Data analysis

12/09/2023

Libraries

```
library(tidyverse)
library(readr)
library(boot)
library(table1)
library(gridExtra)
library(MASS)
library(car)
library(leaps)
library(corrplot)
library(caret)
library(car)
library(ResourceSelection)
library(pROC)
```

Data Clean

```
breastcancer_data =
  read_csv("Project_2_data.csv") |>
  janitor::clean_names()
```

```
## Rows: 4024 Columns: 16
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (11): Race, Marital Status, T Stage, N Stage, 6th Stage, differentiate, ...
## dbl  (5): Age, Tumor Size, Regional Node Examined, Reginol Node Positive, Su...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
summary(breastcancer_data)
```

```
##       age            race           marital_status       t_stage
##  Min.   :30.00   Length:4024        Length:4024        Length:4024
##  1st Qu.:47.00   Class :character   Class :character   Class :character
##  Median :54.00   Mode  :character   Mode  :character   Mode  :character
##  Mean   :53.97
##  3rd Qu.:61.00
```

```
##  Max.   :69.00
##    n_stage            x6th_stage        differentiate         grade
##  Length:4024        Length:4024        Length:4024        Length:4024
##  Class :character   Class :character   Class :character   Class :character
##  Mode  :character   Mode  :character   Mode  :character   Mode  :character
##
##
##
##    a_stage             tumor_size     estrogen_status    progesterone_status
##  Length:4024        Min.   :  1.00   Length:4024        Length:4024
##  Class :character   1st Qu.: 16.00   Class :character   Class :character
##  Mode  :character   Median : 25.00   Mode  :character   Mode  :character
##                     Mean   : 30.47
##                     3rd Qu.: 38.00
##                     Max.   :140.00
##  regional_node_examined reginol_node_positive survival_months
##  Min.   : 1.00          Min.   : 1.000        Min.   :  1.0
##  1st Qu.: 9.00          1st Qu.: 1.000        1st Qu.: 56.0
##  Median :14.00          Median : 2.000        Median : 73.0
##  Mean   :14.36          Mean   : 4.158        Mean   : 71.3
##  3rd Qu.:19.00          3rd Qu.: 5.000        3rd Qu.: 90.0
##  Max.   :61.00          Max.   :46.000        Max.   :107.0
##     status
##  Length:4024
##  Class :character
##  Mode  :character
##
##
##
```

```r
bc = breastcancer_data |>
  mutate(
    race=case_when(
      race == "White" ~ 1,
      race == "Black" ~ 2,
      race == "Other" ~ 3),
    marital_status=case_when(
      marital_status == "Married" ~ 1,
      marital_status == "Divorced" ~ 2,
      marital_status == "Single" ~ 3,
      marital_status == "Widowed" ~ 4,
      marital_status == "Separated" ~ 5),
    t_stage=case_when(
      t_stage == "T1" ~ 1,
      t_stage == "T2" ~ 2,
      t_stage == "T3" ~ 3,
      t_stage == "T4" ~ 4),
    n_stage=case_when(
      n_stage == "N1" ~ 1,
      n_stage == "N2" ~ 2,
      n_stage == "N3" ~ 3),
    x6th_stage=case_when(
      x6th_stage == "IIA" ~ 1,
      x6th_stage == "IIIA" ~ 2,
```

```
    x6th_stage == "IIIC" ~ 3,
    x6th_stage == "IIB" ~ 4,
    x6th_stage == "IIIB" ~ 5),
  differentiate=case_when(
    differentiate == "Poorly differentiated" ~ 1,
    differentiate == "Moderately differentiated" ~ 2,
    differentiate == "Well differentiated" ~ 3,
    differentiate == "Undifferentiated" ~ 4),
  grade=case_when(
    grade == "1" ~ 1,
    grade == "2" ~ 2,
    grade == "3" ~ 3,
    grade == "anaplastic; Grade IV" ~ 4),
  a_stage=case_when(
    a_stage == "Regional" ~ 1,
    a_stage == "Distant" ~ 0),
  estrogen_status=case_when(
    estrogen_status == "Positive" ~ 1,
    estrogen_status == "Negative" ~ 0),
  progesterone_status=case_when(
    progesterone_status == "Positive" ~ 1,
    progesterone_status == "Negative" ~ 0),
  status=case_when(
    status == "Alive" ~ 1,
    status == "Dead" ~ 0)
  )
```

Descriptive statistics for all variables

```
summary(bc)
```

```
##       age             race       marital_status     t_stage
##  Min.   :30.00   Min.   :1.000   Min.   :1.000   Min.   :1.000
##  1st Qu.:47.00   1st Qu.:1.000   1st Qu.:1.000   1st Qu.:1.000
##  Median :54.00   Median :1.000   Median :1.000   Median :2.000
##  Mean   :53.97   Mean   :1.231   Mean   :1.646   Mean   :1.785
##  3rd Qu.:61.00   3rd Qu.:1.000   3rd Qu.:2.000   3rd Qu.:2.000
##  Max.   :69.00   Max.   :3.000   Max.   :5.000   Max.   :4.000
##     n_stage        x6th_stage    differentiate       grade
##  Min.   :1.000   Min.   :1.000   Min.   :1.000   Min.   :1.000
##  1st Qu.:1.000   1st Qu.:1.000   1st Qu.:1.000   1st Qu.:2.000
##  Median :1.000   Median :2.000   Median :2.000   Median :2.000
##  Mean   :1.438   Mean   :2.405   Mean   :1.868   Mean   :2.151
##  3rd Qu.:2.000   3rd Qu.:4.000   3rd Qu.:2.000   3rd Qu.:3.000
##  Max.   :3.000   Max.   :5.000   Max.   :4.000   Max.   :4.000
##     a_stage        tumor_size     estrogen_status  progesterone_status
##  Min.   :0.0000   Min.   :  1.00   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:1.0000   1st Qu.: 16.00   1st Qu.:1.0000   1st Qu.:1.0000
##  Median :1.0000   Median : 25.00   Median :1.0000   Median :1.0000
##  Mean   :0.9771   Mean   : 30.47   Mean   :0.9332   Mean   :0.8265
##  3rd Qu.:1.0000   3rd Qu.: 38.00   3rd Qu.:1.0000   3rd Qu.:1.0000
```

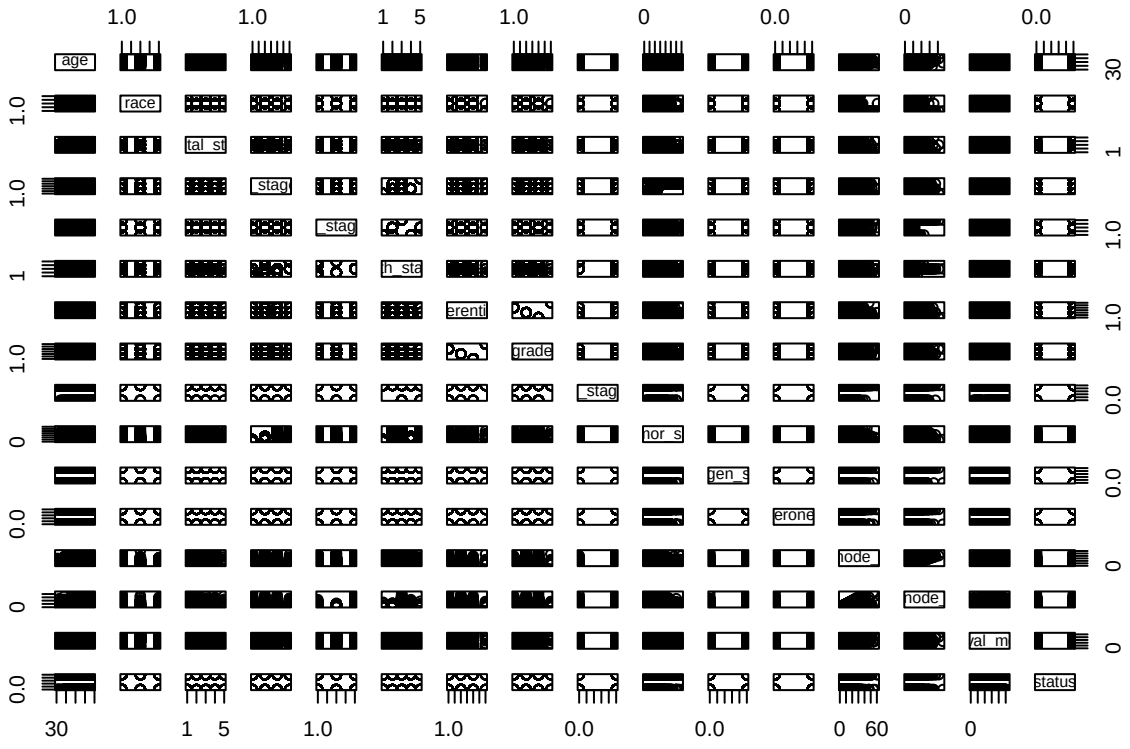
```
##  Max.   :1.0000   Max.   :140.00   Max.   :1.0000   Max.   :1.0000
##  regional_node_examined reginol_node_positive survival_months     status
##  Min.   : 1.00          Min.   : 1.000        Min.   :  1.0   Min.   :0.0000
##  1st Qu.: 9.00          1st Qu.: 1.000        1st Qu.: 56.0   1st Qu.:1.0000
##  Median :14.00          Median : 2.000        Median : 73.0   Median :1.0000
##  Mean   :14.36          Mean   : 4.158        Mean   : 71.3   Mean   :0.8469
##  3rd Qu.:19.00          3rd Qu.: 5.000        3rd Qu.: 90.0   3rd Qu.:1.0000
##  Max.   :61.00          Max.   :46.000        Max.   :107.0   Max.   :1.0000
```

We change race, marital_status, t_stage, n_stage, x6th_stage, differentiate, and grade into multiple numeric levels, while a_stage, estrogen_status, progesterone_status, and status to binary levels. The above variables are categorical variables.

And age, tumor_size, regional_node_examined, reginol_node_positive, and survival_months are numeric variables.

Covariance and Correlation

```
plot(bc)
```



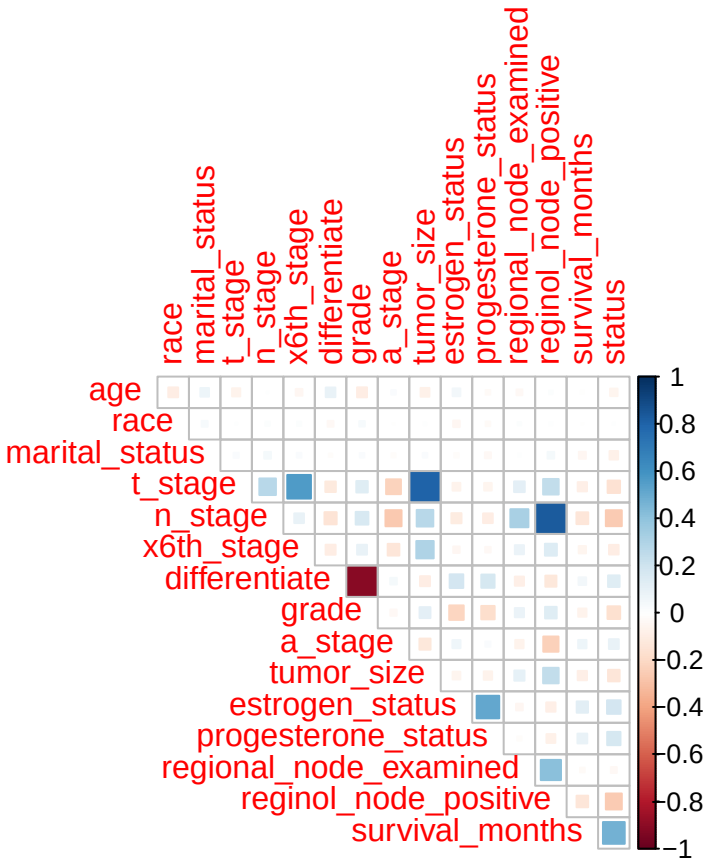

```
cor(bc) |>
  knitr::kable(digits=4,caption="Correlation for all variables")
```

Table 1: Correlation for all variables

	age	race	marital_status	t_stage	n_stage	x6th_stage	differentiate	grade	a_stage	tumor_size	estrogen_status	progesterone_status	regional_node_examined	reginol_node_positive	survival_months	status
age	1.0000	-0.0970	0.0755	-0.0669	0.0029	-0.0450	-0.0932	-0.0993	-0.0209	-0.0772	-0.0598	-0.0213	-0.0333	-0.0126	-0.0094	-0.0559
race	-0.0970	1.0000	0.0349	0.0036	0.0191	0.0173	-0.0336	-0.0301	-0.0020	-0.0071	-0.0425	-0.0209	-0.0113	-0.0090	-0.0025	0.0042
marital_status	0.0755	0.0349	1.0000	0.0257	0.0457	0.0221	-0.0117	-0.0206	-0.0174	-0.0207	-0.0198	-0.0357	-0.0077	-0.0443	-0.0487	-0.0731
t_stage	-0.0669	0.0036	0.0257	1.0000	0.2770	0.5637	-0.1102	-0.1315	-0.2211	-0.8092	-0.0610	-0.0576	-0.1141	-0.2431	-0.0857	-0.1547
n_stage	0.0029	0.0191	0.0457	0.2770	1.0000	0.0939	-0.1488	-0.1625	-0.2606	-0.2779	-0.1020	-0.0937	-0.3283	-0.8381	-0.1396	-0.2558
x6th_stage	0.0450	0.0173	0.0221	0.5637	0.0939	1.0000	-0.0999	-0.0972	-0.1372	-0.3034	-0.0417	-0.0309	-0.0826	-0.1427	-0.0536	-0.0919
differentiate	0.0932	-0.0336	-0.0117	-0.1102	-0.1488	-0.0999	1.0000	-0.9083	-0.0395	-0.1868	-0.2113	-0.1799	-0.0834	-0.1229	-0.0677	-0.1614
grade	-0.0993	0.0301	0.0206	0.1315	0.1625	0.0972	-0.9083	1.0000	-0.1239	0.1194	-0.0596	-0.0699	-0.0690	-0.2328	-0.0869	-0.1342
a_stage	0.0209	-0.0020	-0.0174	-0.2211	-0.2606	-0.1372	0.0395	-0.1239	1.0000	-0.0656	-0.0265	-0.0699	-0.1044	-0.2423	-0.1285	-0.1847
tumor_size	0.0772	0.0071	0.0207	0.8092	0.2779	0.3034	-0.0995	0.1194	-0.1239	1.0000	-0.0596	-0.0699	-0.0448	-0.0860	-0.0960	-0.1771
estrogen_status	0.0598	0.0425	0.0198	0.0610	0.1020	0.0417	-0.2113	0.0596	-0.0265	0.0596	1.0000	0.5133	-0.0181	-0.0781	-0.0221	-0.0348
progesterone_status	0.0213	0.0209	0.0357	0.0576	0.0937	0.0309	-0.1799	0.0699	-0.0699	0.0699	0.5133	1.0000	-0.0181	-0.0781	-0.1352	-0.2566
regional_node_examined	0.0333	0.0113	0.0077	0.1141	0.3283	0.0826	-0.0834	0.0844	-0.0690	0.1044	-0.0448	-0.0181	1.0000	0.4116	-0.0221	-0.0348
reginol_node_positive	0.0126	0.0090	0.0443	0.2431	0.8381	0.1427	-0.1229	0.1353	-0.2328	0.2423	-0.0860	-0.0781	-0.4116	1.0000	-0.1352	-0.2566
survival_months	0.0094	0.0025	0.0487	0.0857	0.1396	0.0536	-0.0677	0.0869	-0.1285	0.0960	-0.0221	-0.1352	-0.0221	-0.1352	1.0000	0.4765
status	-0.0559	0.0042	0.0731	0.1547	0.2558	0.0919	-0.1614	0.1342	-0.1847	0.1771	-0.0348	-0.2566	-0.0348	-0.2566	0.4765	1.0000

