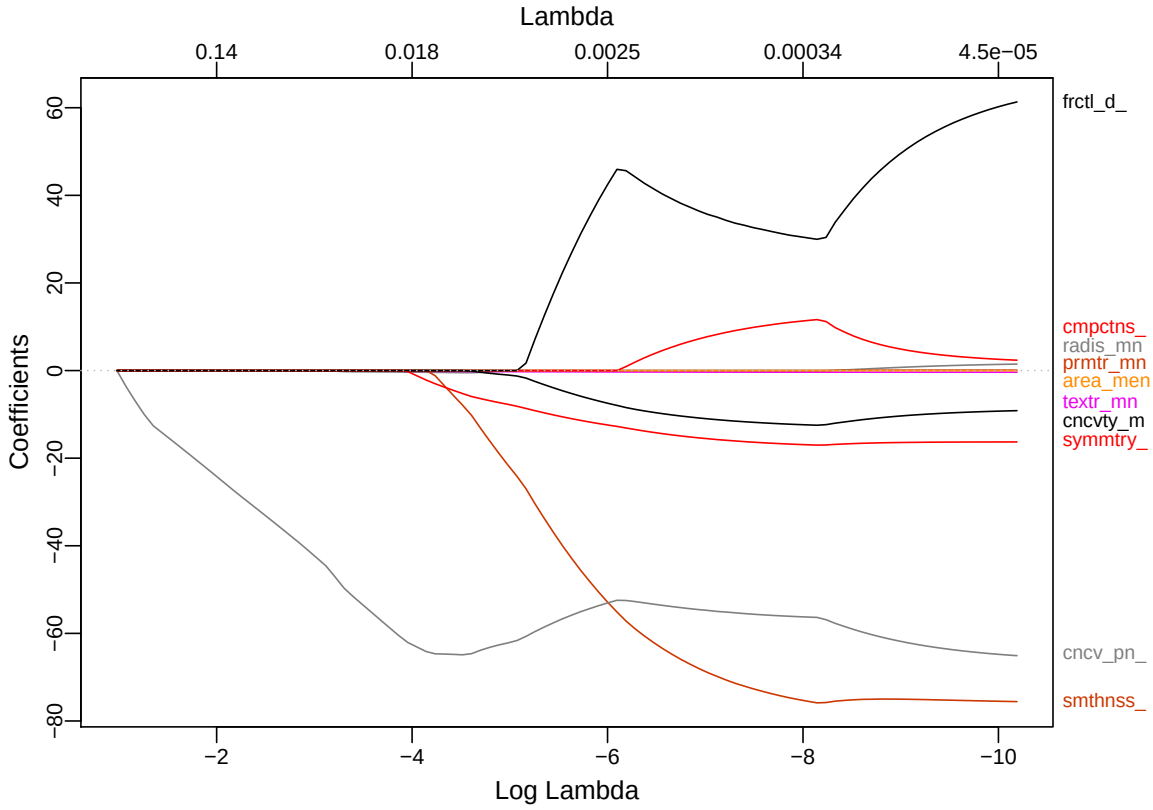
```
binomial_Qlasso = cv_Qlasso(Y,X,bfun)

binomial_Qlasso$cvtable %>%
  unnest(coef) %>%
  filter(term != 0) %>%
  ggplot(aes(x = log(lambda), y = coefficient, color = term)) +
  geom_line() +
  scale_x_reverse() +
  labs(title = "Cross validate Qlasso selection at Binomial Family")
```




```
binomial_glmnet = cv.glmnet(X,Y,family = "binomial")

plotmo::plot_glmnet(binomial_glmnet$glmnet.fit)
```




```
tibble(term = c("intercept",colnames(X)),
       Qlasso = binomial_Qlasso$coef,
       glmnet = coef(binomial_glmnet) %>% as.vector()) %>%
  knitr::kable(caption = "Binomial family result")
```

Table 5: Binomial family result

term	Qlasso	glmnet
intercept	0.373	13.998
radius_mean	0.000	-0.414
texture_mean	0.000	-0.193
perimeter_mean	0.000	0.000
area_mean	0.000	0.000
smoothness_mean	0.000	-1.160
compactness_mean	0.000	0.000
concavity_mean	0.000	0.000
concave_points_mean	0.000	-64.666
symmetry_mean	0.000	-3.006
fractal_dimension_mean	0.000	0.000