Project 2: Breast Cancer Diagnosis

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3/17/2022

Objectives

A mammogram is an X-ray image of breast tissue. It can help save lives because it is easier to treat breast cancer in its early stages before the cancer is big enough to detect or cause symptoms. However, a wrong diagnosis can have a negative impact on patients. For example, if there is a false-positive test result, the doctor sees something that looks like cancer but is not. This could result in overtreatment that causes unnecessary side effects on patients. On the other hand, false-negative test result occurs when a doctor misses cancer tissues, which may delay the treatment. Therefore, building a model that gives an accurate classification of the tissue images is necessary to give proper treatment. In our study, we collected 569 images from both malignant and benign cancer tissues. Our goal is to build a predictive model to facilitate cancer diagnosis.

Dataset

Our data set consistes of 569 rows, with 357 benign and 212 malignant. We denote 0 for benign and 1 for malignant. We also have 30 columns representing the features of the tissue images. They include the mean, standard deviation, and the largest values of the distributions of the following 10 features computed for the cell nuclei:

- 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)

Methods

Variables Selection

Among the 30 explanatory variables that we have, not all of them are necessary for the prediction model. Therefore, we dropped the columns that have high correlation with other columns. The 11 variables we left in the end have correlations less than 0.7 with each other.

Logistic Model

Let y be the vector with 569 binary response variable, X be the 569×30 matrix with 30 numerical explanatory variables, and β be the vector with 30 corresponding coefficients. We also have β_0 as the intercepts.

For our logistic model, the probability of ith row be a malignant tissue is given by:

$$P(y_i = 1|X_i) = \frac{e^{\beta_0+\beta X_i}}{1 + e^{\beta_0+\beta X_i}}.$$

For likelihood function is:

$$L(\beta_0, \beta) = \prod_{i=1}^{n} [(\frac{e^{\beta_0+\beta X_i}}{1 + e^{\beta_0+\beta X_i}})^{y_i} (\frac{1}{1 + e^{\beta_0+\beta X_i}})^{1-y_i}].$$

Maximizing the likelihood is equivalent to maximizing the log likelihood:

$$f(\beta_0, \beta) = \sum_{i=1}^{n} [y_i(\beta_0 + \beta X_i) - \log(1 + e^{\beta_0+\beta X_i})].$$

The gradient of this function is:

$$\nabla f(\beta_0, \beta) = \begin{pmatrix} \sum_{i=1}^{n} y_i - p_i \\ \sum_{i=1}^{n} X_1(y_i - p_i) \\ ... \\ \sum_{i=1}^{n} X_n(y_i - p_i) \end{pmatrix} = X^T(y_i - p_i)$$

where $p_i = P(y_i = 1|X_i)$ as mentioned in previous probability function.

The Hessian is given by

$$\nabla^2 f(\beta_0, \beta) = -XX^T W$$

where $W = p_i(1 - p_i)$.

Results

Conclusions

Appendix

data import and data clean

```r
#load the data
breast_dat = read_csv("breast-cancer.csv") %>%
  janitor::clean_names() %>%
  select(-33) %>% #drop NA column
  add_row(id = 92751, diagnosis = "B", radius_mean = 7.76, texture_mean = 24.54,
          perimeter_mean = 47.92, area_mean = 181, smoothness_mean = 0.05263,
          compactness_mean = 0.04362, concavity_mean = 0,
          concave_points_mean = 0, symmetry_mean = 0.1587,
          fractal_dimension_mean = 0.05884, radius_se = 0.3857,
          texture_se = 1.428, perimeter_se = 2.548, area_se = 19.15,
          smoothness_se = 0.007189, compactness_se = 0.00466, concavity_se = 0,
          concave_points_se = 0, symmetry_se = 0.02676,
          fractal_dimension_se = 0.002783, radius_worst = 9.456,
          texture_worst = 30.37, perimeter_worst = 59.16, area_worst = 268.6,
          smoothness_worst = 0.08996, compactness_worst = 0.06444,
          concavity_worst = 0, concave_points_worst = 0,
          symmetry_worst = 0.2871, fractal_dimension_worst = 0.07039)
  #add missing row


head(breast_dat, 5)
```