Another plot for correlation

```
corrplot(cor(bc), method = "square", type = "upper", diag = FALSE)
```



Exploratory visualisation

```
plot1age =
  breastcancer_data|>
  ggplot(aes(x = age)) +
  geom_histogram(color = "blue", fill = alpha("blue", 0.5), binwidth = 5) +
  theme_minimal() +
  labs(
    title = "Age Distribution",
    x = "Age",
    y = "Frequency"
  )
#plot1age
```

```
plot2race =
  breastcancer_data|>
  ggplot(aes(x = race)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Race Distribution",
    x = "Race",
    y = "Frequency"
```

```
  )
#plot2race
```

```
plot3marital =
  breastcancer_data|>
  ggplot(aes(x = marital_status)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Marital Status Distribution",
    x = "Marital Status",
    y = "Frequency"
  )

#plot3marital
```

```
plot4tstage =
  breastcancer_data|>
  ggplot(aes(x = t_stage)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "T Stage Distribution",
    x = "T Stage",
    y = "Frequency"
  )

#plot4tstage
```

```
plot5nstage =
  breastcancer_data|>
  ggplot(aes(x = n_stage)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "N Stage Distribution",
    x = "N Stage",
    y = "Frequency"
  )

#plot5nstage
```

```
plot6x6thstage =
  breastcancer_data|>
  ggplot(aes(x = x6th_stage)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "x6th Stage Distribution",
    x = "x6th Stage",
    y = "Frequency"
  )
```

```r
#plot6x6thstage
```

```r
plot7differentate =
  breastcancer_data|>
  ggplot(aes(x = differentiate)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Differentate Distribution",
    x = "Differentate Group",
    y = "Frequency"
  )

#plot7differentate
```

```r
plot8grade =
  breastcancer_data|>
  ggplot(aes(x = grade)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Grade Distribution",
    x = "Grade",
    y = "Frequency"
  )

#plot8grade
```

```r
plot9astage =
  breastcancer_data|>
  ggplot(aes(x = a_stage)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "A_stage Distribution",
    x = "A Stage",
    y = "Frequency"
  )

#plot9astage
```

```r
plot10tumorsize =
  breastcancer_data|>
  ggplot(aes(x = tumor_size)) +
  geom_histogram(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Tumor Size Distribution",
    x = "Tumor Size",
    y = "Frequency"
  )

#plot10tumorsize
```

```r
plot11estrogen =
  breastcancer_data|>
  ggplot(aes(x = estrogen_status)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Estrogen Status Distribution",
    x = "Estrogen Status",
    y = "Frequency"
  )

#plot11estrogen
```

```r
plot12progesterone =
  breastcancer_data|>
  ggplot(aes(x = progesterone_status)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Progesterone Status Distribution",
    x = "Progesterone Status",
    y = "Frequency"
  )

#plot12progesterone
```

```r
plot13nodeexamined =
  breastcancer_data|>
  ggplot(aes(x = regional_node_examined)) +
  geom_histogram(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Regional Node Examined Distribution",
    x = "Examined Regional Node",
    y = "Frequency"
  )

#plot13nodeexamined
```

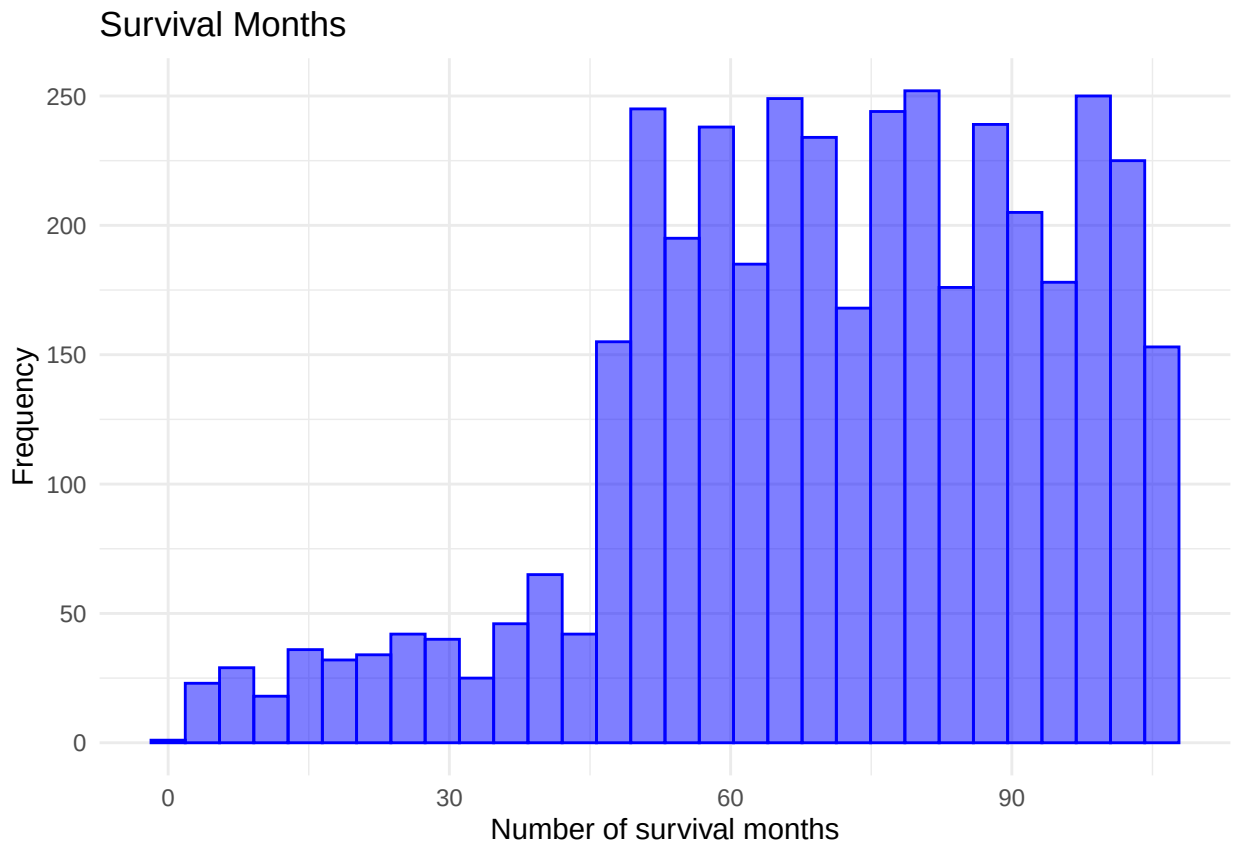
```r
plot14nodepositive =
  breastcancer_data|>
  ggplot(aes(x = reginol_node_positive)) +
  geom_histogram(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Regional Node Positive Distribution",
    x = "Positive Reginol Node",
    y = "Frequency"
  )

#plot14nodepositive
```

Y1 = survive months; (numeric)

Y2 = status; (binary)

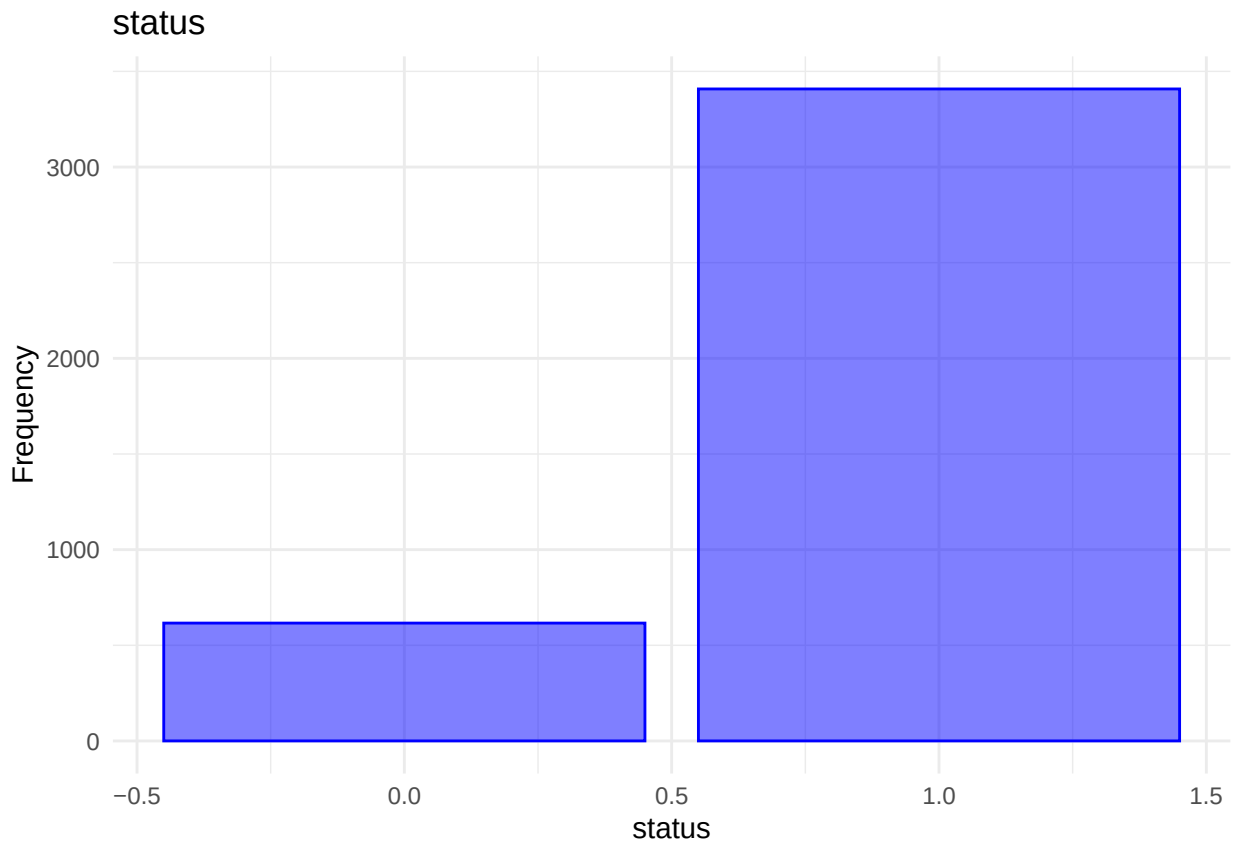
```
plot15survivalmonths =
  breastcancer_data|>
  ggplot(aes(x = survival_months)) +
  geom_histogram(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Survival Months",
    x = "Number of survival months",
    y = "Frequency"
  )

plot15survivalmonths
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
plot16status =
  bc|>
  ggplot(aes(x = status)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
```

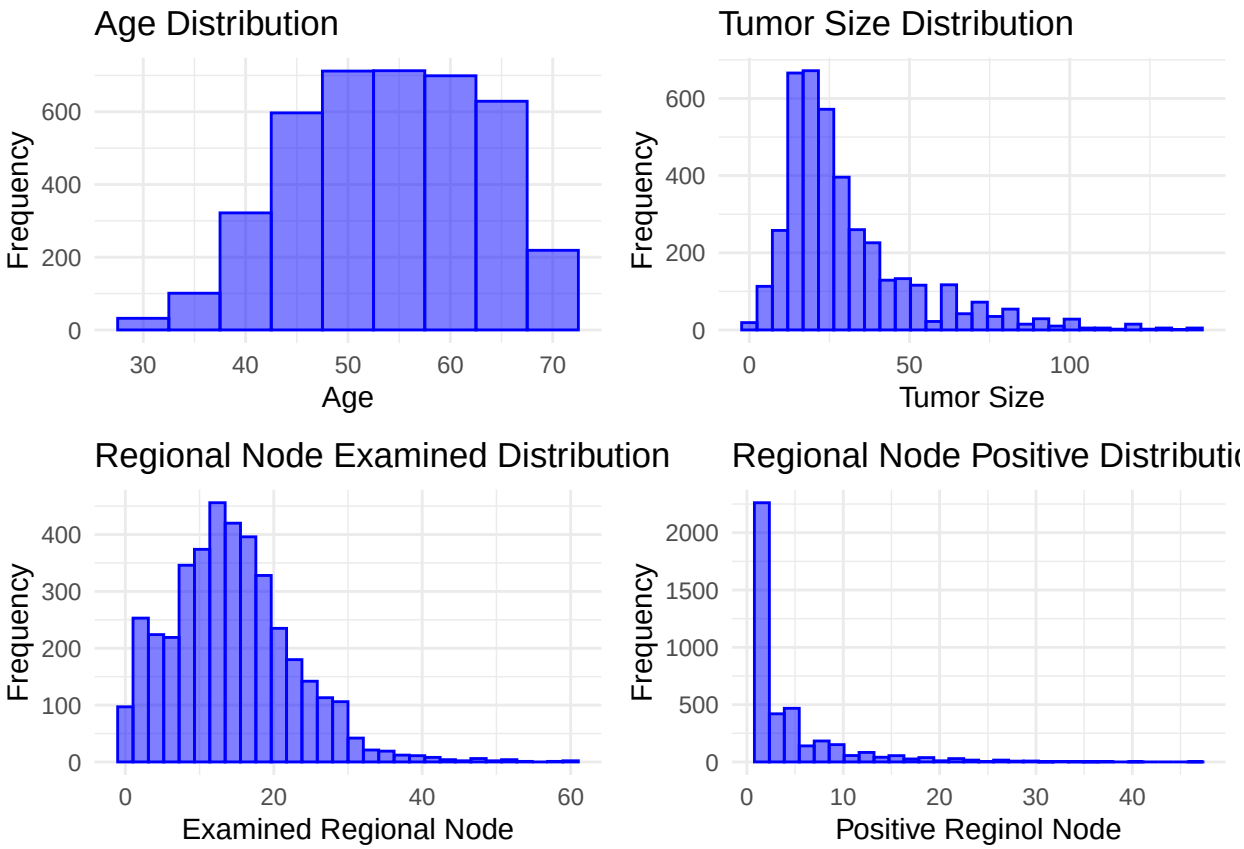
```
    title = "status",
    x = "status",
    y = "Frequency"
  )

plot16status
```



