

# 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
##
##
##
```

---

```

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

```

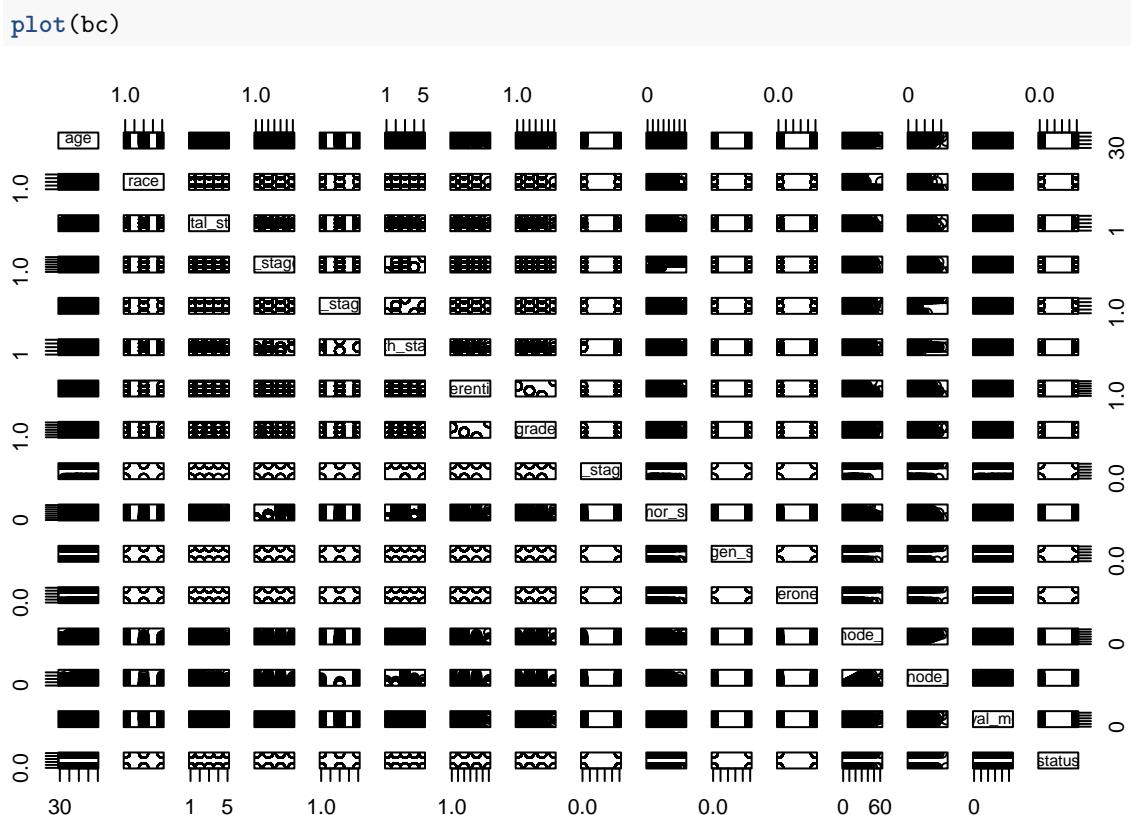
##  Max.   :1.0000   Max.   :140.00   Max.   :1.0000   Max.   :1.0000
##  regional_node_examined  reginol_node_positive survival_months      status
##  Min.   : 1.00          Min.   : 1.000          Min.   : 1.0          Min.   :0.0000
##  1st Qu.: 9.00          1st Qu.: 1.000          1st Qu.: 56.0        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



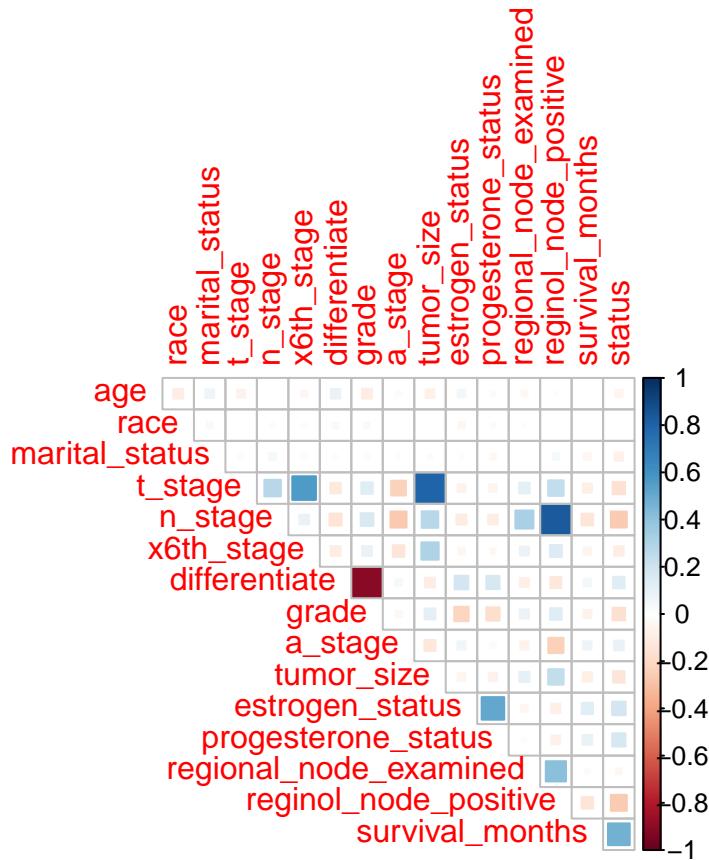
```
cor(bc) |>  
  knitr::kable(digits=4,caption="Correlation for all variables")
```

Table 1: Correlation for all variables

	age	race	marital	<u>stage</u>	<u>stage6</u>	<u>differentiate</u>	<u>grade</u>	<u>stage</u>	<u>noes</u>	<u>size</u>	<u>progesterone</u>	<u>status</u>	<u>regional</u>	<u>node</u>	<u>survival</u>	<u>months</u>
age	1.0000-	0.0755	-	0.0029	-	0.0932	-	0.0209	-	0.0598	-	-	-	0.0126	-	-
		0.0970		0.0669	0.0450		0.0993		0.0772		0.0213	0.0333			0.0094	0.0559
race	-	1.0000	0.0349	0.0036	0.0190	0.0173	-	0.0301	-	0.0071	-	-	0.0113	0.0090	-	0.0042
		0.0970					0.0336		0.0020		0.0425	0.0209			0.0025	
marital	<del>0.0755</del>	0.0349	0.0000	0.0257	0.0457	0.0221	-	0.0206	-	0.0207	-	-	0.0077	0.0443	-	-
							0.0117		0.0174		0.0198	0.0357			0.0487	0.0731
t_stage	-	0.0036	0.0257	1.0000	0.2770	0.5637	-	0.1315	-	0.8092	-	-	0.1141	0.2431	-	-
		0.0669					0.1102		0.2211		0.0610	0.0576			0.0857	0.1547
n_stage	0.0029	0.0190	0.0457	0.2770	0.0000	0.0939	-	0.1625	-	0.2779	-	-	0.3283	0.8381	-	-
							0.1488		0.2606		0.1020	0.0937			0.1396	0.2558
x6th_stage	0.0173	0.0221	0.5637	0.0939	0.0000	-	0.0972	-	0.3034	-	-	0.0826	0.1427	-	-	
