A study of optimization algorithms on a breast cancer diagnosis dataset

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Abstract

This report discusses a study of optimization algorithms on breast cancer diagnosis dataset. Our goal is to build a predictive model based on logistic regression to facilicate cancer diagnosis, and we compared methods including Newton Raphson, Gradient Decent with general logistic regression and Pathwise Coordinate Descent with regularized logistic regression. Our result shows that all of our algorithms were valid and Newton-Raphson was the most efficient according to iteration times. The MSE of these three methods were similar.

Background

Dataset

The data *breast-cancer.csv* have 569 row and 33 columns. The first two columns inclues covariate "ID" which lables individual breast tissue images and covariate "Diagnonsis" which indentifies if the image is coming from cancer tissue or benign cases. 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.

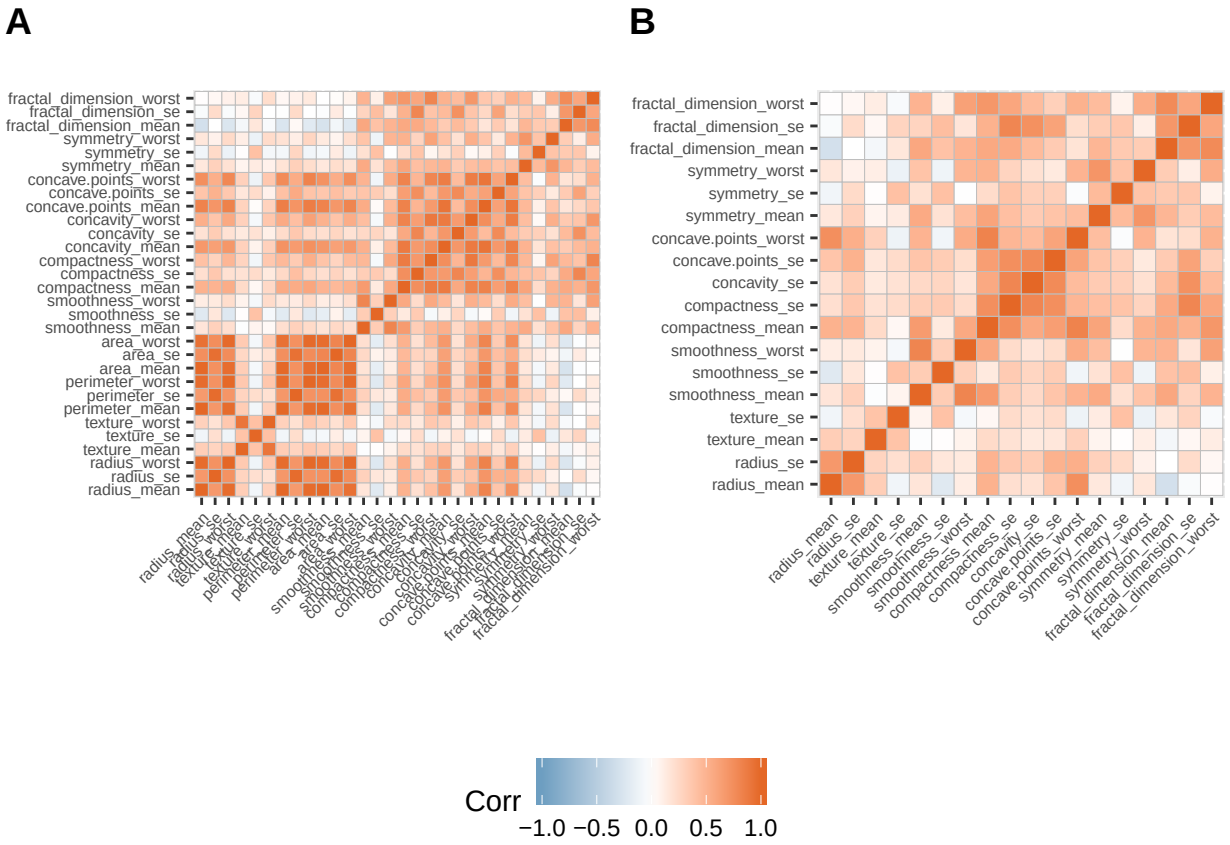
- radius: mean of distances from center to points on the perimeter
- texture: standard deviation of gray-scale values
- perimeter: mean size of the core tumor
- area: mean area of the core tumor
- smoothness: local variation in radius lengths
- compactness: perimeter^2/area - 1.0
- concavity: severity of concave portions of the contour
- concave points: number of concave portions of the contour
- symmetry: symmetry of the tumor
- fractal dimension: "coastline approximation" - 1

Variable selection

There exists multicollinearity within the dataset (**Fig. 1A**), which will casue the correlation matrix to be singular and irreversible. Although the best practice to select variables is according to background information, in our context, we have three random variables, the mean estimate, variance estimate, and extreme value estimate one single background covariate. So we proposed a method to reduce this multicollinearity based on both correlation coefficient and eigenvalue of correlation matrix, that is, the column with high correlation with other columns (e.g., larger than 0.7) and low eigenvalue (e.g., less than 0.01) will be deleted.