Summarized plots for covariates

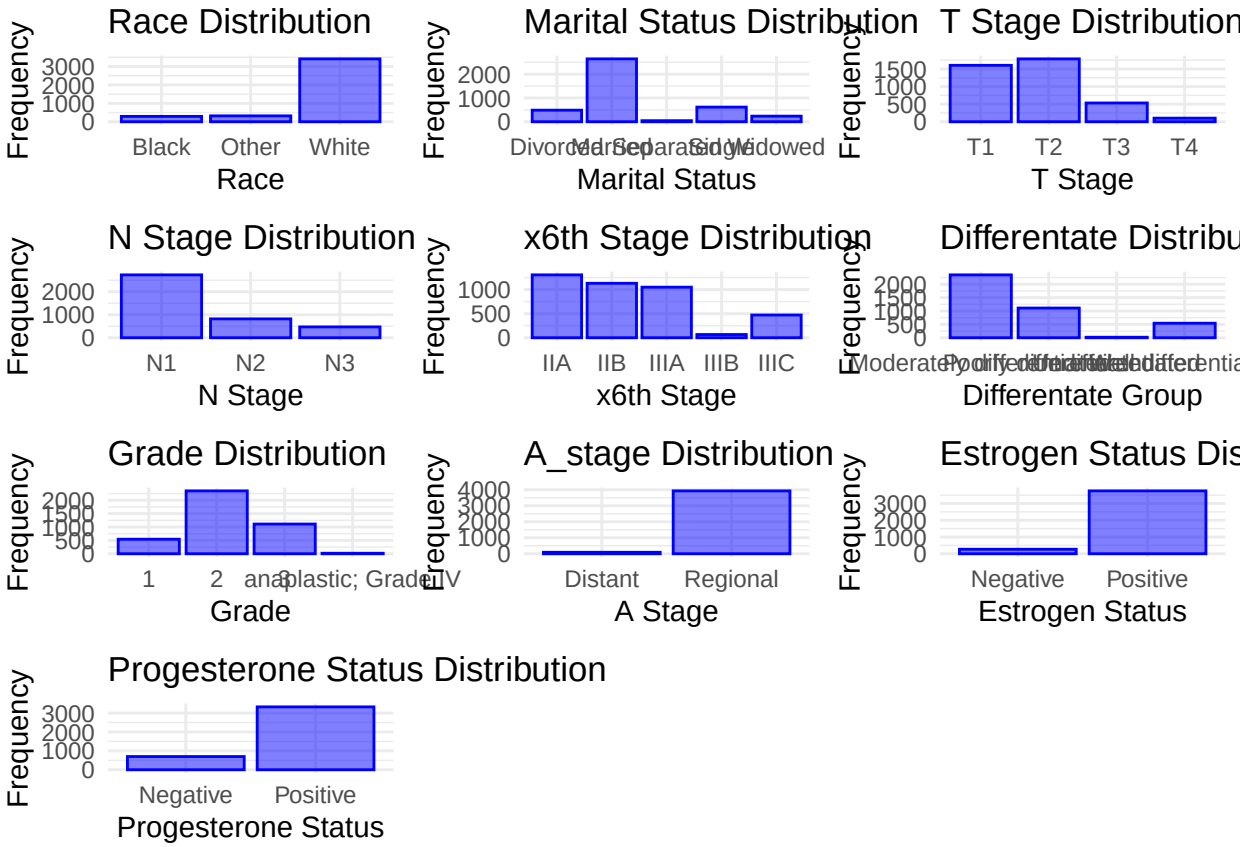
```
grid.arrange(plot1age, plot10tumorsize, plot13nodeexamined,
             plot14nodepositive, ncol = 2)
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



We can see that age is approximately normal, while tumor size, regional node examined, and regional node positive are skewed.

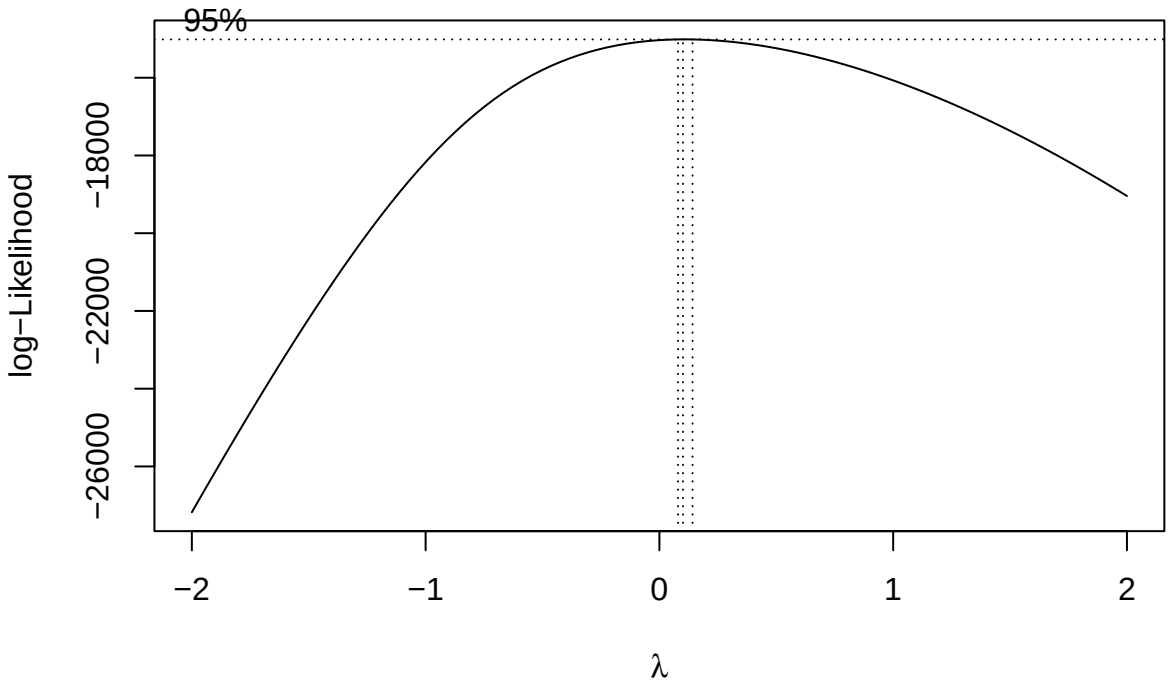
```
grid.arrange(plot2race, plot3marital,plot4tstage,
             plot5nstage, plot6x6thstage,plot7differentate,
             plot8grade,plot9astage,plot11estrogen,plot12progesterone, ncol = 3)
```



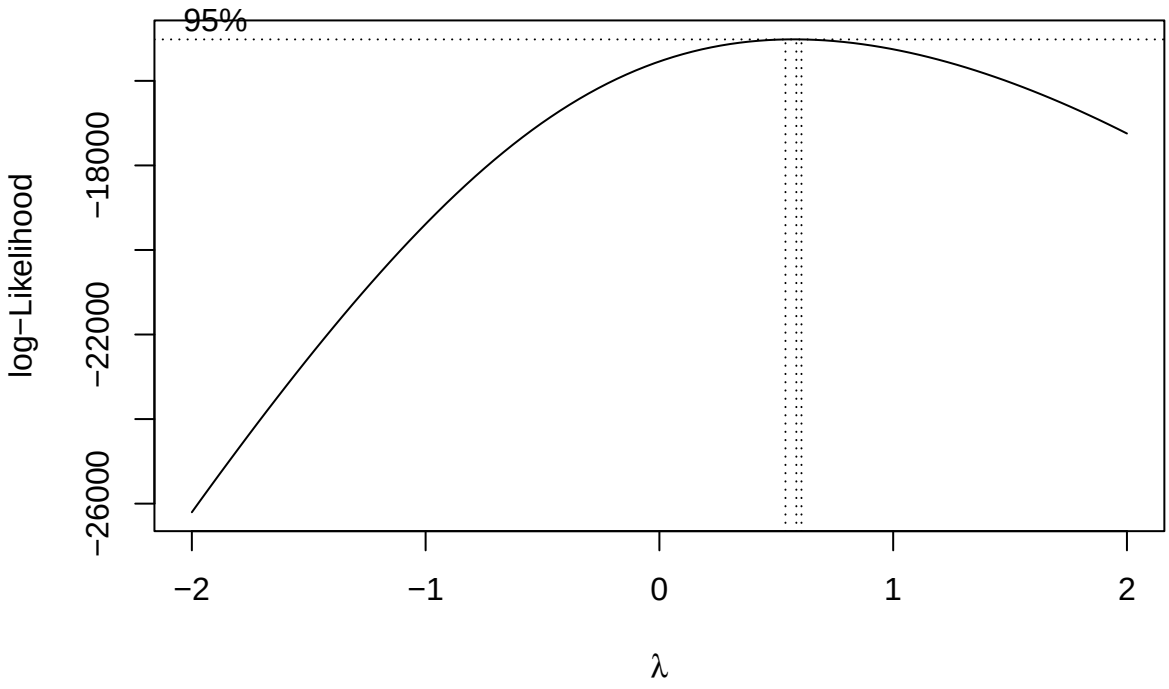
Transformation

We know that the tumor size, regional node examined, and regional node positive are skewed. We should do transformation on these variables. Before the transformation, we can use the Box-Cox plot to check which transformation work the best for them.

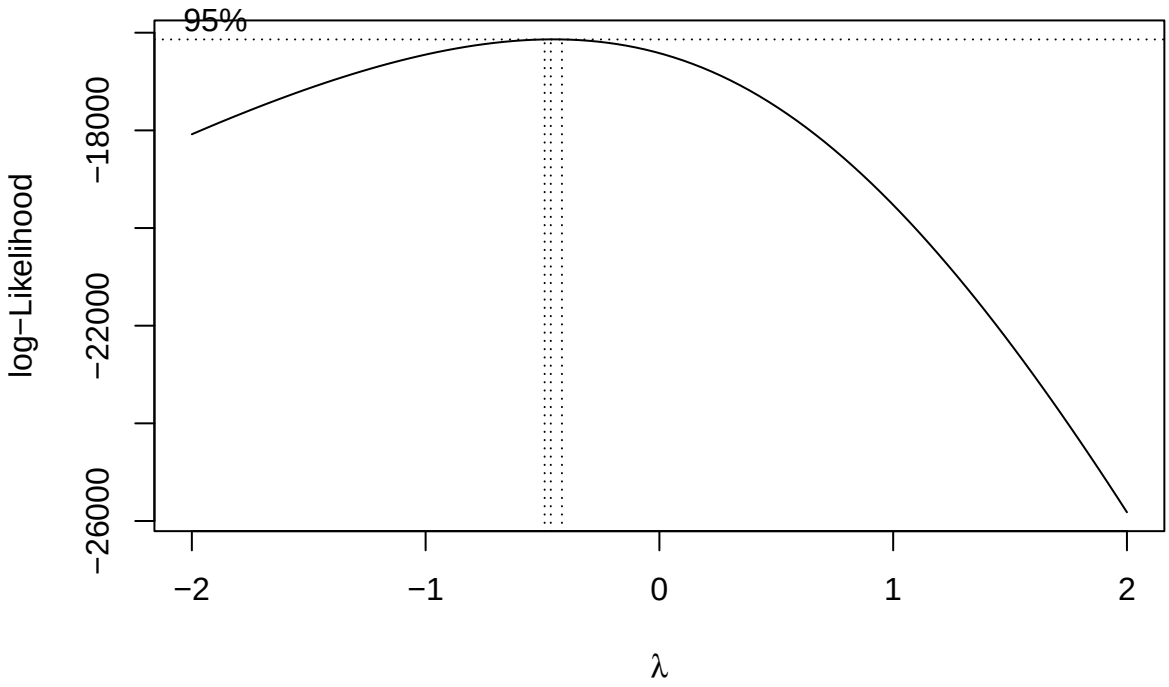
```
bc_transform_tumorsize <- boxcox(breastcancer_data$tumor_size ~ 1, lambda = seq(-2, 2, by=0.1))
```




```
bc_transform_regionalnode_examined <- boxcox(breastcancer_data$regional_node_examined ~ 1, lambda = seq
```

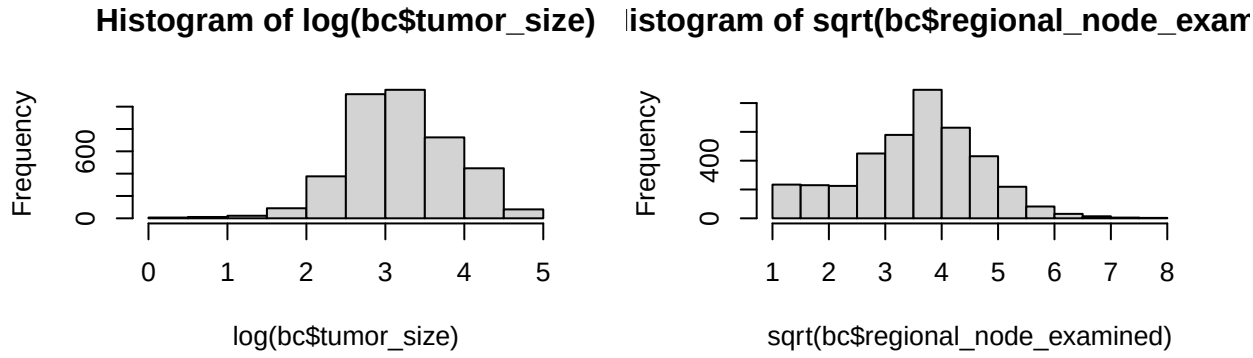


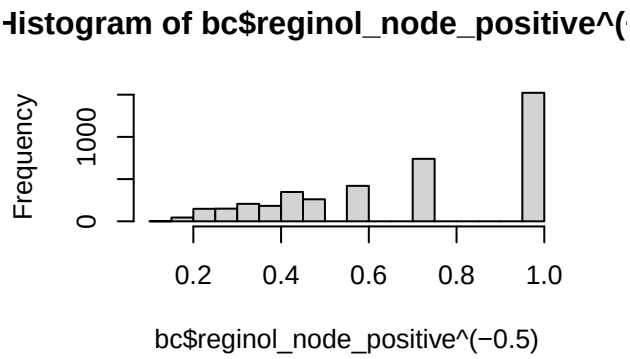

```
bc_transform_regionalnode_pos <- boxcox(breastcancer_data$reginol_node_positive ~ 1, lambda = seq(-2, 2
```



The lambda value of tumor size is close to 0, so we should use log transformation, while the lambda value of regional node examined is around 0.5, we should take a square root to the value, and the lambda value of regional node positive is around -0.5, so we should take a take square root and take an (-1) exponent for transformation.