		0.0450					0.0999		0.1372		0.0417	0.0309			0.0536	0.0919
differentiate	<del>0.0932</del>	-	-	-	-	1.0000	-	0.0437	-	0.1868	0.1758	-	-	0.0584	0.1342	
							0.0336	0.0117	0.1102	0.1488	0.0999	0.9083	0.0995	0.0834	0.1229	
grade	-	0.0300	0.0206	0.1310	0.1620	0.0972	-	1.0000	-	0.1194	-	-	0.0844	0.1353	-	-
		0.0993					0.9083		0.0395		0.2113	0.1799			0.0677	0.1614
a_stage	0.0209	-	-	-	-	0.0437	-	1.0000	-	0.0656	0.0265	-	-	0.0701	0.0966	
							0.0020	0.0174	0.2210	0.2600	0.1372	0.0395	0.1239	0.0690	0.2328	
tumor_size	0.0070	0.0207	0.8090	0.2770	0.3034	-	0.1194	-	1.0000	-	-	0.1044	0.2423	-	-	
		0.0772					0.0995		0.1239		0.0596	0.0699			0.0869	0.1342
estrogen	<del>0.0598</del>	-	-	-	-	0.1868	-	0.0656	-	1.0000	0.5133	-	-	0.1285	0.1847	
							0.0420	0.0198	0.0610	0.1020	0.0417	0.2113	0.0596	0.0448	0.0860	
progesterone_status	-	-	-	-	-	0.1758	-	0.0265	-	0.5133	1.0000	-	-	0.0960	0.1771	
							0.0210	0.0200	0.0357	0.0570	0.0930	0.0309	0.1799	0.0181	0.0781	
regional_node	<del>0.0110</del>	<del>0.0077</del>	<del>0.1140</del>	<del>0.3280</del>	<del>0.0826</del>	-	0.0844	-	0.1044	-	-	1.0000	0.4116	-	-	
							0.0333		0.0834		0.0690	0.0448	0.0181		0.0221	0.0348
reginol_survival	<del>0.0040</del>	<del>0.0090</del>	<del>0.0443</del>	<del>0.2430</del>	<del>0.8380</del>	<del>0.1427</del>	-	0.1353	-	0.2423	-	-	0.4116	1.0000	-	-
							0.1229		0.2328		0.0860	0.0781			0.1352	0.2566
survival_months	-	-	-	-	-	0.0584	-	0.0701	-	0.1285	0.0960	-	-	1.0000	0.4765	
							0.0094	0.0026	0.0487	0.0850	0.1390	0.0536	0.0677	0.0221	0.1352	
status	-	0.0042	-	-	-	-	0.1342	-	0.0966	-	0.1847	0.1771	-	-	0.4765	1.0000
		0.0559					0.0731	0.1540	0.2558	0.0919	0.1614	0.1342	-	0.0348	0.2566	

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"
)
```

