Untitled

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Data import

This dataset has 569 rows and 32 columns. The outcome variable of interst is Diagnosis which takes on values benign or malignant cases. There are 357 benign cases and 212 malignant cases as seen below in Table 1. One variable is id and the rest 30 variables are the mean, sd and largest values of the following criteria.

- 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 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)

Using this dataset models will be compared and compared on their ability to predict cancer diagnosis.

Characteristic	**Benign**, N = 357	**Malignant**, N = 212	**p-value**
radius_mean	12.147 (1.781)	17.463 (3.204)	< 0.001
texture_mean	17.915 (3.995)	21.605 (3.779)	< 0.001
perimeter_mean	78.075 (11.807)	115.365 (21.855)	< 0.001
area_mean	462.790 (134.287)	978.376 (367.938)	< 0.001
smoothness_mean	0.092 (0.013)	0.103 (0.013)	< 0.001
compactness_mean	0.080 (0.034)	0.145 (0.054)	< 0.001
concavity_mean	0.046 (0.043)	0.161 (0.075)	< 0.001
concave.points_mean	0.026 (0.016)	0.088 (0.034)	< 0.001
symmetry_mean	0.174 (0.025)	0.193 (0.028)	< 0.001
fractal_dimension_mean	0.063 (0.007)	0.063 (0.008)	0.5
radius_se	0.284 (0.113)	0.609 (0.345)	< 0.001
texture_se	1.220 (0.589)	1.211 (0.483)	0.6
perimeter_se	2.000 (0.771)	4.324 (2.569)	< 0.001
area_se	21.135 (8.843)	72.672 (61.355)	< 0.001
smoothness_se	0.007 (0.003)	0.007 (0.003)	0.2
compactness_se	0.021 (0.016)	0.032 (0.018)	< 0.001
concavity_se	0.026 (0.033)	0.042 (0.022)	< 0.001
concave.points_se	0.010 (0.006)	0.015 (0.006)	< 0.001
symmetry_se	0.021 (0.007)	0.020 (0.010)	0.028
fractal_dimension_se	0.004 (0.003)	0.004 (0.002)	< 0.001
radius_worst	13.380 (1.981)	21.135 (4.284)	< 0.001
texture_worst	23.515 (5.494)	29.318 (5.435)	< 0.001
perimeter_worst	87.006 (13.527)	141.370 (29.457)	< 0.001
area_worst	558.899 (163.601)	1,422.286 (597.968)	< 0.001
smoothness_worst	0.125 (0.020)	0.145 (0.022)	< 0.001
compactness_worst	0.183 (0.092)	0.375 (0.170)	< 0.001
concavity_worst	0.166 (0.140)	0.451 (0.182)	< 0.001
concave.points_worst	0.074 (0.036)	0.182 (0.046)	< 0.001
symmetry_worst	0.270 (0.042)	0.323 (0.075)	< 0.001
fractal_dimension_worst	0.079 (0.014)	0.092 (0.022)	< 0.001

Build a logistic model to classify the images into malignant/benign

Before building the model we need to first write down the likelihood function, its gradient and Hessian matrix. The likelihood function for our data which has a single binary response and 30 numerical explanatory variables is

$$\pi_i = P(Y_i = 1 | x_{i,1}, \dots x_{i,30}) = \frac{e^{\beta_0 + \beta_1 x_{i,1} + \dots \beta_{30} x_{i,30}}}{1 + e^{\beta_0 + \beta_1 x_{i,1} + \dots \beta_{30} x_{i,30}}} = \frac{e^{\beta_0 + \sum_{j=1}^{30} \beta_i x_{i,j}}}{1 + e^{\beta_0 + \sum_{j=1}^{30} \beta_i x_{i,j}}}$$

Where X_i represents the *i* observation of all 30 of our predictor variables. For the data give we have the likelihood is given by

$$L(\mathbf{X}|\beta) = \prod_{i=1}^{n} \left[\pi_i^{y_i} (1 - \pi_i)^{1 - y_i} \right]$$

Finding the log-likelihood we have

$$l(\mathbf{X}|\vec{\beta}) = \sum_{i=1}^{n} \left[y_i \left(\beta_0 + \sum_{j=1}^{30} \beta_i x_{i,j} \right) - \log \left(1 + \exp \left(\beta_0 + \sum_{j=1}^{30} \beta_i x_{i,j} \right) \right) \right]$$

The gradient can then can be solved for. Observe

$$\nabla l(\mathbf{X}|\vec{\beta}) = \left[\sum_{i=1}^{n} y_i - \pi_i \quad \sum_{i=1}^{n} x_{i,1} (y_i - \pi) \quad \dots \quad \sum_{i=1}^{n} x_{i,30} (y_i - \pi) \right]_{(1 \times 31)}^{T}$$

Finally, with the gradient we can derive our hessian. Note that due to the 30 predictor variables the hessian will be a 31 by 31 matrix.

$$\nabla^2 l(\mathbf{X}|\vec{\beta}) = -\sum_{i=1}^n \begin{pmatrix} 1 \\ X \end{pmatrix} (1 \quad X) \, \pi_i (1 - \pi_i)$$
$$= - \begin{pmatrix} 1 & X \end{pmatrix} diag(\pi_i (1 - \pi_i)) \begin{pmatrix} 1 \\ X \end{pmatrix}$$

Where $X = (x_{i,1}, \dots, x_{i,30})$. Note that this matrix will always be negative definite at all parameters making the this a well behaved problem.