There were 18 variables left as final input predictors, **Fig. 1B** shows the correlation matrix after deletion. As the darker color stands for high correlation, we can see that after variable selection, there is less collinearity between variables.

Figure 1: multicollinearity plot of the dataset



Method

Logistic Regression

Let y be the vector of n response random variable, X denote the $n \times p$ design matrix (X_i denote the ith row) and β denote the $p \times 1$ coefficient. Let $\eta = E(y) = X\beta$ and given the link function as $g(\eta) = \log \frac{\eta}{1-\eta}$, we have the logistic regression model written as:

$$\log(\frac{\eta}{1-\eta}) = X\beta$$

The likelihood of this logistic regression is:

$$L(\beta; X, y) = \prod_{i=1}^{n} \{(\frac{\exp(X_i\beta)}{1+\exp(X_i\beta)})^{y_i} (\frac{1}{1+\exp(X_i\beta)})^{1-y_i}\}$$

Maximizing the likelihood is equivalent to maximizing the log likelihood:

$$l(\beta) = \sum_{i=1}^{n} \{y_i(X_i\beta) - \log(1+\exp(X_i\beta))\}$$

Let p, a vector of n denote $p = \frac{\exp(X\beta)}{1+\exp(X\beta)}$. The gradient of this function is:

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

and the Hessian is given by:

$$\nabla^2 l(\beta) = -X^T W X$$

where $W = diag(p_i(1-p_i)), i = 1, \cdots, n$. Hessian matrix is negative definite and is well behaved.

Newton-Raphson Algorithm

We wanted to search for solutions to the system of equations $\nabla l(\beta) = 0$.

At each step, given the current point β_i, the gradient $\nabla l(\beta)$ for β near β_i may be approximated according to taylor expansion by $\nabla l(\beta_i) + \nabla^2 l(\beta_i)(\beta - \beta_i)$ which defines the plane tangent to $\nabla l(\beta)$ at β_i. The next step in the algorithm is determined by solving the system of the above linear equations, which gives

$$\beta_{i+1} = \beta_i - [\nabla^2 l(\beta_i)]^{-1} \nabla l(\beta_i)$$

Since the hessian is negative definite, the direction of each step is correct, we wanted to optimize the size of each step. We applied step-halving method and the next "current point" is set to be the solution

$$\beta_{i+1}(\gamma) = \beta_i - \gamma[\nabla^2 l(\beta_i)]^{-1} \nabla l(\beta_i)$$

Then compute the full Newton-Raphson step, corresponding to $\gamma = 1$. If $f(\theta_{i+1}(1)) \geq f(\theta_i)$, then set $\theta_{i+1} = \theta_{i+1}(1)$ and go on to the next iteration. Otherwise, search for a value $\gamma \in (0, 1)$ for which $f(\theta_{i+1}(\gamma)) \geq f(\theta_i)$, set $\theta_{i+1} = \theta_{i+1}(\gamma)$ and go on to the next iteration. The algorithm continues like this iteratively choosing a sequence of points $\beta_0, \beta_1, ..., \beta_i, ...$ until convergence is achieved.

For Newton's method with a large p, the computational burden in calculating the inverse of the Hessian Matrix $[\nabla^2 f(\beta_i)]^{-1}$ increases quickly with p. One can update

$$\beta_{i+1} = \beta_i + H_i \nabla f(\beta_i)$$

where $H_i = (X^T X)^{-1}$ for every i. This is easy to compute, but could be slow in convergence. And this is called Gradient Decent algorithm.

The steps are:

- get the objective (loglik,grad,Hess) function;
- use the principle of newton raphson to update the estimate, if the step size too large, step-halving step
- stop searching until the convergences of the estimates.

Pathwise Coordinate Descent with regularized logistic regression

Regularization is the common variable selection approaches for high-dimensional covariates. The best known Regularization is called LASSO, which is to add $L1$-penalty to the objective function. First we consider a linear regression, with penalty term, we are aiming to solve the following problem:

$$\min_{\beta \in \mathbb{R}^{p+1}} \{\frac{1}{2n} \sum_{i=1}^{n} (z_i - \sum_{j=0}^{p} x_{i,j}\beta_j)^2 + \lambda P(\beta))\}$$

When p, the number of predictors is large, the optimization could be challenging, so we could use coordinate-wise descent update with objective function

$$f(\beta_j) = \frac{1}{2n} \sum_{i=1}^{n} (y_i - \sum_{k \neq j} x_{i,k}\tilde{\beta_k} - x_{i,j}\beta_j)^2 + \lambda \sum_{k \neq j} |\tilde{\beta_k}| + \lambda |\beta_j|$$

Minimize $f(\beta_j)$ w.r.t. β_j while having $\tilde{\beta_k}$ fixed, we have

$$\tilde{\beta}_j^{lasso}(\lambda) \leftarrow S(\frac{1}{n} \sum_{i=1}^{n} x_{i,j}(y_i - \tilde{y_i}^{(-j)}), \lambda)$$

where $\tilde{y_i}^{(-j)} = \sum_{k \neq j} x_{i,k}\tilde{\beta_k}$ and $S(\hat{\beta}, \lambda) = sign(\hat{\beta})(|\hat{\beta}| - \lambda)_+$.