*#plot6x6thstage*

```

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

```

*#plot7differentate*

```

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*

```

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*

```

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*

```

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

```

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

```

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

```

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)

```

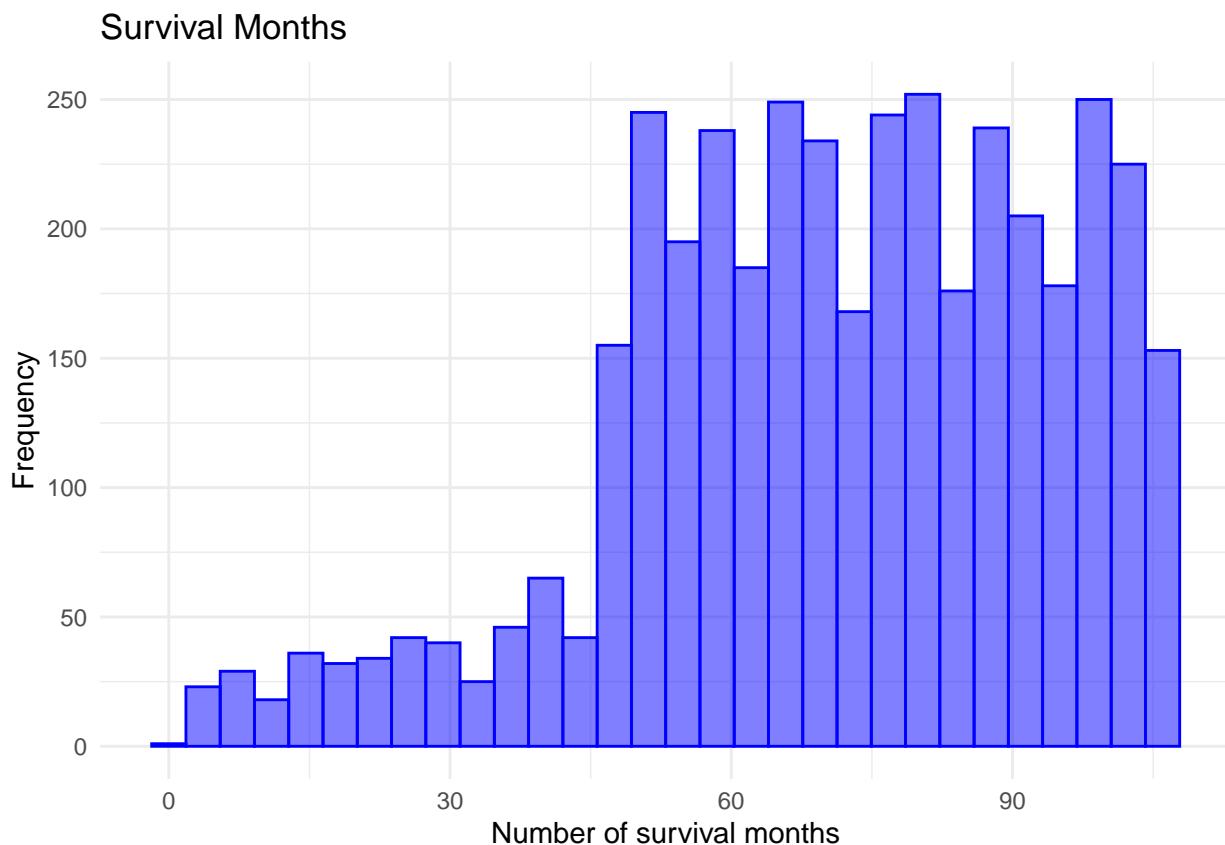
Y2 = status; (binary)

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`.

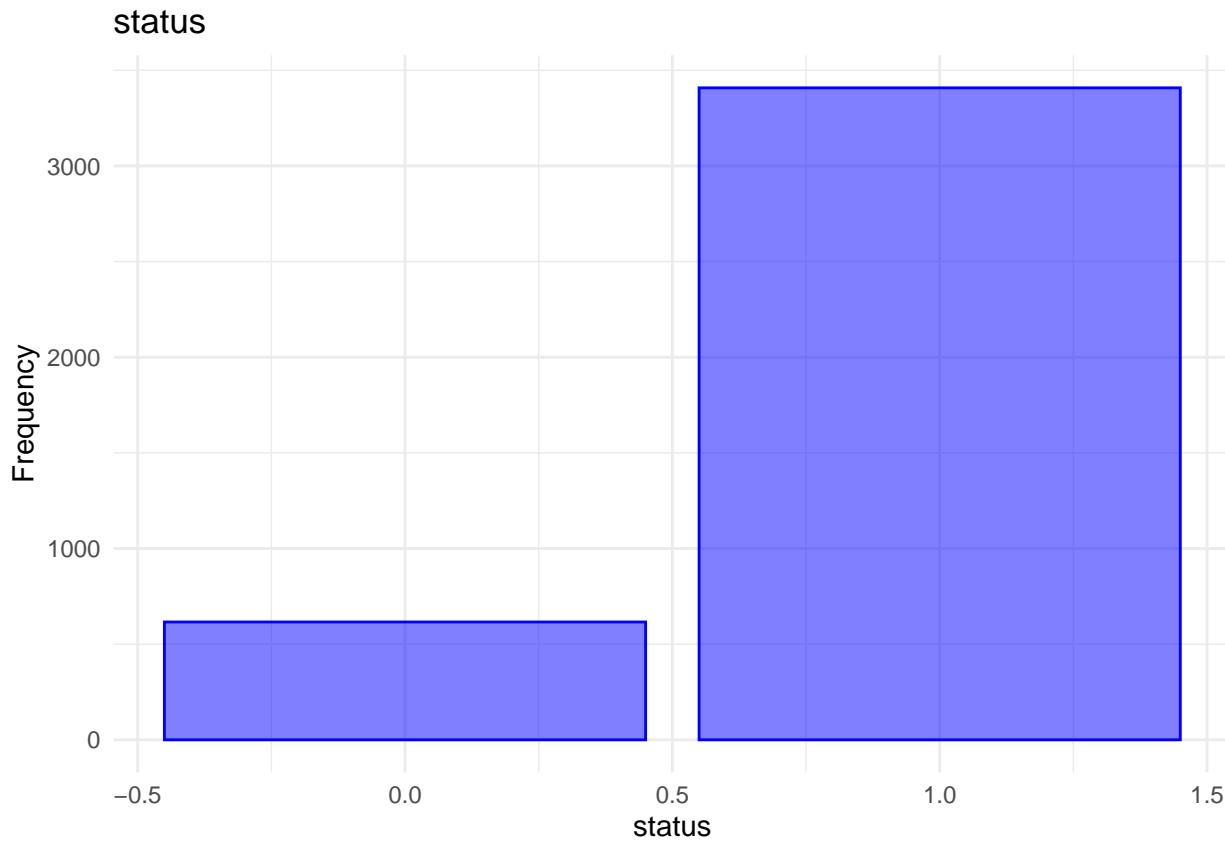


```

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