Develop a Newton-Raphson algorithm to estimate your model

Modifications:

- I include half stepping in the Newton-Raphson method.
- Assent direction

Data Preprocess

```
set.seed(7777)
dat <- bc %>% select(-id) %>%
    rename(y = diagnosis) %>%
    mutate(y = ifelse(y=="B", 0, 1))

#split <- initial_split(dat, prop = 0.8)

training_df <- dat # split %>% training()

#testing_df <- split %>% testing()

#training_df <- training_df[c(1:455),]</pre>
```

Functions

```
loglike_func <- function(dat, betavec){
    # setting up an intercept
    dat_temp = dat %>%
        rename(intercept = y) %>%
        mutate(intercept = rep(1, nrow(dat)))
    dat_x = unname(as.matrix(dat_temp)) # creating the x matrix

# finding the pi values
    u = dat_x %*% betavec
    pi <- exp(u) / (1+exp(u))

# loglikelihood
    loglik <- sum(dat$y*u - log(1 + exp(u)))</pre>
```

```
#qradient
  grad \leftarrow t(dat_x)%*%(dat$y - pi)
  # Hessian
  W = matrix(0, nrow = dim(dat)[1], ncol = dim(dat)[1])
  diag(W) = pi*(1-pi)
 hess = -t(dat_x)%*% W %*% (dat_x)
 return(list(loglik = loglik, grad = grad, hess = hess))
#loglike_func(dat, betavec = c( rep(0.03, 31))) # test!
NewtonRaphson <- function(dat, start, tol = 1e-8, maxiter = 200){
  i = 0
  cur = start
  stuff = loglike_func(dat, cur)
  res <- c(i=0, "loglik" = stuff$loglik, "step" = 1, cur)</pre>
  prevloglik <- -Inf # To make sure it iterates</pre>
  while(i < maxiter && abs(stuff$loglik - prevloglik) > tol) {
    step = 1
    i <- i + 1
    prevloglik <- stuff$loglik</pre>
    # checking negative definite
    eigen_vals = eigen(stuff$hess)
    if(max(eigen_vals$values) <= 0 ){ # check neg def, if not change</pre>
      hess = stuff$hess
    } else{ # if it is pos def then need to adjust
      hess = stuff$hess - (max(eigen_vals$values) + 0.1)*diag(nrow(stuff$hess))
    }
    prev <- cur
    cur <- prev - rep(step, length(prev))*(solve(stuff$hess) %*% stuff$grad)</pre>
    stuff <- loglike_func(dat, cur) # log-lik, gradient, Hessian</pre>
    # doing half stepping
    while(stuff$loglik < prevloglik){</pre>
      stuff <- loglike_func(dat, prev)</pre>
      step <- step / 2 # this is where half steping happens
           <- prev - step*(solve(stuff$hess) %*% stuff$grad)</pre>
      stuff <- loglike_func(dat, cur)</pre>
    }
    # Add current values to results matrix
    res <- rbind(res, c(i, stuff$loglik, step, cur))</pre>
  colnames(res) <- c("i", "loglik", "step", "intercept", names(dat[,-1]))</pre>
  return(res)
#Running the algorithm with random starting values
```

```
betavec = c(rep(0.01, 31))
ans <- NewtonRaphson(training_df, betavec)</pre>
```

Results:

```
##
       i
                 step
                           loglik
## 1
       0 1.000000e+00 -4572.62022
## 2
       1 3.814697e-06 -4305.72478
       2 3.125000e-02 -4106.78557
## 4
       3 2.441406e-04 -1765.78820
## 5
       4 3.125000e-02 -1500.82384
## 6
       5 1.250000e-01 -570.56646
## 7
       6 2.500000e-01
                      -186.64985
## 8
       7 1.000000e+00
                        -95.43908
## 9
       8 1.000000e+00
                        -58.73991
## 10 9 1.000000e+00
                        -39.93848
                        -29.51427
## 11 10 1.000000e+00
## 12 11 1.000000e+00
                        -22.63002
## 13 12 1.000000e+00
                        -18.46245
## 14 13 1.000000e+00
                        -15.99269
## 15 14 1.000000e+00
                        -14.12667
## 16 15 1.000000e+00
                        -11.71059
## 17 16 1.250000e-01
                        -11.28851
## 18 17 1.562500e-02
                        -11.23519
## 19 18 7.812500e-03
                        -11.20859
## 20 19 3.906250e-03
                        -11.19531
## 21 20 1.953125e-03
                        -11.18867
## 22 21 9.765625e-04
                        -11.18536
## 23 22 4.882812e-04
                        -11.18370
## 24 23 1.220703e-04
                        -11.18328
## 25 24 6.103516e-05
                        -11.18308
## 26 25 3.051758e-05
                        -11.18297
## 27 26 9.536743e-07
                        -11.18297
## 28 27 1.192093e-07
                        -11.18297
## 29 28 2.980232e-08
                        -11.18297
## 30 29 1.490116e-08
                        -11.18297
## 31 30 7.450581e-09
                        -11.18297
## 32 31 1.862645e-09
                        -11.18297
```