```
par(mfrow = c(2, 2))
hist(log(bc$tumor_size))
hist(sqrt(bc$regional_node_examined))
hist(bc$reginol_node_positive**(-0.5))
```





We can see that tumor size and regional node examined become approximately normal after log transformation, while the regional node positive is still extremely skewed. Therefore, we may consider not using the variable of reginol_node_positive.

Transformation model

```
newbc = bc |>
  mutate(ln_tumor=log(tumor_size),
         sqrt_examined=sqrt(regional_node_examined)) |>
  dplyr::select(-tumor_size) |>
  dplyr::select(-regional_node_examined) |>
  dplyr::select(-survival_months)
newbc
```

```
## # A tibble: 4,024 x 15
##      age  race marital_status t_stage n_stage x6th_stage differentiate grade
##    <dbl> <dbl>          <dbl>   <dbl>   <dbl>      <dbl>          <dbl> <dbl>
##  1    68     1              1       1       1          1              1     3
##  2    50     1              1       2       2          2              2     2
##  3    58     1              2       3       3          3              2     2
##  4    58     1              1       1       1          1              1     3
##  5    47     1              1       2       1          4              1     3
##  6    51     1              3       1       1          1              2     2
##  7    51     1              1       1       1          1              3     1
```

```
##  8    40     1              1       2       1          4             2     2
##  9    40     1              2       4       3          3             1     3
## 10    69     1              1       4       3          3             3     1
## # i 4,014 more rows
## # i 7 more variables: a_stage <dbl>, estrogen_status <dbl>,
## #   progesterone_status <dbl>, reginol_node_positive <dbl>, status <dbl>,
## #   ln_tumor <dbl>, sqrt_examined <dbl>
```

chi-square tets

```
# Create an empty data frame to store chi-square test results
chi_square_results <- data.frame(Variable = character(),
                                 ChiSquare = numeric(),
                                 PValue = numeric(),
                                 stringsAsFactors = FALSE)

# Specify the dependent variable
dependent_var <- newbc$status

# List of independent variables
independent_vars <- newbc[,-13]

# Perform chi-square test for each independent variable
for (var in names(independent_vars)) {
  # Create a contingency table
  table <- table(dependent_var, newbc[[var]])

  # Perform chi-square test and suppress warnings for expected count less than 5
  test <- try(suppressWarnings(chisq.test(table)), silent = TRUE)

  # Store the results if the test was successful
  if (!inherits(test, "try-error")) {
    chi_square_results <- rbind(chi_square_results, data.frame(Variable = var,
                                                               ChiSquare = test$statistic,
                                                               PValue = test$p.value))
  } else {
    # Store NA if the test failed due to too many zero counts
    chi_square_results <- rbind(chi_square_results, data.frame(Variable = var,
                                                               ChiSquare = NA,
                                                               PValue = NA))
  }
}

chi_square_results
```

```
##                         Variable ChiSquare       PValue
## X-squared                    age  86.47154 1.880216e-05
## X-squared1                  race  27.97001 8.440929e-07
## X-squared2        marital_status  28.26381 1.102769e-05
## X-squared3               t_stage 103.47631 2.779095e-22
## X-squared4               n_stage 269.92914 2.430141e-59
## X-squared5            x6th_stage 281.64844 9.830332e-60
```

```
## X-squared6          differentiate 112.55628 3.091352e-24
## X-squared7                  grade 112.55628 3.091352e-24
## X-squared8                a_stage  35.76473 2.226426e-09
## X-squared9        estrogen_status 135.15574 3.052608e-31
## X-squared10   progesterone_status 124.88539 5.392080e-29
## X-squared11 reginol_node_positive 343.65852 2.292691e-51
## X-squared12              ln_tumor 192.12355 1.560395e-06
## X-squared13         sqrt_examined  71.62539 4.501059e-02
```

Based on the above chi-squared table, each variable listed has been tested for independence with respect to the dependent variable, and each shows a significant relationship.

Indicator Test

When y is status

```r
# indicator test when y is status
categorical_vars <- c("race", "marital_status", "t_stage", "n_stage", "x6th_stage",
                      "differentiate", "grade", "a_stage",
                      "estrogen_status", "progesterone_status")

newbc[categorical_vars] <- lapply(newbc[categorical_vars], factor)

formula <- as.formula("status ~ race + marital_status + t_stage + n_stage + x6th_stage +
                      differentiate + grade + a_stage + estrogen_status + progesterone_status+ln_tumor

model <- glm(formula, data = newbc, family = binomial())

summary(model)
```

```
##
## Call:
## glm(formula = formula, family = binomial(), data = newbc)
##
## Coefficients: (4 not defined because of singularities)
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)           1.826084   0.591231   3.089  0.00201 **
## race2                -0.517829   0.161866  -3.199  0.00138 **
## race3                 0.412988   0.202323   2.041  0.04123 *
## marital_status2      -0.208737   0.141798  -1.472  0.14100
## marital_status3      -0.137065   0.134860  -1.016  0.30946
## marital_status4      -0.226852   0.192395  -1.179  0.23836
## marital_status5      -0.870139   0.369406  -2.356  0.01850 *
## t_stage2             -0.241275   0.214882  -1.123  0.26151
## t_stage3             -0.463184   0.308144  -1.503  0.13280
## t_stage4             -0.911657   0.451201  -2.021  0.04333 *
## n_stage2             -0.652606   0.238058  -2.741  0.00612 **
## n_stage3             -0.757283   0.301072  -2.515  0.01189 *
## x6th_stage2           0.069464   0.294083   0.236  0.81327
## x6th_stage3                 NA         NA      NA       NA
## x6th_stage4          -0.226947   0.231875  -0.979  0.32771
```

```
## x6th_stage5           -0.085418   0.528445  -0.162  0.87159
## differentiate2         0.387813   0.104972   3.694  0.00022 ***
## differentiate3         0.922456   0.193026   4.779 1.76e-06 ***
## differentiate4        -0.970582   0.533726  -1.819  0.06899 .
## grade2                       NA         NA      NA       NA
## grade3                       NA         NA      NA       NA
## grade4                       NA         NA      NA       NA
## a_stage1               0.044840   0.266049   0.169  0.86616
## estrogen_status1       0.733142   0.177768   4.124 3.72e-05 ***
## progesterone_status1   0.589919   0.127619   4.623 3.79e-06 ***
## ln_tumor              -0.053874   0.138931  -0.388  0.69818
## sqrt_examined          0.256137   0.049748   5.149 2.62e-07 ***
## reginol_node_positive -0.074309   0.015040  -4.941 7.78e-07 ***
## age                   -0.023985   0.005625  -4.264 2.01e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2951.6  on 3999  degrees of freedom
## AIC: 3001.6
##
## Number of Fisher Scoring iterations: 5
```

Based on the above indicator test summary, we delete grade and x6th_stage because their output was NA in the output logistic model, since NA indicates these predicts may contribute collinearity.

Model Fitting

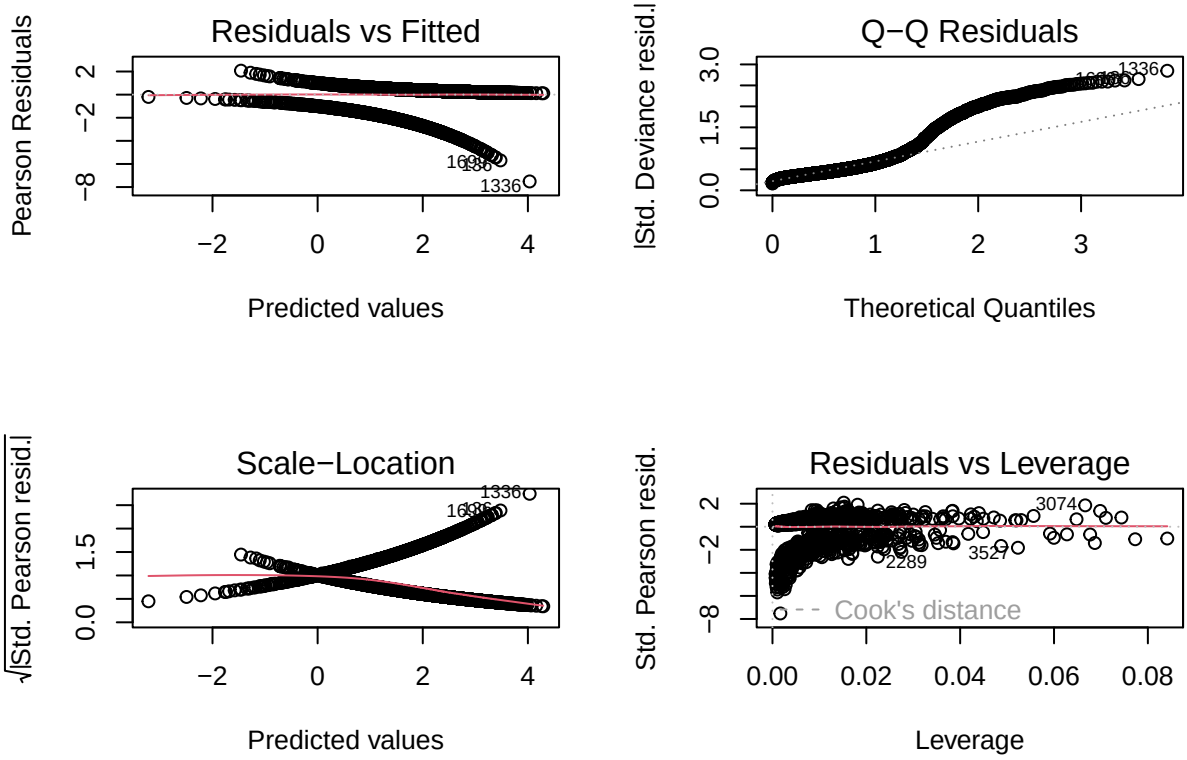
Initial Model

```
glmfit <- glm(status ~ race + marital_status + t_stage + n_stage + differentiate +
              a_stage + estrogen_status + progesterone_status + ln_tumor +
              sqrt_examined + reginol_node_positive + age,
              data = newbc, family = binomial)
summary(glmfit)
```

```
##
## Call:
## glm(formula = status ~ race + marital_status + t_stage + n_stage +
##     differentiate + a_stage + estrogen_status + progesterone_status +
##     ln_tumor + sqrt_examined + reginol_node_positive + age, family = binomial,
##     data = newbc)
##
## Coefficients:
##                        Estimate Std. Error z value Pr(>|z|)
## (Intercept)            1.775787   0.587386   3.023 0.002501 **
## race2                 -0.522765   0.161744  -3.232 0.001229 **
## race3                  0.419131   0.202312   2.072 0.038293 *
## marital_status2       -0.209325   0.141735  -1.477 0.139709
```

```
## marital_status3       -0.140584   0.134542  -1.045 0.296064
## marital_status4       -0.222113   0.192496  -1.154 0.248558
## marital_status5       -0.867369   0.370116  -2.344 0.019104 *
## t_stage2              -0.372488   0.159129  -2.341 0.019243 *
## t_stage3              -0.471905   0.266764  -1.769 0.076894 .
## t_stage4              -1.025962   0.313035  -3.277 0.001047 **
## n_stage2              -0.474091   0.129288  -3.667 0.000245 ***
## n_stage3              -0.637101   0.237639  -2.681 0.007341 **
## differentiate2         0.386027   0.104898   3.680 0.000233 ***
## differentiate3         0.917457   0.192668   4.762 1.92e-06 ***
## differentiate4        -0.947095   0.531127  -1.783 0.074557 .
## a_stage1               0.045211   0.265718   0.170 0.864894
## estrogen_status1       0.737828   0.177538   4.156 3.24e-05 ***
## progesterone_status1   0.588385   0.127499   4.615 3.93e-06 ***
## ln_tumor              -0.055274   0.138631  -0.399 0.690103
## sqrt_examined          0.255997   0.049654   5.156 2.53e-07 ***
## reginol_node_positive -0.074961   0.014984  -5.003 5.65e-07 ***
## age                   -0.023647   0.005618  -4.209 2.56e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2953.4  on 4002  degrees of freedom
## AIC: 2997.4
##
## Number of Fisher Scoring iterations: 5
```

```
par(mfrow = c(2, 2))
plot(glmfit)
```



Indicator Variables categorize by Race

```
# According to our data formating in the upper procedure, in Race:
# 1 represents "white"
# 2 represents "black"
# 3 represents "others"
## A newdataset with "white" as reference

# Ensure race is a factor and not an ordered factor
bc_ref <- newbc |>
  mutate(race = factor(race, ordered = FALSE))

# Relevel to make white as reference
bc_ref <- bc_ref |>
  mutate(race = relevel(race, ref = 1))

## Run a SLR for race only
single_race = glm(status ~ race, family = binomial, bc_ref)

summary(single_race)
```

```
##
## Call:
## glm(formula = status ~ race, family = binomial, data = bc_ref)
```

```
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.73909    0.04801  36.221  < 2e-16 ***
## race2       -0.64505    0.14350  -4.495 6.95e-06 ***
## race3        0.42389    0.18997   2.231   0.0257 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 3418.9  on 4021  degrees of freedom
## AIC: 3424.9
##
## Number of Fisher Scoring iterations: 4
```

```r
## Run a MLR with race ref but without interaction terms
model_ref = glm(status ~ race + marital_status + t_stage + n_stage + differentiate +
                a_stage + estrogen_status + progesterone_status + reginol_node_positive + ln_tumor +
                sqrt_examined + age,
                data = bc_ref, family = binomial)
#model_ref
summary(model_ref)
```

```
##
## Call:
## glm(formula = status ~ race + marital_status + t_stage + n_stage +
##     differentiate + a_stage + estrogen_status + progesterone_status +
##     reginol_node_positive + ln_tumor + sqrt_examined + age, family = binomial,
##     data = bc_ref)
##
## Coefficients:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)              1.775787   0.587386   3.023 0.002501 **
## race2                   -0.522765   0.161744  -3.232 0.001229 **
## race3                    0.419131   0.202312   2.072 0.038293 *
## marital_status2         -0.209325   0.141735  -1.477 0.139709
## marital_status3         -0.140584   0.134542  -1.045 0.296064
## marital_status4         -0.222113   0.192496  -1.154 0.248558
## marital_status5         -0.867369   0.370116  -2.344 0.019104 *
## t_stage2                -0.372488   0.159129  -2.341 0.019243 *
## t_stage3                -0.471905   0.266764  -1.769 0.076894 .
## t_stage4                -1.025962   0.313035  -3.277 0.001047 **
## n_stage2                -0.474091   0.129288  -3.667 0.000245 ***
## n_stage3                -0.637101   0.237639  -2.681 0.007341 **
## differentiate2           0.386027   0.104898   3.680 0.000233 ***
## differentiate3           0.917457   0.192668   4.762 1.92e-06 ***
## differentiate4          -0.947095   0.531127  -1.783 0.074557 .
## a_stage1                 0.045211   0.265718   0.170 0.864894
## estrogen_status1         0.737828   0.177538   4.156 3.24e-05 ***
## progesterone_status1     0.588385   0.127499   4.615 3.93e-06 ***
## reginol_node_positive -0.074961   0.014984  -5.003 5.65e-07 ***
## ln_tumor                -0.055274   0.138631  -0.399 0.690103
```

```
## sqrt_examined          0.255997   0.049654   5.156 2.53e-07 ***
## age                   -0.023647   0.005618  -4.209 2.56e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2953.4  on 4002  degrees of freedom
## AIC: 2997.4
##
## Number of Fisher Scoring iterations: 5
```