```

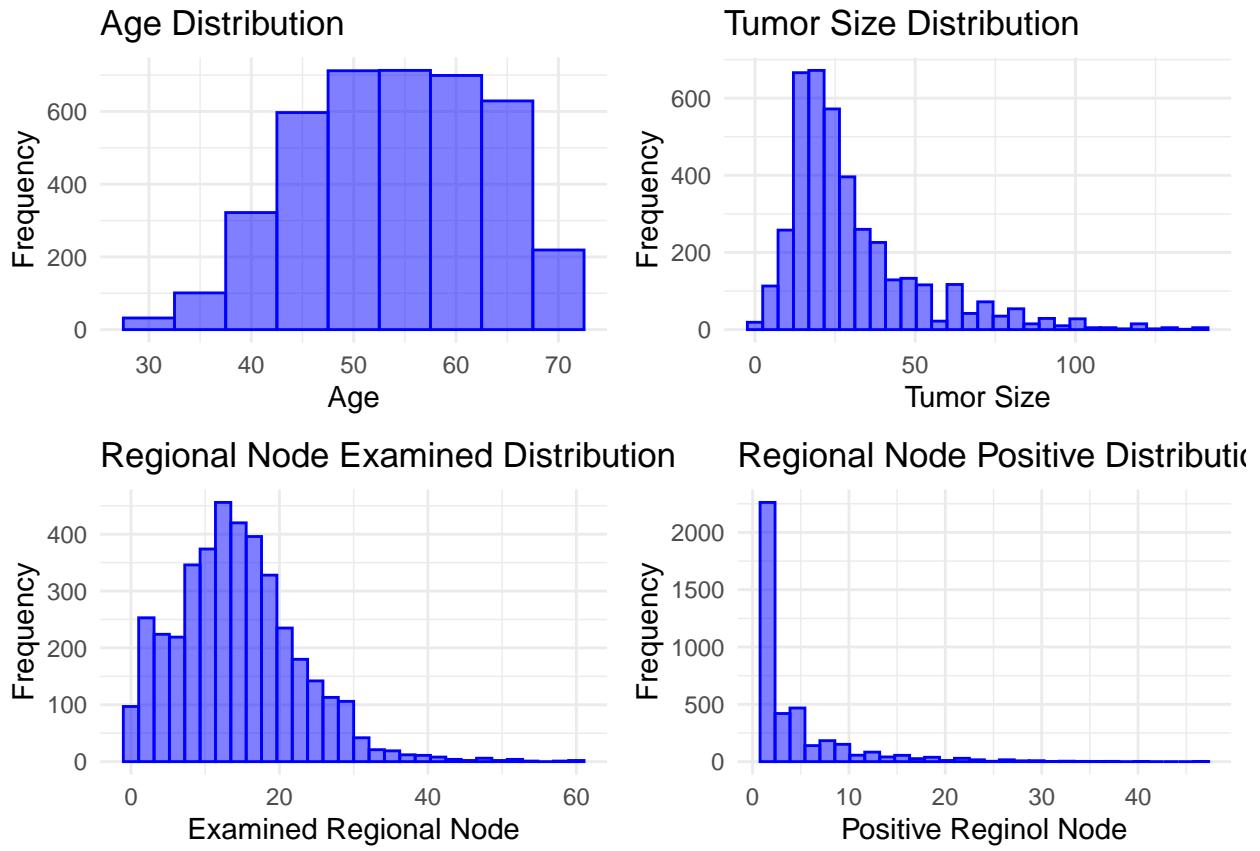
```
)  
plot16status
```



### Summarized plots for covariates

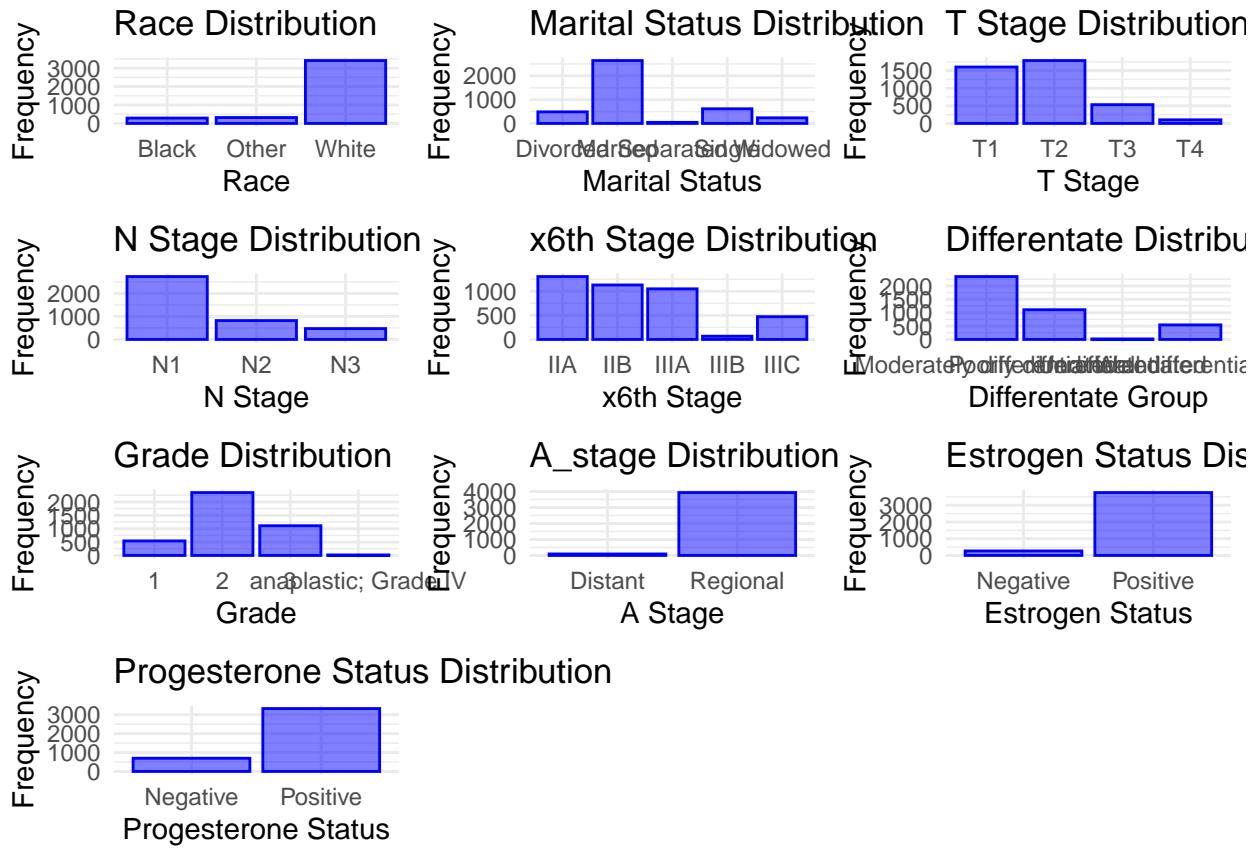
```
grid.arrange(plot1age, plot10tumorsize, plot13nodeexamined,  
            plot14nodepositive, ncol = 2)
```

```
## '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.

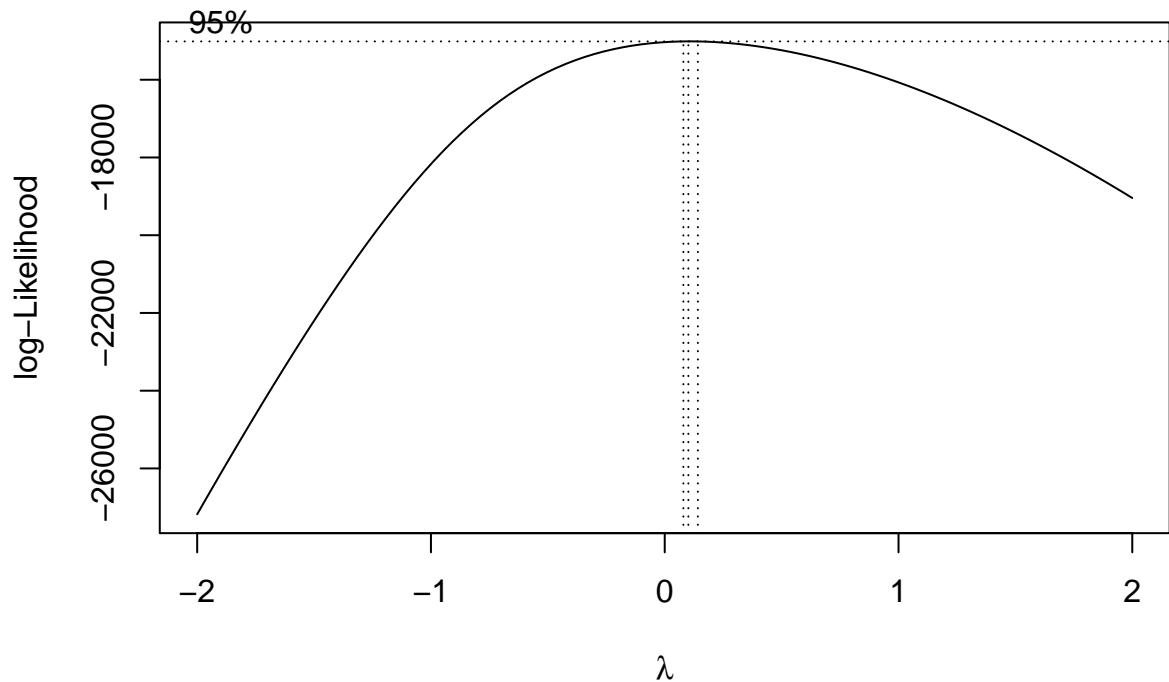
```
grid.arrange(plot2race, plot3marital,plot4tstage,