term	amy_est
intercept	-30.139
radius_mean	-44.734
texture_mean	0.553
perimeter_mean	0.618
area_mean	0.378
smoothness_mean	607.372
compactness_mean	-428.700
concavity_mean	170.327
concave.points_mean	307.008
symmetry_mean	-154.434
fractal_dimension_mean	254.243
radius_se	-15.974
texture_se	-5.739
perimeter_se	-6.772
area_se	1.201
smoothness_se	-110.513
compactness_se	810.326
concavity_se	-655.396
concave.points_se	3058.293
symmetry_se	-716.255
fractal_dimension_se	-8714.163
radius_worst	16.337
texture_worst	1.128
perimeter_worst	0.452
area_worst	-0.118
smoothness_worst	-206.369
compactness_worst	-70.968
concavity_worst	81.319
concave.points_worst	-50.233
symmetry_worst	151.576
fractal_dimension_worst	820.719

Comparing to glm model

Model Implementation

```
# training_df <- training_df[c(1:455),]
glm_fit <- glm(y~., data=training_df, family = "binomial")
result_glm <- summary(glm_fit)

glm_est <- glm_fit %>% broom::tidy() %>%
    select(term, estimate) %>%
    mutate(glm_est = round(estimate, 3)) %>%
    select(-estimate) %>%
    mutate(term = ifelse(term == "(Intercept)", "intercept", term))

library(glmnet)

## Loading required package: Matrix

##
## Attaching package: 'Matrix'
```

```
## The following objects are masked from 'package:tidyr':
##
##
       expand, pack, unpack
## Loaded glmnet 4.0-2
xdat = as.matrix(dat %>% select(-y))
glmnet_fit <- glmnet(x = xdat, y = dat$y, family="binomial", lambda = 0)</pre>
glmnet_est <- as.vector(coef(glmnet_fit)) %>% round(3)
combining
combine_res <- amy_est %>%
 full_join(glm_est) %>%
 mutate(glmnet_est= glmnet_est)
## Joining, by = "term"
combine_res %>%
  mutate(
    glm_est = round(glm_est,2)
  ) %>%
 knitr::kable()
```

term	amy est	glm_est	glmnet est
intercept	-30.139	-2.881303e+06	-63.001
radius mean	-44.734	2.427012e+06	-199.921
texture_mean	0.553	1.957831e+05	4.230
perimeter_mean	0.618	1.473188e + 06	3.056
area mean	0.378	-1.301181e+05	1.656
smoothness_mean	607.372	-1.524522e+08	1694.708
compactness_mean	-428.700	-6.428386e+06	-2296.582
concavity_mean	170.327	1.041553e + 06	1427.085
concave.points_mean	307.008	-1.715686e+07	1217.363
symmetry_mean	-154.434	4.048592e + 07	-821.444
fractal_dimension_mean	254.243	-4.232918e+07	2560.066
radius_se	-15.974	3.328481e+07	214.003
texture_se	-5.739	6.368392e+06	-18.584
perimeter_se	-6.772	1.700716e + 06	-45.148
area_se	1.201	-6.393464e+05	3.775
smoothness_se	-110.513	7.491721e + 08	-3656.025
compactness_se	810.326	-1.773076e+08	3535.532
concavity_se	-655.396	1.528648e + 08	-3157.434
concave.points_se	3058.293	-1.259854e+09	13110.563
symmetry_se	-716.255	2.890109e+08	-4185.736
fractal_dimension_se	-8714.163	1.512103e+09	-30097.121
radius_worst	16.337	-6.130231e+06	46.664
texture_worst	1.128	-5.832457e + 05	3.953
perimeter_worst	0.452	-3.538204e+05	2.667
area_worst	-0.118	8.950446e+04	-0.269
smoothness_worst	-206.369	-2.161128e+07	-287.861
compactness_worst	-70.968	8.986336e+06	-268.719
concavity_worst	81.319	-3.027927e+07	190.525
concave.points_worst	-50.233	1.431304e + 08	365.168
symmetry_worst	151.576	-2.473590e+07	897.403
fractal_dimension_worst	820.719	-3.698324e+07	2691.665