If a weight ω_i is then associated with each observation. In this case the update becomes only slightly more complicated:

$$\tilde{\beta}_j^{lasso}(\lambda) \leftarrow \frac{S(\sum_{i=1}^n \omega_i x_{i,j}(y_i - \tilde{y_i}^{(-j)}), \lambda)}{\sum_{i=1}^n \omega_i x_{i,j}^2}$$

In the context of logistic regression, we are aiming to maximize the penalized log likelihood:

$$\max_{\beta \in \mathbb{R}^{p+1}} \frac{1}{n} \sum_{i=1}^n \{y_i(X_i\beta) - \log(1 + \exp(X_i\beta))\} - \lambda \sum_{j=1}^p |\beta_j|$$

for some $\lambda \geq 0$. Here the $x_{i,j}$ are standardized so that $\sum_i x_{i,j}/n = 0$ and $\sum_i x_{i,j}^2/n = 0$.

The Newton algorithm for maximizing the log likelihood amounts to interatively reweighted least squares. Hence if the current estimate of the parameter is $\tilde{\beta}$, we can form a quardratic approximation to the negative log likelihood by taylor expansion around the current estimate, which is:

$$f(\beta) = -\frac{1}{2n} \sum_{i=1}^n w_i(z_i - \sum_{j=0}^p x_{i,j}\beta_j)^2 + C(\tilde{\beta})$$

where

$$z_i = \tilde{\beta}_0 + x_i^T\tilde{\beta} + \frac{y_i - \tilde{p}(x_i)}{\tilde{p}(x_i)(1 - \tilde{p}(x_i))}, \text{working response}$$
$$w_i = \tilde{p}(x_i)(1 - \tilde{p}(x_i)), \text{working weights}$$

and $\tilde{p}(x_i)$ is evaluated at the current parameters, the last term is constant. The Newton update is obtained by minimizing the $f(\beta)$

The coordinate descent algorithm to solve the penalized weighted least squares problem

$$\min_{\beta \in \mathbb{R}^{p+1}} \{-f(\beta) + \lambda P(\beta)\}$$

The above amounts to a sequence of nested loops:

- outer loop: start with λ that all the coefficients are forced to be zerp, then decrement λ;
- middle loop: update the quardratic $f(\beta)$ using the current estimates of parameters;
- inner loop: run the coordinate descent algorithm on the penalized weighted least square problem.

In our problem, care is taken to avoid coefficients diverging in order to achieve fitted probabilities of 0 or 1 which is the warning message by the R package. When a probability with $\epsilon = 1e - 5$ of 1, we set it to 1, and set the weights to ϵ. 0 is treated similarly.

Results

Estimation path for Lasso

Fig. 2 shows us that as the λ increases, all the variable estimates of parameters shrink accordingly since we penalize all the parameters, though in some. When $\lambda = 0$, the result is the same as least square method and when λ is too large, all the estimates of parameters shrink to 0.