            plot5nstage, plot6x6thstage,plot7differentate,
            plot8grade,plot9astage,plot11estrogen,plot12progesterone, ncol = 3)
```



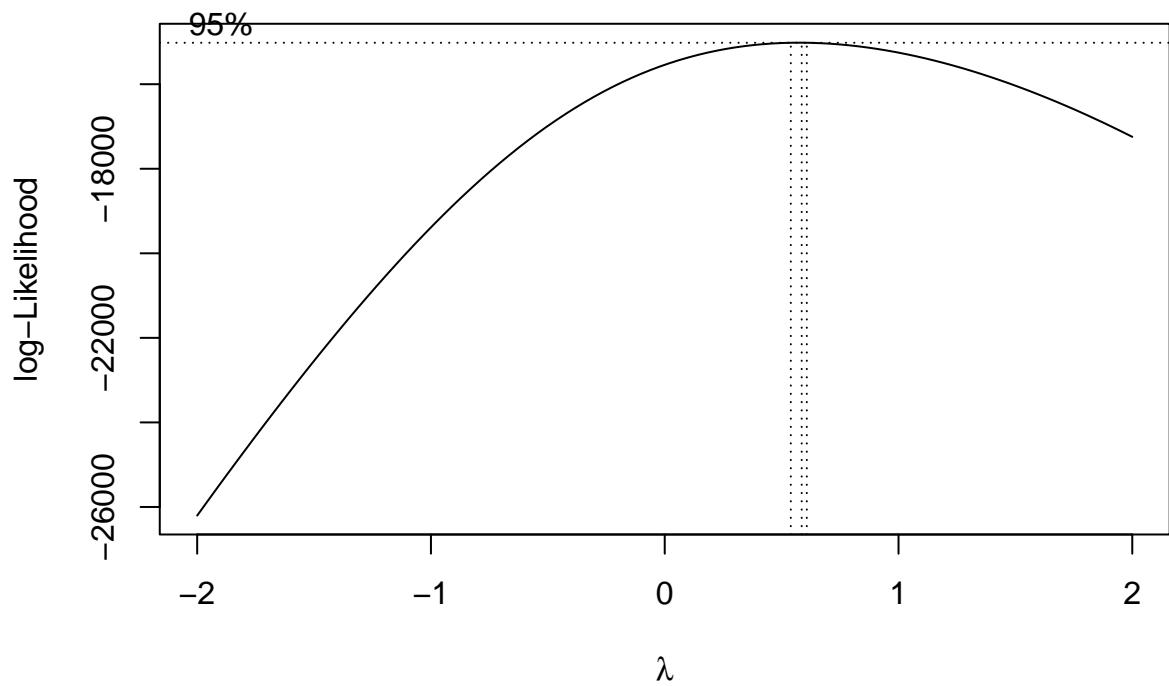
## Transformation

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.

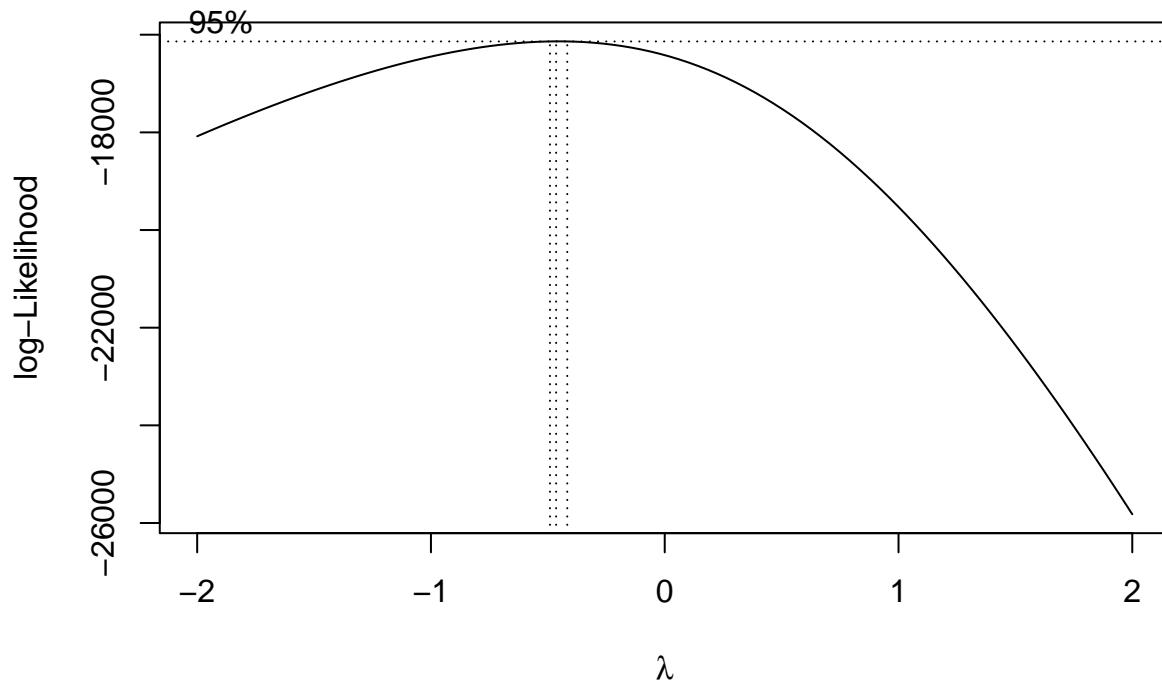
```
bc_transform_tumorsize <- boxcox(breastcancer_data$tumor_size ~ 1, lambda = seq(-2, 2, by=0.1))
```