```
## Run a logistic regression with race ref and with interaction terms
model_refinter = glm(status ~ race + marital_status + t_stage + n_stage + differentiate +
               a_stage + estrogen_status + progesterone_status + reginol_node_positive + ln_tumor +
               sqrt_examined + age +
                race*(marital_status + t_stage + n_stage + differentiate +
               a_stage + estrogen_status + progesterone_status + reginol_node_positive + ln_tumor +
               sqrt_examined + age),
               data = bc_ref, family = binomial)
#model_refinter
summary(model_refinter)
```

```
##
## Call:
## glm(formula = status ~ race + marital_status + t_stage + n_stage +
##     differentiate + a_stage + estrogen_status + progesterone_status +
##     reginol_node_positive + ln_tumor + sqrt_examined + age +
##     race * (marital_status + t_stage + n_stage + differentiate +
##         a_stage + estrogen_status + progesterone_status + reginol_node_positive +
##         ln_tumor + sqrt_examined + age), family = binomial, data = bc_ref)
##
## Coefficients: (1 not defined because of singularities)
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                   2.143663   0.663026   3.233 0.001224 **
## race2                        -3.268199   1.771947  -1.844 0.065123 .
## race3                         5.514563   3.122929   1.766 0.077424 .
## marital_status2              -0.183704   0.152054  -1.208 0.226988
## marital_status3               0.085036   0.158426   0.537 0.591437
## marital_status4              -0.055626   0.220307  -0.252 0.800660
## marital_status5              -0.799662   0.435399  -1.837 0.066266 .
## t_stage2                     -0.275236   0.176881  -1.556 0.119696
## t_stage3                     -0.295508   0.299330  -0.987 0.323529
## t_stage4                     -0.940666   0.342650  -2.745 0.006046 **
## n_stage2                     -0.567320   0.141733  -4.003 6.26e-05 ***
## n_stage3                     -0.843987   0.258302  -3.267 0.001085 **
## differentiate2                0.436042   0.115677   3.769 0.000164 ***
## differentiate3                1.011119   0.214291   4.718 2.38e-06 ***
## differentiate4               -0.948202   0.577004  -1.643 0.100317
## a_stage1                     -0.060677   0.293299  -0.207 0.836106
## estrogen_status1              0.806235   0.196393   4.105 4.04e-05 ***
## progesterone_status1          0.660775   0.138367   4.776 1.79e-06 ***
## reginol_node_positive        -0.065841   0.016154  -4.076 4.59e-05 ***
```

```
## ln_tumor                     -0.165689   0.159061  -1.042 0.297566
## sqrt_examined                 0.278198   0.054658   5.090 3.58e-07 ***
## age                          -0.027956   0.006220  -4.495 6.97e-06 ***
## race2:marital_status2        -0.231457   0.537505  -0.431 0.666750
## race3:marital_status2        -0.493298   0.712072  -0.693 0.488458
## race2:marital_status3        -1.145440   0.409405  -2.798 0.005145 **
## race3:marital_status3        -1.209396   0.612332  -1.975 0.048261 *
## race2:marital_status4        -0.440236   0.601871  -0.731 0.464507
## race3:marital_status4        -2.132622   0.838528  -2.543 0.010981 *
## race2:marital_status5         0.098692   1.175316   0.084 0.933080
## race3:marital_status5        -0.880739   1.347639  -0.654 0.513407
## race2:t_stage2               -0.465403   0.502263  -0.927 0.354128
## race3:t_stage2                0.437497   0.782923   0.559 0.576298
## race2:t_stage3               -0.703756   0.806589  -0.873 0.382931
## race3:t_stage3                1.603080   1.333557   1.202 0.229322
## race2:t_stage4                0.014416   1.193986   0.012 0.990367
## race3:t_stage4               -0.127448   1.726137  -0.074 0.941142
## race2:n_stage2                0.484228   0.476679   1.016 0.309707
## race3:n_stage2                1.082513   0.645862   1.676 0.093724 .
## race2:n_stage3                1.463405   0.897850   1.630 0.103123
## race3:n_stage3                2.525936   1.462710   1.727 0.084188 .
## race2:differentiate2         -0.208584   0.358607  -0.582 0.560802
## race3:differentiate2         -0.109563   0.465485  -0.235 0.813919
## race2:differentiate3         -0.381274   0.682640  -0.559 0.576483
## race3:differentiate3         -0.140078   0.835274  -0.168 0.866816
## race2:differentiate4         -0.724327   1.669867  -0.434 0.664460
## race3:differentiate4                NA         NA      NA       NA
## race2:a_stage1                1.903928   1.021605   1.864 0.062369 .
## race3:a_stage1               -1.581496   1.588021  -0.996 0.319303
## race2:estrogen_status1       -0.686042   0.595097  -1.153 0.248982
## race3:estrogen_status1        1.820519   0.981128   1.856 0.063520 .
## race2:progesterone_status1   -0.050826   0.451620  -0.113 0.910394
## race3:progesterone_status1   -2.784800   0.946246  -2.943 0.003251 **
## race2:reginol_node_positive  -0.121505   0.064782  -1.876 0.060712 .
## race3:reginol_node_positive  -0.153094   0.089011  -1.720 0.085442 .
## race2:ln_tumor                0.776264   0.361491   2.147 0.031762 *
## race3:ln_tumor               -1.194039   0.762242  -1.566 0.117236
## race2:sqrt_examined          -0.085330   0.168637  -0.506 0.612859
## race3:sqrt_examined          -0.162959   0.213679  -0.763 0.445681
## race2:age                     0.008341   0.019360   0.431 0.666599
## race3:age                     0.035269   0.024348   1.449 0.147466
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2898.0  on 3965  degrees of freedom
## AIC: 3016
##
## Number of Fisher Scoring iterations: 6
```

```
## Run a logistic regression with race ref and with interaction terms selected
model_inter = glm(status ~ race + marital_status + t_stage + n_stage + differentiate +
```

```
              a_stage + estrogen_status + progesterone_status + reginol_node_positive + ln_tumor +
              sqrt_examined + age +
               race*(marital_status + progesterone_status + ln_tumor),
              data = bc_ref, family = binomial)
#model_inter
summary(model_inter)
```

```
##
## Call:
## glm(formula = status ~ race + marital_status + t_stage + n_stage +
##     differentiate + a_stage + estrogen_status + progesterone_status +
##     reginol_node_positive + ln_tumor + sqrt_examined + age +
##     race * (marital_status + progesterone_status + ln_tumor),
##     family = binomial, data = bc_ref)
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                  1.882124   0.611049   3.080 0.002069 **
## race2                       -1.131478   0.754804  -1.499 0.133864
## race3                        3.214161   1.374949   2.338 0.019405 *
## marital_status2             -0.186741   0.151851  -1.230 0.218785
## marital_status3              0.086222   0.158014   0.546 0.585299
## marital_status4             -0.076745   0.219242  -0.350 0.726303
## marital_status5             -0.780653   0.435332  -1.793 0.072935 .
## t_stage2                    -0.338441   0.160266  -2.112 0.034708 *
## t_stage3                    -0.375302   0.269563  -1.392 0.163844
## t_stage4                    -0.973119   0.315838  -3.081 0.002063 **
## n_stage2                    -0.495290   0.130427  -3.797 0.000146 ***
## n_stage3                    -0.664599   0.239253  -2.778 0.005473 **
## differentiate2               0.405297   0.105478   3.842 0.000122 ***
## differentiate3               0.947648   0.194613   4.869 1.12e-06 ***
## differentiate4              -0.997840   0.537651  -1.856 0.063464 .
## a_stage1                     0.057824   0.268010   0.216 0.829180
## estrogen_status1             0.768781   0.180131   4.268 1.97e-05 ***
## progesterone_status1         0.684689   0.134874   5.077 3.84e-07 ***
## reginol_node_positive       -0.075918   0.015092  -5.030 4.89e-07 ***
## ln_tumor                    -0.125372   0.146813  -0.854 0.393129
## sqrt_examined                0.258396   0.049886   5.180 2.22e-07 ***
## age                         -0.024851   0.005663  -4.389 1.14e-05 ***
## race2:marital_status2       -0.128238   0.518941  -0.247 0.804820
## race3:marital_status2       -0.373279   0.702629  -0.531 0.595238
## race2:marital_status3       -1.109358   0.385796  -2.876 0.004034 **
## race3:marital_status3       -1.349766   0.576548  -2.341 0.019226 *
## race2:marital_status4       -0.427490   0.551410  -0.775 0.438182
## race3:marital_status4       -1.600358   0.671688  -2.383 0.017191 *
## race2:marital_status5       -0.542786   1.006774  -0.539 0.589795
## race3:marital_status5       -0.911159   1.284113  -0.710 0.477975
## race2:progesterone_status1  -0.516652   0.357042  -1.447 0.147887
## race3:progesterone_status1  -1.646000   0.561267  -2.933 0.003361 **
## race2:ln_tumor               0.436542   0.213238   2.047 0.040638 *
## race3:ln_tumor              -0.336268   0.352855  -0.953 0.340594
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2922.3  on 3990  degrees of freedom
## AIC: 2990.3
##
## Number of Fisher Scoring iterations: 5
```

- From the logistic regression for single race variable, we can see that the race group of black has a P-value of 6.95*10^(-6) and other race group has a P-value of 0.0257 both smaller than 0.05, so there are statistically significant difference between that to the reference of group white.
- From the logistic regression model without interaction terms, we can see that the AIC is around 2997.4 which is smaller than the original full model, when for both race2 and race3 we have a P-value smaller than 0.05 indicating significance, so we considering adding interaction terms.
- From the logistic regression model with race interaction terms added, we can see that the AIC is around 3016 which is getting larger, so we may have too many unnecessary interaction terms, and from the P-values we can see most the interaction covariates are insignificant except some terms in: race:marital_status, race:progesterone_status, race:ln_tumor.
- Therefore, we have the 3rd logistic regression model with race interaction terms selected, and we get a model with AIC of 2990.3 dropped sharply and the interaction term is included.

Step-wise: both direction/AiC

Step-wise for MLR without interaction term:

```r
set.seed(123)
# Full Model
full_model <- glm(status ~ race + marital_status + t_stage + n_stage + differentiate +
                  a_stage + estrogen_status + progesterone_status + reginol_node_positive +
                  ln_tumor + sqrt_examined + age,
                  data = newbc, family = binomial)

# Minimal Model (Intercept Only)
min_model <- glm(status ~ 1, data = newbc, family = binomial)

# Forward Selection
forward_model <- step(min_model, scope = list(lower = min_model, upper = full_model),
                      direction = "forward", trace = FALSE)

# Backward Elimination
backward_model <- step(full_model, direction = "backward", trace = FALSE)

# Both Directions
stepwise_model <- step(min_model, scope = list(lower = min_model, upper = full_model),
                       direction = "both", trace = FALSE)

# Print the summary of the chosen model
summary(forward_model)
```

```
##
```

```
## Call:
## glm(formula = status ~ n_stage + progesterone_status + differentiate +
##     t_stage + age + race + estrogen_status + sqrt_examined +
##     reginol_node_positive, family = binomial, data = newbc)
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)             1.623139   0.371232   4.372 1.23e-05 ***
## n_stage2               -0.474258   0.128697  -3.685 0.000229 ***
## n_stage3               -0.644148   0.234160  -2.751 0.005943 **
## progesterone_status1    0.600531   0.127305   4.717 2.39e-06 ***
## differentiate2          0.389412   0.104623   3.722 0.000198 ***
## differentiate3          0.908192   0.191600   4.740 2.14e-06 ***
## differentiate4         -0.954165   0.525800  -1.815 0.069571 .
## t_stage2               -0.429230   0.112954  -3.800 0.000145 ***
## t_stage3               -0.561433   0.148563  -3.779 0.000157 ***
## t_stage4               -1.122611   0.242936  -4.621 3.82e-06 ***
## age                    -0.024052   0.005443  -4.419 9.90e-06 ***
## race2                  -0.574227   0.158413  -3.625 0.000289 ***
## race3                   0.430601   0.201848   2.133 0.032901 *
## estrogen_status1        0.731594   0.176812   4.138 3.51e-05 ***
## sqrt_examined           0.259110   0.049645   5.219 1.80e-07 ***
## reginol_node_positive -0.076301   0.014939  -5.107 3.27e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2961.5  on 4008  degrees of freedom
## AIC: 2993.5
##
## Number of Fisher Scoring iterations: 5
```

```
# or summary(backward_model)
summary(backward_model)
```

```
##
## Call:
## glm(formula = status ~ race + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + reginol_node_positive +
##     sqrt_examined + age, family = binomial, data = newbc)
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)             1.623139   0.371232   4.372 1.23e-05 ***
## race2                  -0.574227   0.158413  -3.625 0.000289 ***
## race3                   0.430601   0.201848   2.133 0.032901 *
## t_stage2               -0.429230   0.112954  -3.800 0.000145 ***
## t_stage3               -0.561433   0.148563  -3.779 0.000157 ***
## t_stage4               -1.122611   0.242936  -4.621 3.82e-06 ***
## n_stage2               -0.474258   0.128697  -3.685 0.000229 ***
## n_stage3               -0.644148   0.234160  -2.751 0.005943 **
## differentiate2          0.389412   0.104623   3.722 0.000198 ***
```

```
## differentiate3         0.908192   0.191600   4.740 2.14e-06 ***
## differentiate4        -0.954165   0.525800  -1.815 0.069571 .
## estrogen_status1       0.731594   0.176812   4.138 3.51e-05 ***
## progesterone_status1   0.600531   0.127305   4.717 2.39e-06 ***
## reginol_node_positive -0.076301   0.014939  -5.107 3.27e-07 ***
## sqrt_examined          0.259110   0.049645   5.219 1.80e-07 ***
## age                   -0.024052   0.005443  -4.419 9.90e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2961.5  on 4008  degrees of freedom
## AIC: 2993.5
##
## Number of Fisher Scoring iterations: 5
```

```
# or summary(stepwise_model)
summary(stepwise_model)
```

```
##
## Call:
## glm(formula = status ~ n_stage + progesterone_status + differentiate +
##     t_stage + age + race + estrogen_status + sqrt_examined +
##     reginol_node_positive, family = binomial, data = newbc)
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)             1.623139   0.371232   4.372 1.23e-05 ***
## n_stage2               -0.474258   0.128697  -3.685 0.000229 ***
## n_stage3               -0.644148   0.234160  -2.751 0.005943 **
## progesterone_status1    0.600531   0.127305   4.717 2.39e-06 ***
## differentiate2          0.389412   0.104623   3.722 0.000198 ***
## differentiate3          0.908192   0.191600   4.740 2.14e-06 ***
## differentiate4         -0.954165   0.525800  -1.815 0.069571 .
## t_stage2               -0.429230   0.112954  -3.800 0.000145 ***
## t_stage3               -0.561433   0.148563  -3.779 0.000157 ***
## t_stage4               -1.122611   0.242936  -4.621 3.82e-06 ***
## age                    -0.024052   0.005443  -4.419 9.90e-06 ***
## race2                  -0.574227   0.158413  -3.625 0.000289 ***
## race3                   0.430601   0.201848   2.133 0.032901 *
## estrogen_status1        0.731594   0.176812   4.138 3.51e-05 ***
## sqrt_examined           0.259110   0.049645   5.219 1.80e-07 ***
## reginol_node_positive -0.076301   0.014939  -5.107 3.27e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2961.5  on 4008  degrees of freedom
## AIC: 2993.5
##
```