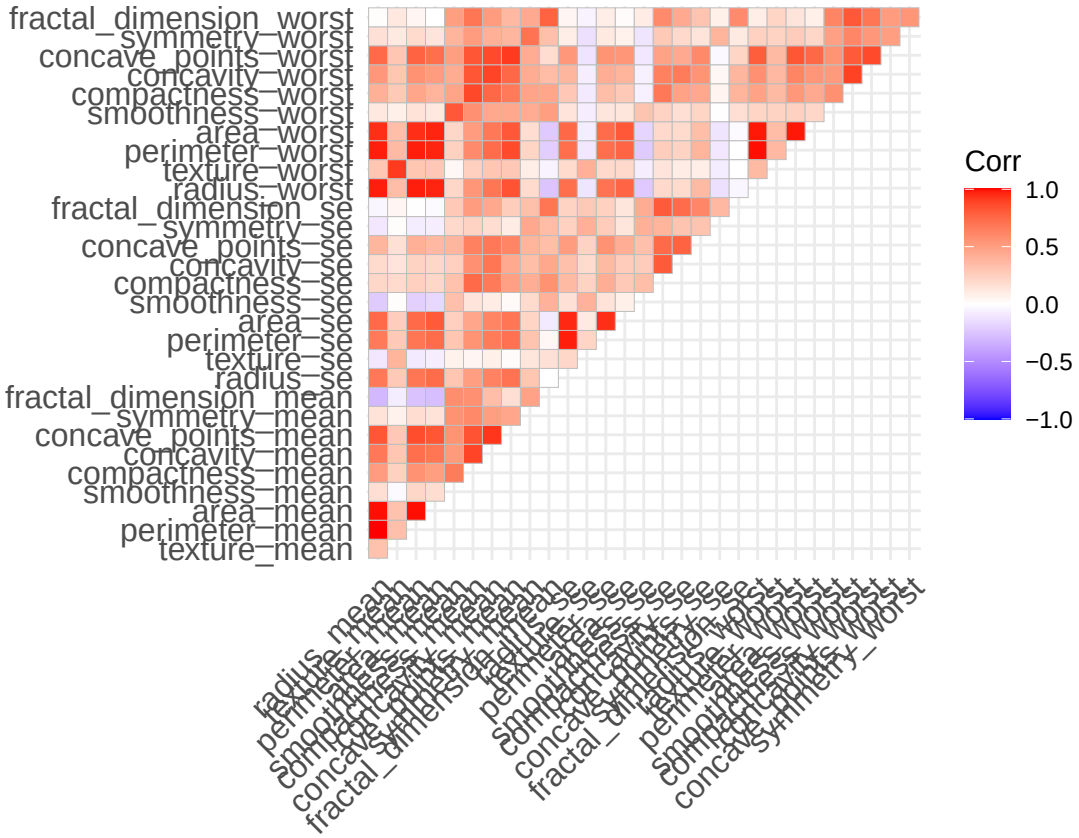
```
## # A tibble: 5 x 32
##         id diagnosis radius_mean texture_mean perimeter_mean area_mean
##      <dbl> <chr>           <dbl>        <dbl>          <dbl>     <dbl>
## 1   842302 M                18.0         10.4          123.      1001
## 2   842517 M                20.6         17.8          133.      1326
## 3 84300903 M                19.7         21.2          130       1203
## 4 84348301 M                11.4         20.4           77.6      386.
## 5 84358402 M                20.3         14.3          135.      1297
## # ... with 26 more variables: smoothness_mean <dbl>, compactness_mean <dbl>,
## #   concavity_mean <dbl>, concave_points_mean <dbl>, symmetry_mean <dbl>,
## #   fractal_dimension_mean <dbl>, radius_se <dbl>, texture_se <dbl>,
## #   perimeter_se <dbl>, area_se <dbl>, smoothness_se <dbl>,
## #   compactness_se <dbl>, concavity_se <dbl>, concave_points_se <dbl>,
## #   symmetry_se <dbl>, fractal_dimension_se <dbl>, radius_worst <dbl>,
## #   texture_worst <dbl>, perimeter_worst <dbl>, area_worst <dbl>, ...
```

```r
r = dim(breast_dat)[1] #row number
c = dim(breast_dat)[2] #column number

var_names = names(breast_dat)[-c(1,2)] #variable names

standardize = function(col) {
  mean = mean(col)
  sd = sd(col)
  return((col - mean)/sd)
}

stand_df = breast_dat %>%
  dplyr::select(radius_mean:fractal_dimension_worst) %>%
  map_df(.x = ., standardize) #standardize
```

```
X = stand_df #predictors
y = as.vector(ifelse(breast_dat[,2] == "M", 1, 0))#response
```