```
bc_transformRegionalnode_examined <- boxcox(breastcancer_data$regional_node_examined ~ 1, lambda = seq(-2, 2, 0.01))
```



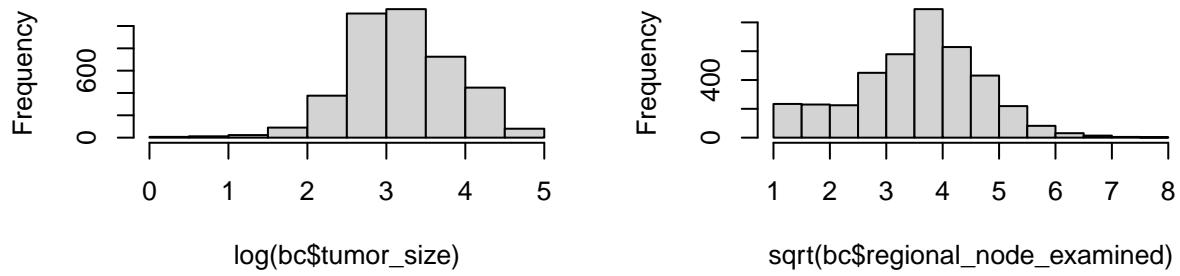
```
bc_transformRegionalnode_pos <- boxcox(breastcancer_data$regional_node_positive ~ 1, lambda = seq(-2, 2, 0.01))
```



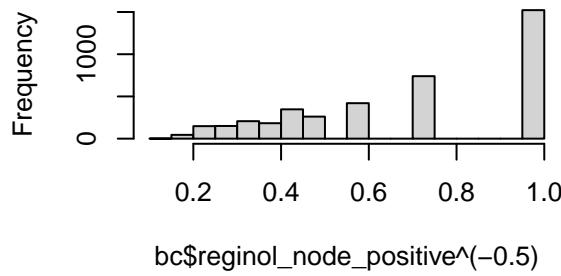
The lambda value of tumor size is close to 0, so we should use log transformation, while the lambda value of regional node examined is around 0.5, we should take a square root to the value, and the lambda value of regional node positive is around -0.5, so we should take a take square root and take an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

## Histogram of log(bc\$tumor\_size) | histogram of sqrt(bc\$regional\_node\_examined)



## histogram of bc\$reginol\_node\_positive^(



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        1        2         2            2     2
## 3     58     1         1        2        3         3            3     2
## 4     58     1         1        1        1         1            1     3
## 5     47     1         1        1        2         1            4     1
## 6     51     1         1        3        1         1            1     2
## 7     51     1         1        1        1         1            1     3
## 8     40     1         1        1        2         1            4     2
## 9     40     1         1        2        4         3            3     1
## 10    69     1         1        1        4         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 tests