Figure 2: A path of solutions with a sequence of descending lambda's

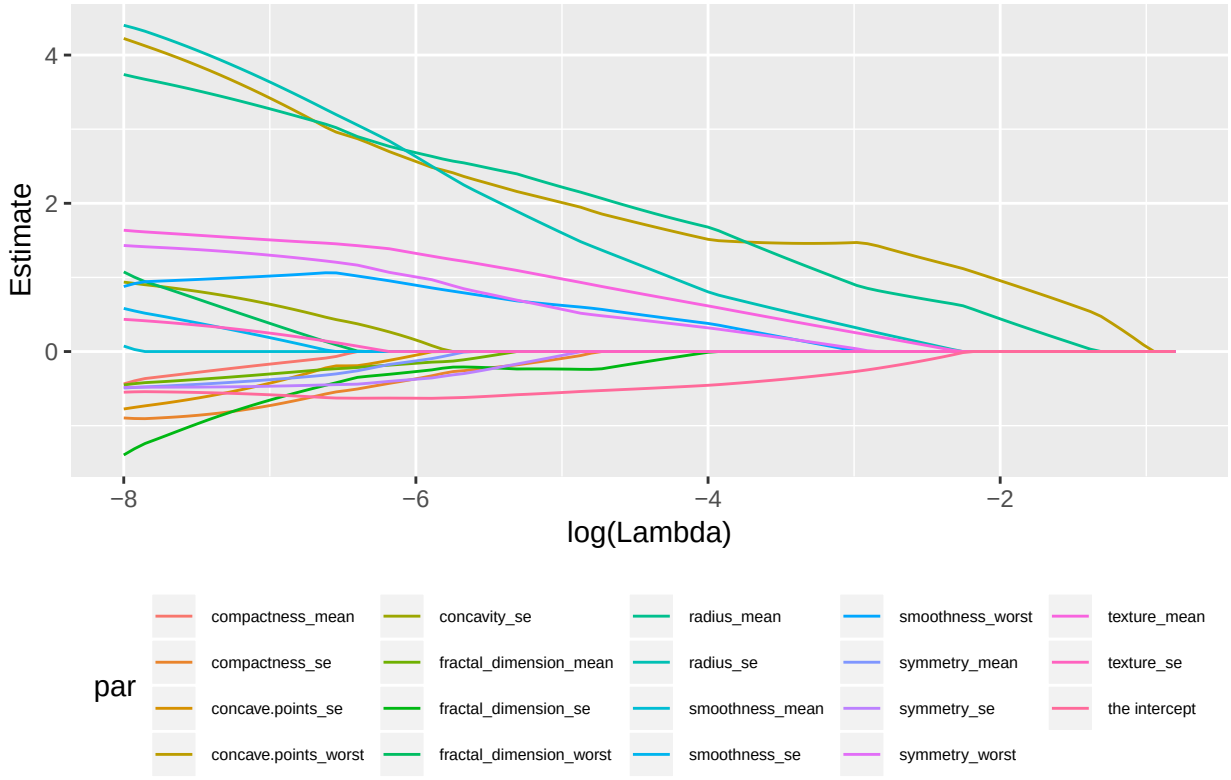
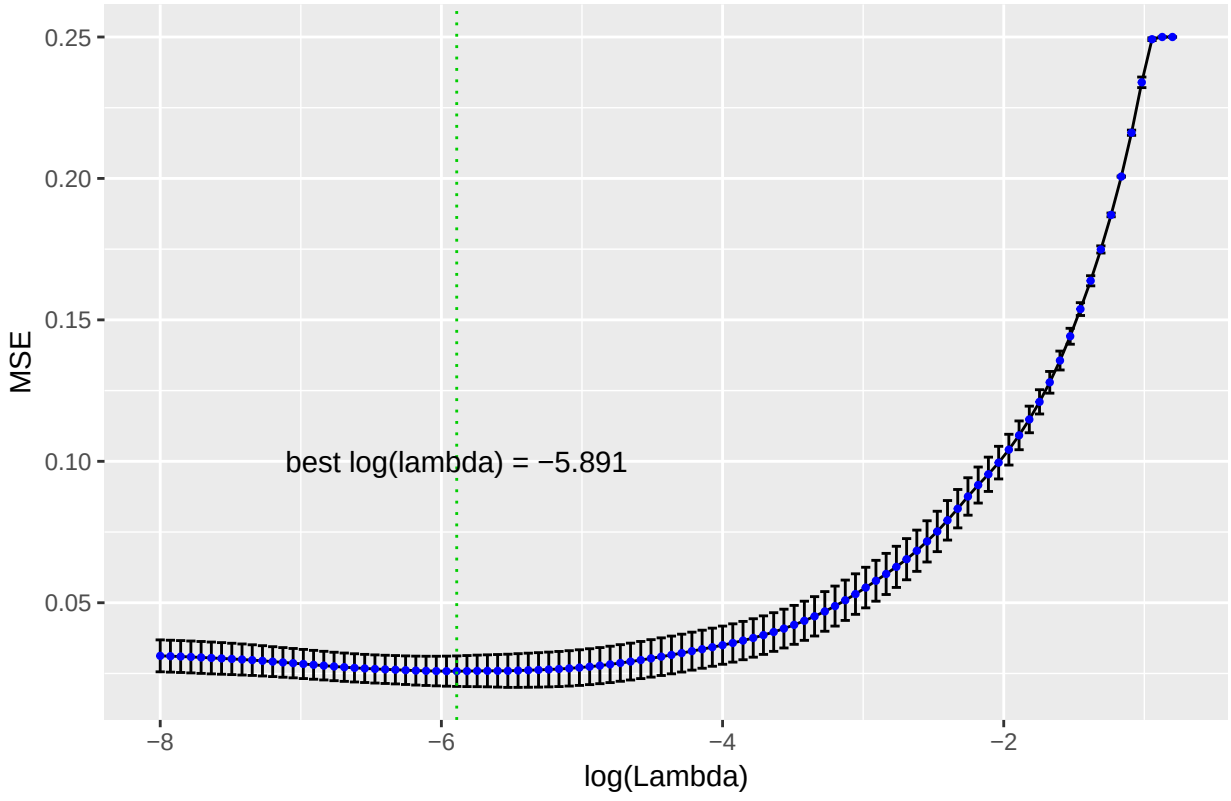


Figure 3: Lasso regression by 5 fold cross validation



Cross validation for lasso

We used 5-fold cross-validation to choose the best λ such that the objective function with penalty term can achieve its extreme value. We calculate the mean squared error (MSE) and its $\pm 1\sigma$ interval as the output. **Fig. 3** shows us the trajectory that as the penalty term gets larger, the penalized likelihood achieves its minimum and then increase gradually. the λ with the lowest MSE is 0.0028.