check collinearity

```
corr = stand_df %>%
  cor()

ggcorrplot(corr, type = "upper")
```




```
#X = stand_df %>%
  #select(radius_mean, texture_mean, smoothness_mean, compactness_mean,
         #symmetry_mean, fractal_dimension_mean, radius_se, texture_se,
         #smoothness_se, concavity_se, symmetry_se)

#corr_new = X %>% cor()
#corr_new

#ggcorrplot(corr_new, type = "upper", lab = TRUE)
```

```
logdata = cbind.data.frame(y, X)
log_model = glm(y ~ ., family = binomial(link = "logit"),data = logdata)
summary(log_model)
```

```
##
## Call:
## glm(formula = y ~ ., family = binomial(link = "logit"), data = logdata)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
##  -8.49   -8.49   -8.49    8.49    8.49
##
## Coefficients:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 253916      23548  10.783  < 2e-16 ***
## radius_mean                8552881     948876   9.014  < 2e-16 ***
## texture_mean                842067      63252  13.313  < 2e-16 ***
## perimeter_mean            35796847     598698  59.791  < 2e-16 ***
## area_mean                -45790271    1375034 -33.301  < 2e-16 ***
## smoothness_mean           -2144100     117586 -18.234  < 2e-16 ***
## compactness_mean           -339500     169667  -2.001  0.04540 *
## concavity_mean               83032     112278   0.740  0.45959
## concave_points_mean        -665733     208830  -3.188  0.00143 **
## symmetry_mean              1109889      21306  52.093  < 2e-16 ***
## fractal_dimension_mean     -298858      15312 -19.519  < 2e-16 ***
## radius_se                  9230274     324119  28.478  < 2e-16 ***
## texture_se                 3513102     110604  31.763  < 2e-16 ***
## perimeter_se               3438590      95432  36.032  < 2e-16 ***
## area_se                  -29084420     834804 -34.840  < 2e-16 ***
## smoothness_se              2249396      36747  61.213  < 2e-16 ***
## compactness_se            -3175247     102656 -30.931  < 2e-16 ***
## concavity_se               4614370     161208  28.624  < 2e-16 ***
## concave_points_se         -7773633     247582 -31.398  < 2e-16 ***
## symmetry_se                2389064      34103  70.054  < 2e-16 ***
## fractal_dimension_se       4001120     174560  22.921  < 2e-16 ***
## radius_worst             -29628795    1035752 -28.606  < 2e-16 ***
## texture_worst             -3584767     149772 -23.935  < 2e-16 ***
## perimeter_worst          -11889227     409644 -29.023  < 2e-16 ***
## area_worst                50959831    1560436  32.657  < 2e-16 ***
## smoothness_worst           -493436      75304  -6.553 5.66e-11 ***
## compactness_worst          1413874      62922  22.470  < 2e-16 ***
## concavity_worst           -6316972     317828 -19.875  < 2e-16 ***
## concave_points_worst       9408268     359616  26.162  < 2e-16 ***
## symmetry_worst            -1530342      20986 -72.923  < 2e-16 ***
## fractal_dimension_worst    -667962      96441  -6.926 4.33e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance:   751.44  on 568  degrees of freedom
## Residual deviance: 32006.76  on 538  degrees of freedom
## AIC: 32069
##
## Number of Fisher Scoring iterations: 25
```