```
## Number of Fisher Scoring iterations: 5
```

From the both direction step-wise, the best model without interaction term has lowest AIC of 2993.5 is: status ~ n_stage + progesterone_status + differentiate + t_stage + age + race + estrogen_status + sqrt_examined + reginol_node_positive

Step-wise for MLR with interaction term:

```
# Full Model with Interaction Terms
full_interaction_model <- glm(status ~ race + marital_status + t_stage + n_stage + differentiate +
               a_stage + estrogen_status + progesterone_status + reginol_node_positive + ln_tumor +
               sqrt_examined + age +
                race*(marital_status + progesterone_status + ln_tumor),
                             data = bc_ref, family = binomial)

# Minimal Model (Intercept Only)
min_model <- glm(status ~ 1, data = bc_ref, family = binomial)

# Stepwise Selection (Forward, Backward, or Both)
stepwise_interaction_model <- step(min_model, scope = list(lower = min_model, upper = full_interaction_
                                  direction = "both", trace = FALSE)

# Print the summary of the chosen model
summary(stepwise_interaction_model)
```

```
##
## Call:
## glm(formula = status ~ n_stage + progesterone_status + differentiate +
##     t_stage + age + race + estrogen_status + sqrt_examined +
##     reginol_node_positive + marital_status + progesterone_status:race +
##     race:marital_status, family = binomial, data = bc_ref)
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                  1.570840   0.383329   4.098 4.17e-05 ***
## n_stage2                    -0.496361   0.129955  -3.819 0.000134 ***
## n_stage3                    -0.679178   0.236559  -2.871 0.004091 **
## progesterone_status1         0.687634   0.134627   5.108 3.26e-07 ***
## differentiate2               0.401059   0.105340   3.807 0.000140 ***
## differentiate3               0.952710   0.194356   4.902 9.49e-07 ***
## differentiate4              -0.947664   0.540209  -1.754 0.079387 .
## t_stage2                    -0.406468   0.113944  -3.567 0.000361 ***
## t_stage3                    -0.534698   0.149840  -3.568 0.000359 ***
## t_stage4                    -1.100569   0.245075  -4.491 7.10e-06 ***
## age                         -0.024541   0.005655  -4.340 1.43e-05 ***
## race2                        0.224318   0.383613   0.585 0.558716
## race3                        2.011663   0.542750   3.706 0.000210 ***
## estrogen_status1             0.769528   0.179823   4.279 1.87e-05 ***
## sqrt_examined                0.257377   0.049803   5.168 2.37e-07 ***
## reginol_node_positive       -0.075272   0.015097  -4.986 6.16e-07 ***
## marital_status2             -0.191812   0.151472  -1.266 0.205399
## marital_status3              0.078126   0.157546   0.496 0.619971
```

```
## marital_status4            -0.082890   0.218859  -0.379 0.704885
## marital_status5            -0.779425   0.434517  -1.794 0.072849 .
## progesterone_status1:race2 -0.465115   0.359360  -1.294 0.195566
## progesterone_status1:race3 -1.605449   0.549534  -2.921 0.003484 **
## race2:marital_status2      -0.036425   0.525651  -0.069 0.944755
## race3:marital_status2      -0.293014   0.695570  -0.421 0.673567
## race2:marital_status3      -1.051902   0.387355  -2.716 0.006616 **
## race3:marital_status3      -1.315085   0.567928  -2.316 0.020581 *
## race2:marital_status4      -0.421867   0.561169  -0.752 0.452193
## race3:marital_status4      -1.585759   0.660762  -2.400 0.016400 *
## race2:marital_status5      -0.519846   1.015055  -0.512 0.608556
## race3:marital_status5      -0.931811   1.284515  -0.725 0.468195
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2927.9  on 3994  degrees of freedom
## AIC: 2987.9
##
## Number of Fisher Scoring iterations: 5
```

From the both direction step-wise, the best model with interaction term has lowest AIC of 2987.9 is: status ~ n_stage + progesterone_status + differentiate + t_stage + age + race + estrogen_status + sqrt_examined + reginol_node_positive + marital_status + progesterone_status:race + race:marital_status.

VIF

```
# Calculate VIF for the model without interaction
vif_result_bic <- vif(stepwise_model)
print(vif_result_bic)
```

```
##                           GVIF Df GVIF^(1/(2*Df))
## n_stage                3.835937  2        1.399484
## progesterone_status    1.426727  1        1.194457
## differentiate          1.112306  3        1.017897
## t_stage                1.098462  3        1.015775
## age                    1.042599  1        1.021077
## race                   1.020862  2        1.005175
## estrogen_status        1.471867  1        1.213205
## sqrt_examined          1.423764  1        1.193216
## reginol_node_positive 4.073707  1        2.018343
```

```
# Calculate VIF for the interaction model
vif_result_aic <- vif(stepwise_interaction_model, type = 'predictor')
```

```
## Warning in vif.lm(stepwise_interaction_model, type = "predictor"): type = 'predictor' is available or
##   type = 'terms' will be used
```

```r
print(vif_result_aic)
```

```
##                              GVIF Df GVIF^(1/(2*Df))
## n_stage                  3.884443  2        1.403887
## progesterone_status      1.565824  1        1.251329
## differentiate            1.133420  3        1.021093
## t_stage                  1.114696  3        1.018262
## age                      1.120454  1        1.058515
## race                    43.194842  2        2.563646
## estrogen_status          1.476767  1        1.215223
## sqrt_examined            1.426509  1        1.194365
## reginol_node_positive    4.094125  1        2.023394
## marital_status           3.129525  4        1.153280
## progesterone_status:race 24.566818  2        2.226318
## race:marital_status      14.850111  8        1.183677
```

Partial Test

Partial Test for binary Y

```r
# Model without Interaction Terms
model_no_interaction <- glm(status ~ n_stage + progesterone_status + differentiate + t_stage +
                            age + race + estrogen_status + sqrt_examined + reginol_node_positive,
                            data = newbc, family = binomial)

# Model with Selected Interaction Terms
model_with_interaction <- glm(status ~ n_stage + progesterone_status + differentiate + t_stage +
                              age + race + estrogen_status + sqrt_examined + reginol_node_positive +
                              marital_status + progesterone_status:race + race:marital_status,
                              data = bc_ref, family = binomial)

# Partial Test
anova(model_no_interaction, model_with_interaction, test = "Chisq")
```

```
## Analysis of Deviance Table
##
## Model 1: status ~ n_stage + progesterone_status + differentiate + t_stage +
##     age + race + estrogen_status + sqrt_examined + reginol_node_positive
## Model 2: status ~ n_stage + progesterone_status + differentiate + t_stage +
##     age + race + estrogen_status + sqrt_examined + reginol_node_positive +
##     marital_status + progesterone_status:race + race:marital_status
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      4008     2961.5
## 2      3994     2927.9 14   33.565 0.002386 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The p-value is below the common alpha level of 0.05, indicating that the inclusion of interaction terms in the model significantly improves the fit compared to the model without interaction terms. This result supports selecting the model with interaction terms, as it provides a better explanation of the variation in the response variable (status).

global F test for binary Y

```
anova_result1 <- anova(model_with_interaction)
print(anova_result1)
```

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: status
##
## Terms added sequentially (first to last)
##
##
##                           Df Deviance Resid. Df Resid. Dev
## NULL                                       4023     3444.7
## n_stage                    2  230.650      4021     3214.0
## progesterone_status        1   85.373      4020     3128.7
## differentiate              3   43.629      4017     3085.0
## t_stage                    3   27.748      4014     3057.3
## age                        1   19.891      4013     3037.4
## race                       2   18.417      4011     3019.0
## estrogen_status            1   15.880      4010     3003.1
## sqrt_examined              1   15.282      4009     2987.8
## reginol_node_positive      1   26.334      4008     2961.5
## marital_status             4    7.907      4004     2953.6
## progesterone_status:race   2    9.500      4002     2944.1
## race:marital_status        8   16.158      3994     2927.9
```

```
summary(model_with_interaction)
```

```
##
## Call:
## glm(formula = status ~ n_stage + progesterone_status + differentiate +
##     t_stage + age + race + estrogen_status + sqrt_examined +
##     reginol_node_positive + marital_status + progesterone_status:race +
##     race:marital_status, family = binomial, data = bc_ref)
##
## Coefficients:
##                             Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 1.570840   0.383329   4.098 4.17e-05 ***
## n_stage2                   -0.496361   0.129955  -3.819 0.000134 ***
## n_stage3                   -0.679178   0.236559  -2.871 0.004091 **
## progesterone_status1        0.687634   0.134627   5.108 3.26e-07 ***
## differentiate2              0.401059   0.105340   3.807 0.000140 ***
## differentiate3              0.952710   0.194356   4.902 9.49e-07 ***
## differentiate4             -0.947664   0.540209  -1.754 0.079387 .
## t_stage2                   -0.406468   0.113944  -3.567 0.000361 ***
## t_stage3                   -0.534698   0.149840  -3.568 0.000359 ***
## t_stage4                   -1.100569   0.245075  -4.491 7.10e-06 ***
## age                        -0.024541   0.005655  -4.340 1.43e-05 ***
## race2                       0.224318   0.383613   0.585 0.558716
```

```
## race3                         2.011663   0.542750   3.706 0.000210 ***
## estrogen_status1              0.769528   0.179823   4.279 1.87e-05 ***
## sqrt_examined                 0.257377   0.049803   5.168 2.37e-07 ***
## reginol_node_positive        -0.075272   0.015097  -4.986 6.16e-07 ***
## marital_status2              -0.191812   0.151472  -1.266 0.205399
## marital_status3               0.078126   0.157546   0.496 0.619971
## marital_status4              -0.082890   0.218859  -0.379 0.704885
## marital_status5              -0.779425   0.434517  -1.794 0.072849 .
## progesterone_status1:race2 -0.465115   0.359360  -1.294 0.195566
## progesterone_status1:race3 -1.605449   0.549534  -2.921 0.003484 **
## race2:marital_status2        -0.036425   0.525651  -0.069 0.944755
## race3:marital_status2        -0.293014   0.695570  -0.421 0.673567
## race2:marital_status3        -1.051902   0.387355  -2.716 0.006616 **
## race3:marital_status3        -1.315085   0.567928  -2.316 0.020581 *
## race2:marital_status4        -0.421867   0.561169  -0.752 0.452193
## race3:marital_status4        -1.585759   0.660762  -2.400 0.016400 *
## race2:marital_status5        -0.519846   1.015055  -0.512 0.608556
## race3:marital_status5        -0.931811   1.284515  -0.725 0.468195
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2927.9  on 3994  degrees of freedom
## AIC: 2987.9
##
## Number of Fisher Scoring iterations: 5
```

With p significant p value, we have enough evidence to show that the model performs well, which is status ~ n_stage + progesterone_status + differentiate + t_stage + age + race + estrogen_status + sqrt_examined + reginol_node_positive + marital_status + progesterone_status:race + race:marital_status

Criterion procedures

Model with Interaction terms

```
aic_selected_bin_model1 <- stepAIC(model_with_interaction, direction = "both")
```

```
## Start:  AIC=2987.91
## status ~ n_stage + progesterone_status + differentiate + t_stage +
##     age + race + estrogen_status + sqrt_examined + reginol_node_positive +
##     marital_status + progesterone_status:race + race:marital_status
##
##                             Df Deviance    AIC
## <none>                           2927.9 2987.9
## - race:marital_status        8   2944.1 2988.1
## - progesterone_status:race   2   2939.1 2995.1
## - n_stage                    2   2943.2 2999.2
## - estrogen_status            1   2946.0 3004.0
## - age                        1   2947.1 3005.1
```

```
## - t_stage                   3   2956.0 3010.0
## - reginol_node_positive     1   2953.0 3011.0
## - sqrt_examined             1   2955.0 3013.0
## - differentiate             3   2963.2 3017.2
```

```
summary(aic_selected_bin_model1)
```

```
##
## Call:
## glm(formula = status ~ n_stage + progesterone_status + differentiate +
##     t_stage + age + race + estrogen_status + sqrt_examined +
##     reginol_node_positive + marital_status + progesterone_status:race +
##     race:marital_status, family = binomial, data = bc_ref)
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                  1.570840   0.383329   4.098 4.17e-05 ***
## n_stage2                    -0.496361   0.129955  -3.819 0.000134 ***
## n_stage3                    -0.679178   0.236559  -2.871 0.004091 **
## progesterone_status1         0.687634   0.134627   5.108 3.26e-07 ***
## differentiate2               0.401059   0.105340   3.807 0.000140 ***
## differentiate3               0.952710   0.194356   4.902 9.49e-07 ***
## differentiate4              -0.947664   0.540209  -1.754 0.079387 .
## t_stage2                    -0.406468   0.113944  -3.567 0.000361 ***
## t_stage3                    -0.534698   0.149840  -3.568 0.000359 ***
## t_stage4                    -1.100569   0.245075  -4.491 7.10e-06 ***
## age                         -0.024541   0.005655  -4.340 1.43e-05 ***
## race2                        0.224318   0.383613   0.585 0.558716
## race3                        2.011663   0.542750   3.706 0.000210 ***
## estrogen_status1             0.769528   0.179823   4.279 1.87e-05 ***
## sqrt_examined                0.257377   0.049803   5.168 2.37e-07 ***
## reginol_node_positive       -0.075272   0.015097  -4.986 6.16e-07 ***
## marital_status2             -0.191812   0.151472  -1.266 0.205399
## marital_status3              0.078126   0.157546   0.496 0.619971
## marital_status4             -0.082890   0.218859  -0.379 0.704885
## marital_status5             -0.779425   0.434517  -1.794 0.072849 .
## progesterone_status1:race2 -0.465115   0.359360  -1.294 0.195566
## progesterone_status1:race3 -1.605449   0.549534  -2.921 0.003484 **
## race2:marital_status2       -0.036425   0.525651  -0.069 0.944755
## race3:marital_status2       -0.293014   0.695570  -0.421 0.673567
## race2:marital_status3       -1.051902   0.387355  -2.716 0.006616 **
## race3:marital_status3       -1.315085   0.567928  -2.316 0.020581 *
## race2:marital_status4       -0.421867   0.561169  -0.752 0.452193
## race3:marital_status4       -1.585759   0.660762  -2.400 0.016400 *
## race2:marital_status5       -0.519846   1.015055  -0.512 0.608556
## race3:marital_status5       -0.931811   1.284515  -0.725 0.468195
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2927.9  on 3994  degrees of freedom
## AIC: 2987.9
```

```
##
## Number of Fisher Scoring iterations: 5
```

```
bic_selected_bin_model1 <- stepAIC(model_with_interaction, direction = "both", family = binomial, k = lo
```