Model comparison

We finally compared these methods: Classic Logistic Regression (GLM package), Newton-Raphson Algorithm, Gradient Decent and Pathwise Coordinate descent penalized Logistic regression. **Table 1** shows the MSE and the iteration times they need to converge. All three algorithms were valid with MSE approximately equal to 0.02. Newton Raphson method needs the lowest iteration times while Gradient Decent method needs more than 1000 times to converge. **Table 2** shows the final parameter estimation calculated by these methods compared to the results from built in R package, which can help prove the validity of our algorithm. The Gradient Decent result is similar to Newton Raphson. With the best λ, Lasso results in turning 6 parameters to 0. The difference between the estimates of our algorithm and built-in package may come from the fact that we include intercept into penalty term while the built-in one doesn't.

Table 1: The comparison of performance for estimation algorithms and models

	GLM package	Newton Raphson	Gradient Decent	Lasso package	Logistic Lasso
iteration times	NA	12	1001	100	NA
MSE	0.02	0.02	0.02	0.02	0.02

[a] Dataset: Breast Cancer Diagnosis

Table 2: The comparison of performance for estimation algorithms and models

	GLM package	Newton Raphson	Gradient Decent	Lasso package	Logistic Lasso
radius_mean	4.43	4.43	3.18	2.71	2.63
texture_mean	1.89	1.89	1.34	1.37	1.29
smoothness_mean	0.78	0.78	0.47	0.00	0.00
compactness_mean	-1.14	-1.14	-0.59	0.00	0.00
symmetry_mean	-0.63	-0.63	-0.44	-0.14	-0.10
fractal_dimension_mean	-0.66	-0.66	-0.72	-0.21	-0.14
radius_se	5.13	5.13	3.28	2.58	2.50
texture_se	0.59	0.59	0.46	0.00	0.00
smoothness_se	1.10	1.10	0.77	0.00	0.00
compactness_se	-0.80	-0.80	-0.68	-0.38	-0.33
concavity_se	1.24	1.24	0.88	0.19	0.08
concave.points_se	-1.11	-1.11	-0.80	0.00	0.00
symmetry_se	-0.53	-0.53	-0.39	-0.42	-0.36
fractal_dimension_se	-2.73	-2.73	-1.55	-0.31	-0.25
smoothness_worst	0.31	0.31	0.31	0.92	0.86
concave.points_worst	5.13	5.13	3.65	2.62	2.48
symmetry_worst	1.60	1.60	1.28	1.06	0.97
fractal_dimension_worst	2.19	2.19	1.41	0.00	0.00
intercept	-0.62	-0.62	-0.71	-0.77	-0.63

[a] Dataset: Breast Cancer Diagnosis

Conclusions

In this study, we used Newton-Raphson algorithm, Gradient Decent and Pathwise Coordinate descent to build three different predictive models for the breast cancer dataset. The variable selection was based on the correlation coefficient and eigenvalue of correlation matrix to remove the multicollinearity within the dataset. The results of our methods are compared to the the same parameter estimation as R's built-in packages. Newton-Raphson has the convincing estimation and it converged quickly. Gradient decent method showed similar estimation as Newton-Raphson method but it was less efficient. For Pathwise Coordinate descent with LASSO logistic, according to the result of 5 fold cross validation and estimation result, the lambda with the lowest MSE was 0.00276 and it shrunk 6 parameters to 0, which is comparable to the result by R's built-in packages.

References

1 Friedman, Jerome, Trevor Hastie, and Rob Tibshirani. "Regularization paths for generalized linear models via coordinate descent." Journal of statistical software 33.1 (2010): 1.