```

# 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

```

# 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 *

```

```

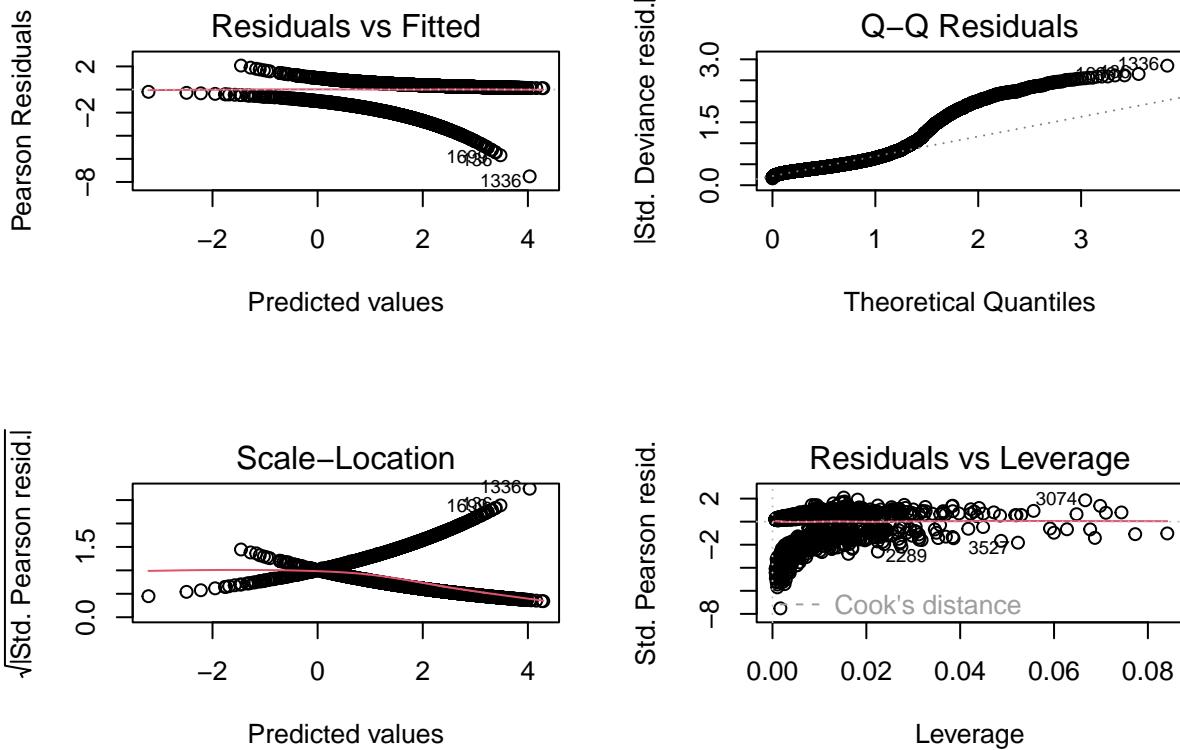
## t_stage2          -0.372488  0.159129 -2.341 0.019243 *
## t_stage3          -0.471905  0.266764 -1.769 0.076894 .
## t_stage4          -1.025962  0.313035 -3.277 0.001047 **
## n_stage2          -0.474091  0.129288 -3.667 0.000245 ***
## n_stage3          -0.637101  0.237639 -2.681 0.007341 **
## 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  
  
## 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  $6.95 \times 10^{-6}$  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:

```

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:  
 $\text{status} \sim \text{n\_stage} + \text{progesterone\_status} + \text{differentiate} + \text{t\_stage} + \text{age} + \text{race} + \text{estrogen\_status} + \text{sqrt\_examined} + \text{reginol\_node\_positive}$

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_model),
                                     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.

## Partial Test

### Partial Test for binary Y

```
# 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 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)
## 
```

```

##      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 = 10)

```

```

## 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  $\text{status} \sim \text{race} + \text{marital\_status} + \text{t\_stage} + \text{n\_stage} + \text{differentiate} + \text{estrogen\_status} + \text{progesterone\_status} + \text{reginol\_node\_positive} + \ln\text{\_tumor} + \sqrt{\text{\_examined}} + \text{age} + \text{race:marital\_status} + \text{race:progesterone\_status} + \text{race:ln\_tumor}$ .

The BIC selected model is  $\text{status} \sim \text{race} + \text{differentiate} + \text{estrogen\_status} + \text{progesterone\_status} + \text{reginol\_node\_positive} + \ln\text{\_tumor} + \sqrt{\text{\_examined}} + \text{age}$ .

### 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.

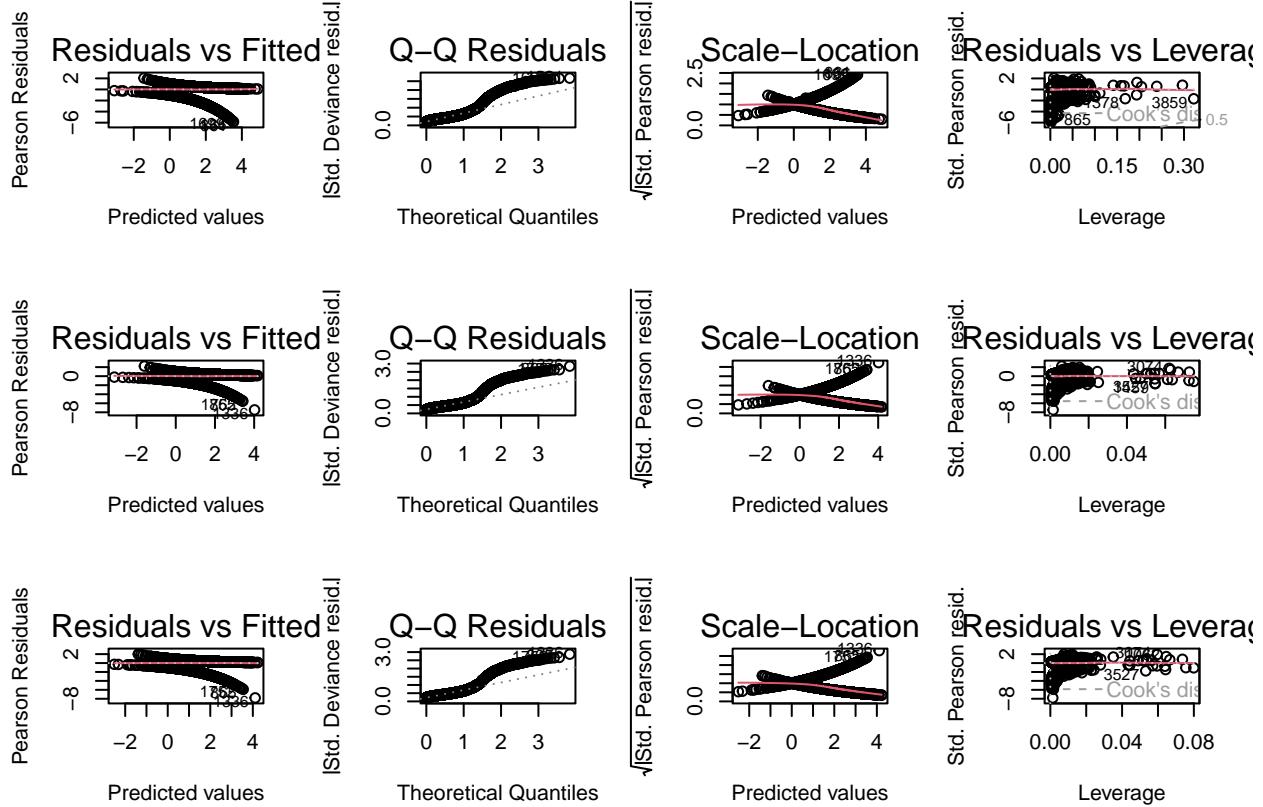
The BIC selected model is status ~ progesterone\_status + differentiate + t\_stage + age + race + estrogen\_status + sqrt\_examined + reginol\_node\_positive with AIC value of 3003.7.

#### Plots to check the model assumptions:

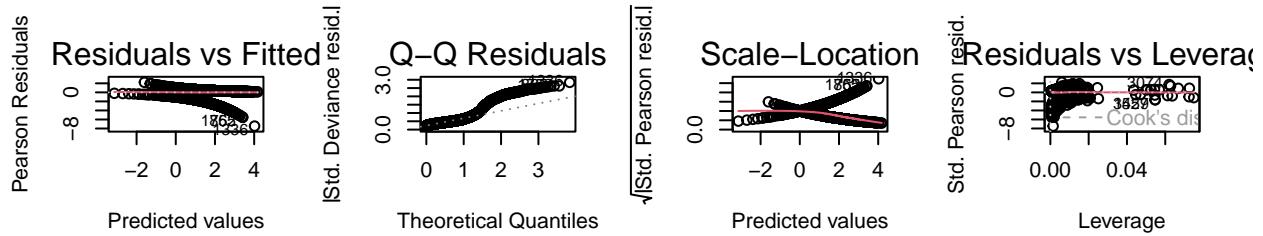
```