```
## Start:  AIC=3176.91
## status ~ n_stage + progesterone_status + differentiate + t_stage +
##     age + race + estrogen_status + sqrt_examined + reginol_node_positive +
##     marital_status + progesterone_status:race + race:marital_status
##
##                             Df Deviance    AIC
## - race:marital_status        8   2944.1 3126.7
## - progesterone_status:race   2   2939.1 3171.5
## - n_stage                    2   2943.2 3175.6
## <none>                           2927.9 3176.9
## - t_stage                    3   2956.0 3180.1
## - estrogen_status            1   2946.0 3186.7
## - differentiate              3   2963.2 3187.3
## - age                        1   2947.1 3187.8
## - reginol_node_positive      1   2953.0 3193.7
## - sqrt_examined              1   2955.0 3195.7
##
## Step:  AIC=3126.67
## status ~ n_stage + progesterone_status + differentiate + t_stage +
##     age + race + estrogen_status + sqrt_examined + reginol_node_positive +
##     marital_status + progesterone_status:race
##
##                             Df Deviance    AIC
## - marital_status             4   2952.3 3101.7
## - progesterone_status:race   2   2953.6 3119.6
## - n_stage                    2   2957.9 3123.9
## <none>                           2944.1 3126.7
## - t_stage                    3   2973.0 3130.7
## - differentiate              3   2977.7 3135.4
## - estrogen_status            1   2962.7 3137.0
## - age                        1   2962.9 3137.2
## - reginol_node_positive      1   2970.2 3144.5
## - sqrt_examined              1   2971.1 3145.4
## + race:marital_status        8   2927.9 3176.9
##
## Step:  AIC=3101.69
## status ~ n_stage + progesterone_status + differentiate + t_stage +
##     age + race + estrogen_status + sqrt_examined + reginol_node_positive +
##     progesterone_status:race
##
##                             Df Deviance    AIC
## - progesterone_status:race   2   2961.5 3094.3
## - n_stage                    2   2966.0 3098.8
## <none>                           2952.3 3101.7
## - t_stage                    3   2982.2 3106.7
## - differentiate              3   2985.8 3110.3
## - estrogen_status            1   2970.7 3111.8
## - age                        1   2973.1 3114.2
## - reginol_node_positive      1   2979.5 3120.6
```

```
## - sqrt_examined             1   2980.1 3121.2
## + marital_status            4   2944.1 3126.7
##
## Step:  AIC=3094.28
## status ~ n_stage + progesterone_status + differentiate + t_stage +
##     age + race + estrogen_status + sqrt_examined + reginol_node_positive
##
##                            Df Deviance    AIC
## - n_stage                   2   2975.7 3091.9
## <none>                          2961.5 3094.3
## - race                      2   2980.3 3096.5
## - t_stage                   3   2992.1 3100.0
## + progesterone_status:race  2   2952.3 3101.7
## - estrogen_status           1   2978.4 3102.9
## - differentiate             3   2995.1 3103.0
## - age                       1   2981.4 3105.9
## - progesterone_status       1   2982.6 3107.1
## - reginol_node_positive     1   2987.8 3112.3
## - sqrt_examined             1   2989.1 3113.6
## + marital_status            4   2953.6 3119.6
##
## Step:  AIC=3091.86
## status ~ progesterone_status + differentiate + t_stage + age +
##     race + estrogen_status + sqrt_examined + reginol_node_positive
##
##                            Df Deviance    AIC
## <none>                          2975.7 3091.9
## + n_stage                   2   2961.5 3094.3
## - race                      2   2995.5 3095.1
## + progesterone_status:race  2   2966.0 3098.8
## - estrogen_status           1   2993.4 3101.3
## - age                       1   2995.6 3103.5
## - differentiate             3   3012.4 3103.7
## - t_stage                   3   3013.8 3105.1
## - progesterone_status       1   2997.5 3105.4
## - sqrt_examined             1   3002.0 3109.9
## + marital_status            4   2967.9 3117.3
## - reginol_node_positive     1   3128.6 3236.5
```

```
summary(bic_selected_bin_model1)
```

```
##
## Call:
## glm(formula = status ~ progesterone_status + differentiate +
##     t_stage + age + race + estrogen_status + sqrt_examined +
##     reginol_node_positive, family = binomial, data = bc_ref)
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)           1.597330   0.369903   4.318 1.57e-05 ***
## progesterone_status1  0.610172   0.126822   4.811 1.50e-06 ***
## differentiate2        0.408222   0.104130   3.920 8.84e-05 ***
## differentiate3        0.949277   0.191071   4.968 6.76e-07 ***
## differentiate4       -0.925654   0.516388  -1.793 0.073044 .
```

```
## t_stage2              -0.476223   0.112076  -4.249 2.15e-05 ***
## t_stage3              -0.636738   0.147043  -4.330 1.49e-05 ***
## t_stage4              -1.211832   0.241560  -5.017 5.26e-07 ***
## age                   -0.024010   0.005429  -4.422 9.76e-06 ***
## race2                 -0.595527   0.157330  -3.785 0.000154 ***
## race3                  0.425009   0.201922   2.105 0.035307 *
## estrogen_status1       0.744754   0.175621   4.241 2.23e-05 ***
## sqrt_examined          0.249258   0.048899   5.097 3.44e-07 ***
## reginol_node_positive -0.108237   0.008844 -12.239  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2975.7  on 4010  degrees of freedom
## AIC: 3003.7
##
## Number of Fisher Scoring iterations: 5
```

In the interaction model, the AIC selected model is status ~ race + marital_status + t_stage + n_stage + differentiate + estrogen_status + progesterone_status + reginol_node_positive + ln_tumor + sqrt_examined + age + race:marital_status + race:progesterone_status + race:ln_tumor.

The BIC selected model is status ~ race + differentiate + estrogen_status + progesterone_status + reginol_node_positive + ln_tumor + sqrt_examined + age.

Model without Interaction Terms

```
aic_selected_bin_model2 <- stepAIC(model_no_interaction, direction = "both")
```

```
## Start:  AIC=2993.48
## status ~ n_stage + progesterone_status + differentiate + t_stage +
##     age + race + estrogen_status + sqrt_examined + reginol_node_positive
##
##                          Df Deviance    AIC
## <none>                        2961.5 2993.5
## - n_stage                 2   2975.7 3003.7
## - race                    2   2980.3 3008.3
## - estrogen_status         1   2978.4 3008.4
## - age                     1   2981.4 3011.4
## - progesterone_status     1   2982.6 3012.6
## - reginol_node_positive   1   2987.8 3017.8
## - t_stage                 3   2992.1 3018.1
## - sqrt_examined           1   2989.1 3019.1
## - differentiate           3   2995.1 3021.1
```

```
summary(aic_selected_bin_model2)
```

```
##
## Call:
```

```
## glm(formula = status ~ n_stage + progesterone_status + differentiate +
##     t_stage + age + race + estrogen_status + sqrt_examined +
##     reginol_node_positive, family = binomial, data = newbc)
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)             1.623139   0.371232   4.372 1.23e-05 ***
## n_stage2               -0.474258   0.128697  -3.685 0.000229 ***
## n_stage3               -0.644148   0.234160  -2.751 0.005943 **
## progesterone_status1    0.600531   0.127305   4.717 2.39e-06 ***
## differentiate2          0.389412   0.104623   3.722 0.000198 ***
## differentiate3          0.908192   0.191600   4.740 2.14e-06 ***
## differentiate4         -0.954165   0.525800  -1.815 0.069571 .
## t_stage2               -0.429230   0.112954  -3.800 0.000145 ***
## t_stage3               -0.561433   0.148563  -3.779 0.000157 ***
## t_stage4               -1.122611   0.242936  -4.621 3.82e-06 ***
## age                    -0.024052   0.005443  -4.419 9.90e-06 ***
## race2                  -0.574227   0.158413  -3.625 0.000289 ***
## race3                   0.430601   0.201848   2.133 0.032901 *
## estrogen_status1        0.731594   0.176812   4.138 3.51e-05 ***
## sqrt_examined           0.259110   0.049645   5.219 1.80e-07 ***
## reginol_node_positive -0.076301   0.014939  -5.107 3.27e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2961.5  on 4008  degrees of freedom
## AIC: 2993.5
##
## Number of Fisher Scoring iterations: 5
```

```
bic_selected_bin_model2 <- stepAIC(model_no_interaction, direction = "both", family = binomial, k = log
```

```
## Start:  AIC=3094.28
## status ~ n_stage + progesterone_status + differentiate + t_stage +
##     age + race + estrogen_status + sqrt_examined + reginol_node_positive
##
##                          Df Deviance    AIC
## - n_stage                 2   2975.7 3091.9
## <none>                        2961.5 3094.3
## - race                    2   2980.3 3096.5
## - t_stage                 3   2992.1 3100.0
## - estrogen_status         1   2978.4 3102.9
## - differentiate           3   2995.1 3103.0
## - age                     1   2981.4 3105.9
## - progesterone_status     1   2982.6 3107.1
## - reginol_node_positive   1   2987.8 3112.3
## - sqrt_examined           1   2989.1 3113.6
##
## Step:  AIC=3091.86
## status ~ progesterone_status + differentiate + t_stage + age +
##     race + estrogen_status + sqrt_examined + reginol_node_positive
```

```
##
##                          Df Deviance    AIC
## <none>                        2975.7 3091.9
## + n_stage                 2   2961.5 3094.3
## - race                    2   2995.5 3095.1
## - estrogen_status         1   2993.4 3101.3
## - age                     1   2995.6 3103.5
## - differentiate           3   3012.4 3103.7
## - t_stage                 3   3013.8 3105.1
## - progesterone_status     1   2997.5 3105.4
## - sqrt_examined           1   3002.0 3109.9
## - reginol_node_positive   1   3128.6 3236.5
```

```
summary(bic_selected_bin_model2)
```

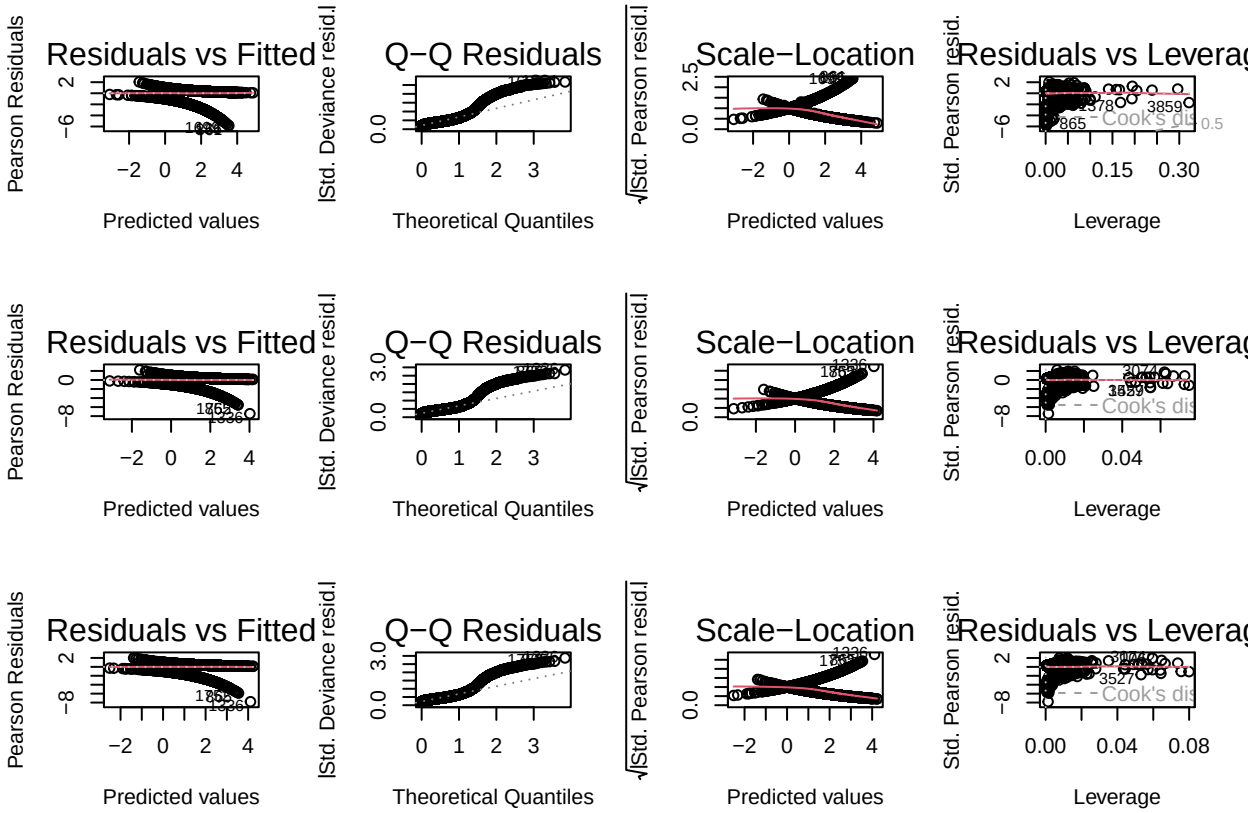
```
##
## Call:
## glm(formula = status ~ progesterone_status + differentiate +
##     t_stage + age + race + estrogen_status + sqrt_examined +
##     reginol_node_positive, family = binomial, data = newbc)
##
## Coefficients:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)              1.597330   0.369903   4.318 1.57e-05 ***
## progesterone_status1     0.610172   0.126822   4.811 1.50e-06 ***
## differentiate2           0.408222   0.104130   3.920 8.84e-05 ***
## differentiate3           0.949277   0.191071   4.968 6.76e-07 ***
## differentiate4          -0.925654   0.516388  -1.793 0.073044 .
## t_stage2                -0.476223   0.112076  -4.249 2.15e-05 ***
## t_stage3                -0.636738   0.147043  -4.330 1.49e-05 ***
## t_stage4                -1.211832   0.241560  -5.017 5.26e-07 ***
## age                     -0.024010   0.005429  -4.422 9.76e-06 ***
## race2                   -0.595527   0.157330  -3.785 0.000154 ***
## race3                    0.425009   0.201922   2.105 0.035307 *
## estrogen_status1         0.744754   0.175621   4.241 2.23e-05 ***
## sqrt_examined            0.249258   0.048899   5.097 3.44e-07 ***
## reginol_node_positive -0.108237   0.008844 -12.239  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2975.7  on 4010  degrees of freedom
## AIC: 3003.7
##
## Number of Fisher Scoring iterations: 5
```

In the model without interaction, the AIC selected model is status ~ n_stage + progesterone_status + differentiate + t_stage + age + race + estrogen_status + sqrt_examined + reginol_node_positive, having a AIC value of 2961.5.

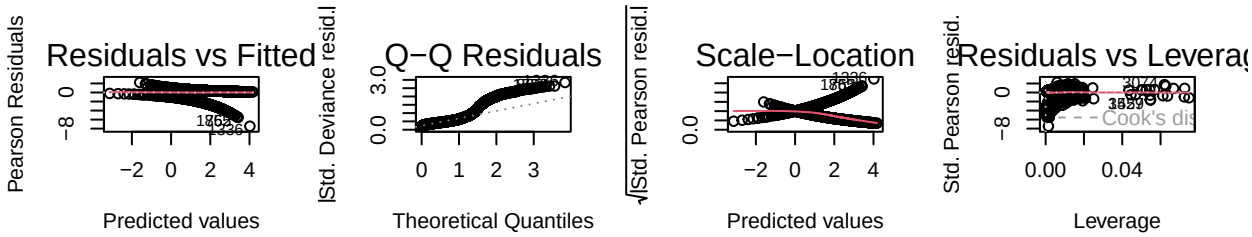
The BIC selected model is status ~ progesterone_status + differentiate + t_stage + age + race + estrogen_status + sqrt_examined + reginol_node_positive with AIC value of 3003.7.

Plots to check the model assumptions:

```
par(mfrow = c(3,4))
plot(aic_selected_bin_model1)
plot(bic_selected_bin_model1)
plot(aic_selected_bin_model2)
```



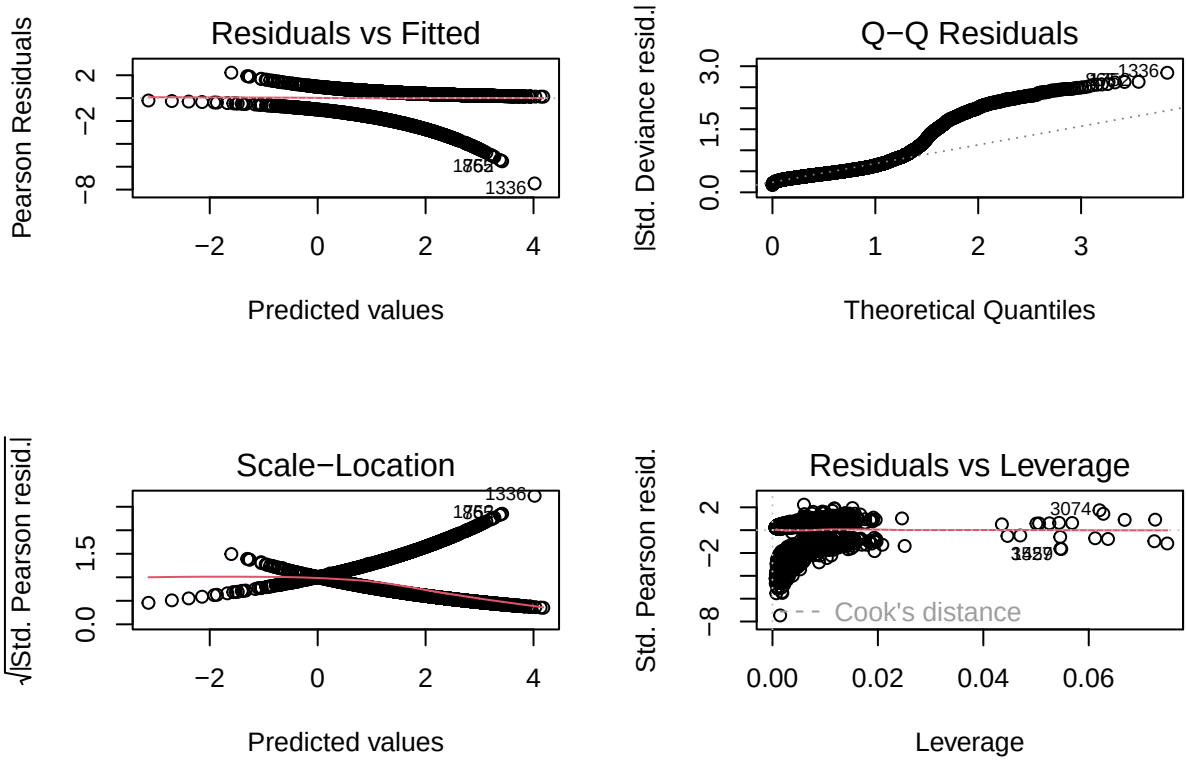

```
plot(bic_selected_bin_model2)
```




```
# final model assumption check
finalmodel <- glm(status ~ progesterone_status + differentiate + t_stage + age +
                  race + estrogen_status + sqrt_examined + reginol_node_positive,
                  data=bc_ref, family=binomial)
# check multicollinearity
vif(finalmodel)
```

```
##                            GVIF Df GVIF^(1/(2*Df))
## progesterone_status    1.427852  1        1.194928
## differentiate          1.104522  3        1.016707
## t_stage                1.070019  3        1.011343
## age                    1.042426  1        1.020993
## race                   1.019906  2        1.004940
## estrogen_status        1.473140  1        1.213730
## sqrt_examined          1.393878  1        1.180626
## reginol_node_positive 1.413722  1        1.189000
```

```
# Model diagnostics - Plotting to check for influential outliers, equal variance
par(mfrow = c(2, 2))
plot(finalmodel)
```




```
# Compute AUC for model assessment
roc_result <- roc(bc_ref$status, fitted(finalmodel))
```

```
## Setting levels: control = 0, case = 1
```

```
## Setting direction: controls < cases
```

```
auc_result <- auc(roc_result)
print(auc_result)
```

```
## Area under the curve: 0.7499
```

For the final model: The diagnostic charts for the logistic regression model imply that the assumptions are largely met. The residuals versus fitted values plot shows a pattern that could hint at some non-linearity, but it's subtle. Few outliers are suggested by slight departures from the expected line in the tails of the normal Q-Q plot. The scale-location plot suggests consistent variance across the data. While the residuals versus leverage plot points to a few outliers, these do not appear to drastically influence the model's predictions. VIF values also suggest that the predictors in the final model are relatively independent of each other. An Area Under the Receiver Operating Characteristic (ROC) Curve (AUC) of 0.7499 indicates that the logistic regression model has good discriminative ability.

Cross Validation

```r
y <- bc_ref[["status"]] # Target column
trainIndex <- caret::createDataPartition(y, p = 0.9, list = FALSE)

# Create training and testing sets
train=bc_ref[trainIndex,]
test=bc_ref[-trainIndex,]
head(train)
```

```
## # A tibble: 6 x 15
##     age race  marital_status t_stage n_stage x6th_stage differentiate grade
##   <dbl> <fct> <fct>          <fct>   <fct>   <fct>      <fct>         <fct>
## 1    68 1     1              1       1       1          1             3
## 2    50 1     1              2       2       2          2             2
## 3    58 1     2              3       3       3          2             2
## 4    58 1     1              1       1       1          1             3
## 5    47 1     1              2       1       4          1             3
## 6    51 1     1              1       1       1          3             1
## # i 7 more variables: a_stage <fct>, estrogen_status <fct>,
## #   progesterone_status <fct>, reginol_node_positive <dbl>, status <dbl>,
## #   ln_tumor <dbl>, sqrt_examined <dbl>
```

```r
# Fit logistic regression model with cross-validation
set.seed(123)
train_control1 <- trainControl(method = "cv", number = 10, classProbs = TRUE)
formula1 <- formula(aic_selected_bin_model1$model)
cvmodel1 <- train(formula1, data = train, method = "glm", family = "binomial",
                  trControl = train_control1)
```

```
## Warning in train.default(x, y, weights = w, ...): You are trying to do
## regression and your outcome only has two possible values Are you trying to do
## classification? If so, use a 2 level factor as your outcome column.

## Warning in train.default(x, y, weights = w, ...): cannnot compute class
## probabilities for regression
```

```r
print(cvmodel1)
```

```
## Generalized Linear Model
##
## 3622 samples
##   10 predictor
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 3259, 3260, 3260, 3260, 3260, 3260, ...
## Resampling results:
##
##   RMSE       Rsquared   MAE
##   0.3371806  0.1317748  0.2243656
```

```r
fitted_model1 <- glm(formula1, data = train, family = "binomial")
yhat1 <- predict(fitted_model1, newdata = test, type = "response")
binary_predictions1 <- ifelse(yhat1 > 0.5, 1, 0)
confusionMatrix(factor(binary_predictions1), factor(test[["status"]]))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0   6   9
##          1  49 338
##
##                Accuracy : 0.8557
##                  95% CI : (0.8175, 0.8886)
##     No Information Rate : 0.8632
##     P-Value [Acc > NIR] : 0.6988
##
##                   Kappa : 0.1198
##
##  Mcnemar's Test P-Value : 3.04e-07
##
##             Sensitivity : 0.10909
##             Specificity : 0.97406
##          Pos Pred Value : 0.40000
##          Neg Pred Value : 0.87339
##              Prevalence : 0.13682
##          Detection Rate : 0.01493
##    Detection Prevalence : 0.03731
##       Balanced Accuracy : 0.54158
##
##        'Positive' Class : 0
##
```

RMSE = 0.3352855 Rsquared = 0.1364786 MAE = 0.2235504

Accuracy : 0.8433

```r
set.seed(123)
train_control2 <- trainControl(method = "cv", number = 10, classProbs = TRUE)
formula2 <- formula(bic_selected_bin_model1$model)
cvmodel2 <- train(formula2, data = train, method = "glm", family = "binomial",
                  trControl = train_control2)
```

```
## Warning in train.default(x, y, weights = w, ...): You are trying to do
## regression and your outcome only has two possible values Are you trying to do
## classification? If so, use a 2 level factor as your outcome column.
```

```
## Warning in train.default(x, y, weights = w, ...): cannnot compute class
## probabilities for regression
```

```r
print(cvmodel2)
```

```
## Generalized Linear Model
##
## 3622 samples
##    8 predictor
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 3259, 3260, 3260, 3260, 3260, 3260, ...
## Resampling results:
##
##   RMSE       Rsquared   MAE
##   0.3368148  0.1322284  0.2261111
```

```
fitted_model2 <- glm(formula2, data = train, family = "binomial")
yhat2 <- predict(fitted_model2, newdata = test, type = "response")
binary_predictions2 <- ifelse(yhat1 > 0.5, 1, 0)
confusionMatrix(factor(binary_predictions2), factor(test[["status"]]))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0   6   9
##          1  49 338
##
##                Accuracy : 0.8557
##                  95% CI : (0.8175, 0.8886)
##     No Information Rate : 0.8632
##     P-Value [Acc > NIR] : 0.6988
##
##                   Kappa : 0.1198
##
##  Mcnemar's Test P-Value : 3.04e-07
##
##             Sensitivity : 0.10909
##             Specificity : 0.97406
##          Pos Pred Value : 0.40000
##          Neg Pred Value : 0.87339
##              Prevalence : 0.13682
##          Detection Rate : 0.01493
##    Detection Prevalence : 0.03731
##       Balanced Accuracy : 0.54158
##
##        'Positive' Class : 0
##
```

RMSE = 0.3351174 Rsquared = 0.1362244 MAE = 0.2244595

Accuracy : 0.8433

```
set.seed(123)
train_control3 <- trainControl(method = "cv", number = 10, classProbs = TRUE)
formula3 <- formula(aic_selected_bin_model2$model)
```

```r
cvmodel3 <- train(formula3, data = train, method = "glm", family = "binomial",
                  trControl = train_control3)
```

```
## Warning in train.default(x, y, weights = w, ...): You are trying to do
## regression and your outcome only has two possible values Are you trying to do
## classification? If so, use a 2 level factor as your outcome column.
```

```
## Warning in train.default(x, y, weights = w, ...): cannnot compute class
## probabilities for regression
```

```r
print(cvmodel3)
```

```
## Generalized Linear Model
##
## 3622 samples
##    9 predictor
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 3259, 3260, 3260, 3260, 3260, 3260, ...
## Resampling results:
##
##   RMSE       Rsquared   MAE
##   0.3363876  0.1344513  0.2255846
```

```r
fitted_model3 <- glm(formula3, data = train, family = "binomial")
yhat3 <- predict(aic_selected_bin_model2, newdata = test, type = "response")
binary_predictions3 <- ifelse(yhat3 > 0.5, 1, 0)
confusionMatrix(factor(binary_predictions3), factor(test[["status"]]))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0   6   8
##          1  49 339
##
##                Accuracy : 0.8582
##                  95% CI : (0.8202, 0.8908)
##     No Information Rate : 0.8632
##     P-Value [Acc > NIR] : 0.6473
##
##                   Kappa : 0.1254
##
##  Mcnemar's Test P-Value : 1.17e-07
##
##             Sensitivity : 0.10909
##             Specificity : 0.97695
##          Pos Pred Value : 0.42857
##          Neg Pred Value : 0.87371
##              Prevalence : 0.13682
```

```
##          Detection Rate : 0.01493
##    Detection Prevalence : 0.03483
##       Balanced Accuracy : 0.54302
##
##        'Positive' Class : 0
##
```

RMSE = 0.3363186 Rsquared = 0.1288768 MAE = 0.2262781

Accuracy : 0.8507

```
set.seed(123)
train_control4 <- trainControl(method = "cv", number = 10, classProbs = TRUE)
formula4 <- formula(bic_selected_bin_model2$model)
cvmodel4 <- train(formula4, data = train, method = "glm", family = "binomial",
                  trControl = train_control4)
```

```
## Warning in train.default(x, y, weights = w, ...): You are trying to do
## regression and your outcome only has two possible values Are you trying to do
## classification? If so, use a 2 level factor as your outcome column.

## Warning in train.default(x, y, weights = w, ...): cannnot compute class
## probabilities for regression
```

```
print(cvmodel4)
```

```
## Generalized Linear Model
##
## 3622 samples
##    8 predictor
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 3259, 3260, 3260, 3260, 3260, 3260, ...
## Resampling results:
##
##   RMSE       Rsquared   MAE
##   0.3368148  0.1322284  0.2261111
```

```
fitted_model4 <- glm(formula4, data = train, family = "binomial")
yhat4 <- predict(bic_selected_bin_model2, newdata = test, type = "response")
binary_predictions4 <- ifelse(yhat4 > 0.5, 1, 0)
confusionMatrix(factor(binary_predictions4), factor(test[["status"]]))
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0   6  11
##          1  49 336
##
##                Accuracy : 0.8507
```

```
##                  95% CI : (0.8121, 0.8841)
##     No Information Rate : 0.8632
##     P-Value [Acc > NIR] : 0.7895
##
##                   Kappa : 0.1091
##
##  Mcnemar's Test P-Value : 1.782e-06
##
##             Sensitivity : 0.10909
##             Specificity : 0.96830
##          Pos Pred Value : 0.35294
##          Neg Pred Value : 0.87273
##              Prevalence : 0.13682
##          Detection Rate : 0.01493
##    Detection Prevalence : 0.04229
##       Balanced Accuracy : 0.53870
##
##        'Positive' Class : 0
##
```

RMSE = 0.3363186 Rsquared = 0.1288768 MAE = 0.2262781

Accuracy : 0.8507

3.0 transformation edited 3.1 interaction transformation ?? 3.2 partial test 3.3 diagnostic boxcox 4. Stepwise: forward/ backward /AIC 5. final model 6. model assumption (check multicolinearity (VIF)) 7. cross validation