2 Friedman, Jerome, et al. "Pathwise coordinate optimization." The annals of applied statistics 1.2 (2007): 302-332.

Appendix A

```
knitr::opts_chunk$set(echo = FALSE, message = FALSE, warning = FALSE, comment = "")
library(tidyverse)
library(Hmisc)#for errvar
library(ggcorrplot) # for correlation heatmap
library(ggpubr) # common legend
library(matrixcalc) #is.negative.def
library(kableExtra) # table
library(glmnet) # lasso
set.seed(99999)
options(knitr.table.format = "latex")
###### data manipulation
mydata <- read.csv("breast-cancer-1.csv")
n <- dim(mydata)[1]
p <- dim(mydata)[2]
list <- c(3:(p - 1))
namesX <- names(mydata)[-c(1,2,p)]
# standardize
dataX <- do.call(cbind, lapply(list, function(x) (mydata[,x] - mean(mydata[,x]))/sd(mydata[,x])))
# design matrix
X <- data.frame(dataX) %>%
  mutate(., intercept = 1)
# response
resp <- as.vector(ifelse(mydata[,2] == "M", 1, 0))
###### plot to check collinearity
colnames(dataX) <- namesX
colinearity.plot <- function(data){
  data.frame(data) %>%
  select(starts_with("radius"),
         starts_with("texture"),
         starts_with("perimeter"),
```

```
         starts_with("area"),
         starts_with("smooth"),
         starts_with("compact"),
         starts_with("concavity"),
         starts_with("concave"),
         starts_with("symmetry"),
         starts_with("fractal")) %>%
  cor() %>%
  ggcorrplot(.,ggtheme = ggplot2::theme_gray,
             colors = c("#6D9EC1", "white", "#E46726"),
             tl.cex = 6)}
g1 <- colinearity.plot(dataX)

###### variable selection
eig <- eigen(cor(dataX))$values
# found values very close to 0, multicolinearity exists
# function: find the maximum correlation between i and j, at least 0.5
max.corr <- function(data){
  len = dim(data)[2]
  a <- 0.5
  for (i in 1:(len-1)) {
    for (j in (i+1):len) {
      if (abs(cor(data[,i],data[,j])) > a) a <- cor(data[,i],data[,j])
    }
  }
  return(round(a,3))
}
# function: update dataset according to several rules: eigenvalues and corr
selection <- function(data, eigen.tol, corr.tol) {
  while (min(eigen(cor(data))$values) <= eigen.tol & max.corr(data) >= corr.tol) {
       temp <- data
       data <- temp[,-(which(round(abs(cor(temp)),3) == max.corr(temp), arr.ind = TRUE)[1,1])]
      }
  return(data)}
newdataX <- selection(dataX, eigen.tol = 2e-2, corr.tol = 0.7)
g2 <- colinearity.plot(newdataX)
eigpost <- eigen(cor(newdataX))$values
# look at the difference of the deleted colums
delnames <- setdiff(colnames(dataX),colnames(newdataX))
ggarrange(g1,g2, ncol=2, nrow=1, common.legend = TRUE, legend = "bottom", labels = "AUTO")
###### 0.logistic regression
# logfit.0 <- glm(resp~dataX, family = binomial(link = "logit"))
# algorithm didn't converge without delete colinearity
logdata <- cbind.data.frame(resp,newdataX)
logfit.1 <- glm(resp~., family = binomial(link = "logit"),data = logdata)
logit.beta <- coef(logfit.1)
##### 1. classical newton raphson
newX <- data.frame(newdataX) %>%
  mutate(., intercept = 1)
newdat <- list(y = resp, X = as.matrix(newX))
# function: calcualte loglik, gradient, hessian
logisticstuff <- function(dat, betavec){
  u <- dat$X %*% betavec
```

```
  expu <- exp(u)
  loglik <- t(u) %*% dat$y - sum((log(1 + expu)))
  prob <- expu / (1 + expu)
  grad <- t(dat$X) %*% (dat$y - prob)
  Hess <- -t(dat$X) %*% diag(as.vector(prob*(1 - prob))) %*% dat$X
  return(list(loglik = loglik, grad = grad, Hess = Hess))}

NewtonRaphson <- function(dat, func, start, tol=1e-10, maxiter =200){
  i <- 0
  cur <- start
  stuff <- func(dat, cur)
  res <- c(0, stuff$loglik, cur)
  prevloglik <- -Inf
  while (i < maxiter && abs(stuff$loglik - prevloglik) > tol && stuff$loglik > -Inf) {
    i <- i + 1
    prevloglik <- stuff$loglik
    prev <- cur
    lambda = 0
    cur <- prev - ((1/(2^lambda)) * solve(stuff$Hess)) %*% stuff$grad
    while (func(dat, cur)$loglik < prevloglik){ # step-halving
      lambda = lambda + 1
      cur <- prev - ((1/(2^lambda)) * solve(stuff$Hess)) %*% stuff$grad
    }
    stuff <- func(dat, cur)
    res <- rbind(res, c(i, stuff$loglik, cur))}

  return(res)