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)
```

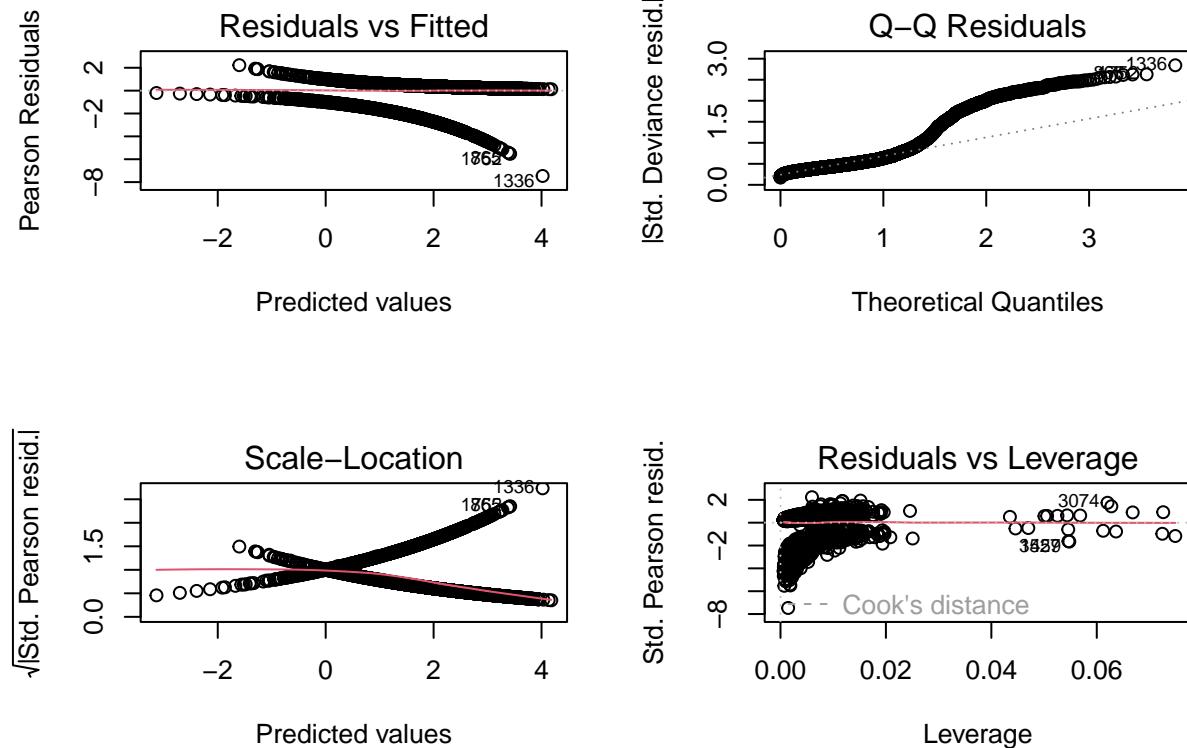


```
# final model assumption check
finalmodel <- glm(status ~ progesterone_status + differentiate + t_stage + age +
                      race + estrogen_status + sqrt_examined + reginol_node_positive,
                      data=bc_ref, family=binomial)

# 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

```
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>
## 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>

# 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)
cvmmodel1 <- 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, ...): cannot compute class
## probabilities for regression

print(cvmmodel1)

## 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
```

```

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

```

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

```
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)

```

```

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

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

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 multicollinearity (VIF)) 7. cross validation