}
newres <- NewtonRaphson(newdat,logisticstuff, start = rep(0, dim(newdat$X)[2]))
# check convergence
check <- tail(newres)[,1:2]
newton.beta <- newres[nrow(newres),3:dim(newres)[2]]
##### 2. gradient descent
gradient <- function(dat, func, start, tol=1e-10, maxiter = 200){
  i <- 0
  cur <- start
  pp <- length(start)
  stuff <- func(dat, cur)
  hessinversed <- solve(t(dat$X) %*% (dat$X))
  res <- c(0, stuff$loglik, cur)
  prevloglik <- -Inf
  while (i < maxiter && abs(stuff$loglik - prevloglik) > tol && stuff$loglik > -Inf) {
    i <- i + 1
    prevloglik <- stuff$loglik
    prev <- cur
    cur <- prev + hessinversed %*% (stuff$grad)
    stuff <- func(dat, cur)
    res <- rbind(res, c(i, stuff$loglik, cur))}
  return(res)
}
gradres <- gradient(newdat, logisticstuff, start = rep(0, dim(newdat$X)[2]), maxiter = 1000)
# check convergence
check <- tail(gradres)[,1:2]
```

```r
grad.beta <- gradres[nrow(gradres),3:dim(gradres)[2]]
##### 3. coordinate-wise logistic lasso
sfun <- function(beta,lambda) sign(beta) * max(abs(beta)-lambda, 0)
coordinatelasso <- function(lambda, dat, s, tol=1e-10, maxiter = 200){
  i <- 0
  pp <- length(s)
  n <- length(dat$y)
  betavec <- s
  loglik <- 1e6
  res <- c(0, loglik, betavec)
  prevloglik <- Inf # To make sure it iterates
  while (i < maxiter && abs(loglik - prevloglik) > tol && loglik < Inf) {
    i <- i + 1
    prevloglik <- loglik
    for (j in 1:pp) {
      u <- dat$X %*% betavec
      expu <- exp(u)
      prob <- expu/(expu+1)
      w <- prob*(1-prob) # weighted
      # avoid coeffcients diverging in order to achieve fitted  probabilities of 0 or 1.
      w <- ifelse(abs(w-0) < 1e-5, 1e-5, w)
      z <- u + (dat$y-prob)/w
      # calculate noj
      znoj <- dat$X[,-j] %*% betavec[-j]
      # revise the formula to be z
      betavec[j] <- sfun(mean(w*(dat$X[,j])*(z - znoj)), lambda)/(mean(w*dat$X[,j]*dat$X[,j]))
    }
    loglik <- sum(w*(z-dat$X %*% betavec)^2)/(2*n) + lambda * sum(abs(betavec))
    res <- rbind(res, c(i, loglik, betavec))}
  return(res)
}
corres <- coordinatelasso(lambda = exp(-8e-1), newdat, s = rep(0, dim(newdat$X)[2]) ,maxiter = 2000)
check <- tail(corres)[,1:2]
cor.beta <- corres[nrow(corres),3:dim(corres)[2]]
# logmod <- glmnet(newdat$X[,-dim(newdat$X)[2]], y=newdat$y, alpha=1, family="binomial",lambda=1e-2)
# check: coef.glmnet(logmod)
logmod <- cv.glmnet(newdat$X[,-dim(newdat$X)[2]], y=newdat$y, alpha=1, family="binomial",type.measure="
# check: plot(logmod)
# check: logmod$lambda.min
# impletement the pathwise coordinatewise optimization algorithm to obtain a path of solutions
path <- function(inputx,inputy,grid){
  start <- rep(0, dim(inputx)[2])
  betas <- NULL
  for (x in 1:100) {
  cv.errors <- vector()
    cor.result <- coordinatelasso(lambda = grid[x],
                                  dat = list(X=as.matrix(inputx),y=inputy),
                                  s= start)
    lasbeta <- cor.result[nrow(cor.result),3:dim(cor.result)[2]]
    start <- lasbeta
    betas <- rbind(betas,c(lasbeta))
  }
  return(data.frame(cbind(grid,betas)))
```

```
}
path.out <- path(newX,resp,grid=exp(seq(-8e-1,-8, length=100)))
colnames(path.out) <- c("grid",colnames(newdataX),"the intercept")
# plot a path of solutions
path.plot <- path.out %>%
  gather(key = par, value = estimate, c(2:dim(path.out)[2])) %>%
  ggplot(aes(x = log(grid), y = estimate, group = par, col = par)) +
  geom_line()+
  ggtitle("Figure 2: A path of solutions with a sequence of descending lambda's") +
  xlab("log(Lambda)") +
  ylab("Estimate") +
  theme(legend.position = "bottom",
        legend.text = element_text(size = 6))
path.plot


##### 5-fold cross-validation and pathwise coordinatewise optimization algorithm
# when lambda = 0.5, all the betas go to 0
cvresult <- function(inputx,inputy,grid,K){
  n <- dim(inputx)[1]
  folds <- sample(1:K, n, replace=TRUE)
  start <- rep(0, dim(inputx)[2])
  cv.error <- vector()
  cv.se <- vector()
  for (x in 1:length(grid)) {
  cv.errors <- vector()
  for (i in 1:K){
    cor.result <- coordinatelasso(lambda = grid[x],
                                  dat = list(X=as.matrix(inputx[folds!=i,]),y=inputy[folds!=i]),
                                  s = start)
    lasbeta <- cor.result[nrow(cor.result),3:dim(cor.result)[2]]
    u <- as.matrix(inputx[folds == i,]) %*% lasbeta
    expu <- exp(u)
    prob <- expu / (1 + expu)
    y <- as.vector(inputy[folds==i])
    cv.errors[i] = mean((y-prob)^2) #MSE
    start <- lasbeta
  }
  cv.error[x] <- mean(cv.errors)
  cv.se[x] <- sqrt(var(cv.errors)/K)
  }
  return(cbind(grid,cv.error,cv.se))
}

result <- cvresult(newX,resp,grid=exp(seq(-8e-1,-8, length=100)),K=5)
# result <- cvresult(X,resp,grid=seq(0.5, 1e-2, length=100),K=5)
best.lambda <- result[which.min(result[,2]),1]
# need rewrite
finlasso <- as.matrix(path(newX,resp,grid=exp(seq(-8e-1,log(best.lambda), length=100))))
lasso.beta <- finlasso[nrow(finlasso),2:dim(finlasso)[2]]

# plot for cross validation
result <- data.frame(result)
```

```
cv.plot <-
    ggplot(result, aes(x=log(result$grid), y=result$cv.error)) +
    geom_errorbar(aes(ymin=result$cv.error-result$cv.se, ymax=result$cv.error+result$cv.se),
                  colour=1) +
    geom_line() +
    geom_point(size=0.8,colour = 4) +
    ggtitle("Figure 3: Lasso regression by 5 fold cross validation")+
    xlab("log(Lambda)") + ylab("MSE") +
    geom_vline(xintercept = log(best.lambda),col=3,lty=3) +
    annotate("text", log(best.lambda), 0.1, label = paste("best log(lambda) = ", round(log(best.lambda)
cv.plot
######## compare prediction performance of all results
pred.fun <- function(outcome,input, beta){
    u <- as.matrix(input) %*% beta
    expu <- exp(u)
    prob <- expu / (1 + expu)
    pred.error = mean((as.vector(outcome)-prob)^2)
    return(pred.error)
}

# logistic regression by GLM
log.beta <- c(logit.beta[2:length(logit.beta)],logit.beta[1])
pred <- predict(logfit.1)
log.pred <- mean((resp-exp(pred)/(1+exp(pred)))^2) # abs(mean(logfit.1$residuals))
# newton's method
newton.ite <- nrow(newres)
newton.beta <- newres[nrow(newres),3:dim(newres)[2]]
newton.pred <- pred.fun(resp,newX,newton.beta)
# gradient decent
grad.ite <- nrow(gradres)
grad.beta <- gradres[nrow(gradres),3:dim(gradres)[2]]
grad.pred <- pred.fun(resp,newX,grad.beta)
logmod.cv <- cv.glmnet(newdat$X[,-dim(newdat$X)[2]], y=newdat$y, alpha=1, family="binomial")
best.lambda.func <- logmod$lambda.min
logmod <- glmnet(newdat$X[,-dim(newdat$X)[2]], y=newdat$y, alpha=1, family="binomial",lambda = best.lam
glmnet.beta <- c(coef.glmnet(logmod)[2:length(coef.glmnet(logmod))],coef.glmnet(logmod)[1])
glmnet.pred <- predict(logmod,newdataX,type="response", lambda = best.lambda.func)
glmnet.pred <- mean((resp-glmnet.pred)^2)
# lasso logistic
lasso.ite <- nrow(finlasso)
lasso.beta <- lasso.beta
lasso.pred <-  pred.fun(resp,newX,lasso.beta)

beta.res <- round(as.matrix(rbind(log.beta,newton.beta,grad.beta,glmnet.beta,lasso.beta)),2)
colnames(beta.res) <- colnames(newX)
rownames(beta.res) <- c("GLM package","Newton Raphson","Gradient Decent","Lasso package","Logistic Lass
perf.res <- matrix(rep(NA),ncol = 2, nrow = 5)
colnames(perf.res) <- c("iteration times","MSE")
rownames(perf.res) <- c("GLM package","Newton Raphson","Gradient Decent","Lasso package","Logistic Lass
perf.res[1,1] <- "NA"
perf.res[1,2] <- round(log.pred ,2)
perf.res[2,1] <- newton.ite
perf.res[2,2] <- round(newton.pred,2)
```

```
perf.res[3,1] <- grad.ite
perf.res[3,2] <- round(grad.pred,2)
perf.res[4,1] <- lasso.ite
perf.res[4,2] <- round(lasso.pred,2)
perf.res[5,1] <- "NA"
perf.res[5,2] <- round(glmnet.pred,2)

# output-performace
kable(t(perf.res), "latex", caption = "The comparison of performance for estimation algorithms and model
  kable_styling(latex_options = c("hold_position", "scale_down")) %>%
  add_footnote(c("Dataset: Breast Cancer Diagnosis"),
               notation = "alphabet")
# output-beta
kable(t(beta.res), "latex", caption = "The comparison of performance for estimation algorithms and model
  kable_styling(latex_options = c("hold_position", "scale_down")) %>%
  add_footnote(c("Dataset: Breast Cancer Diagnosis"),
               notation = "alphabet")
```