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
```

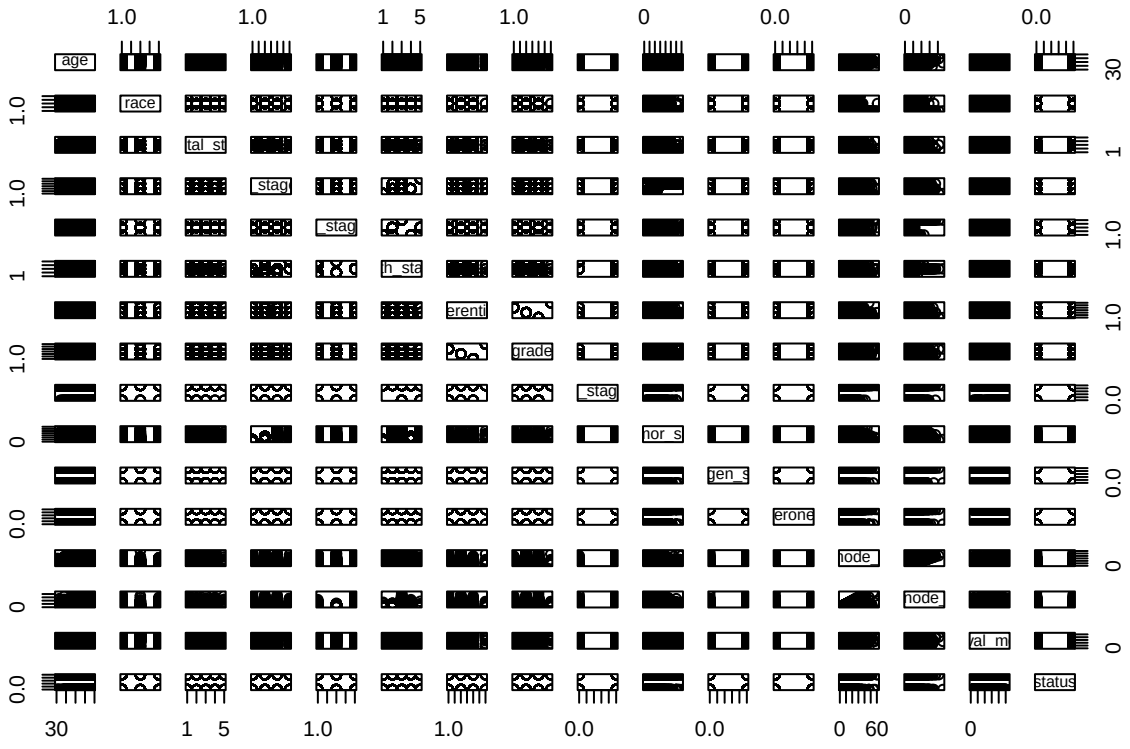
```
##  Max.   :1.0000   Max.   :140.00   Max.   :1.0000   Max.   :1.0000
##  regional_node_examined reginol_node_positive survival_months     status
##  Min.   : 1.00          Min.   : 1.000        Min.   :  1.0   Min.   :0.0000
##  1st Qu.: 9.00          1st Qu.: 1.000        1st Qu.: 56.0   1st Qu.:1.0000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



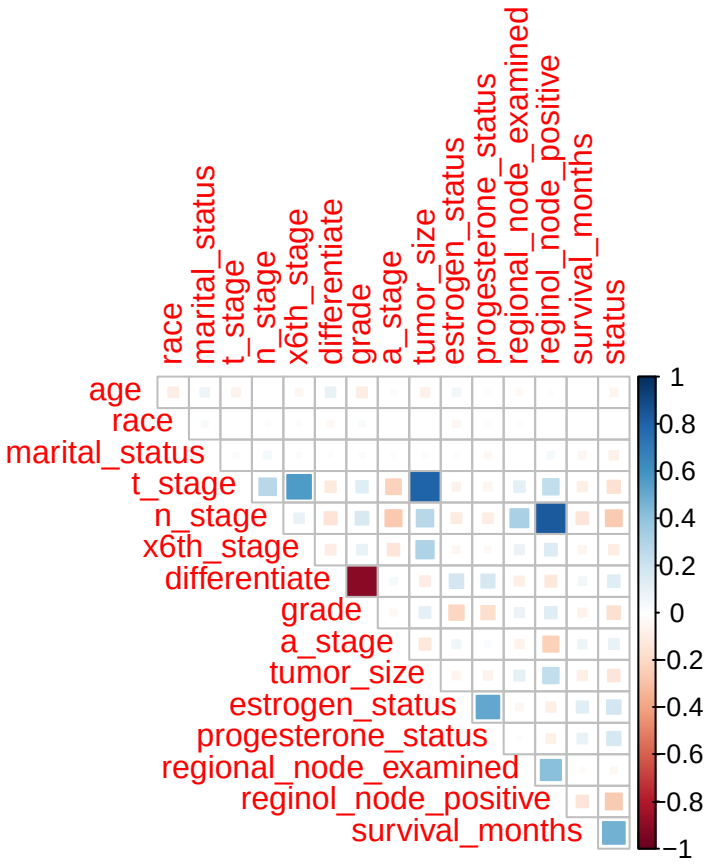

```
cor(bc) |>
  knitr::kable(digits=4,caption="Correlation for all variables")
```

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
```

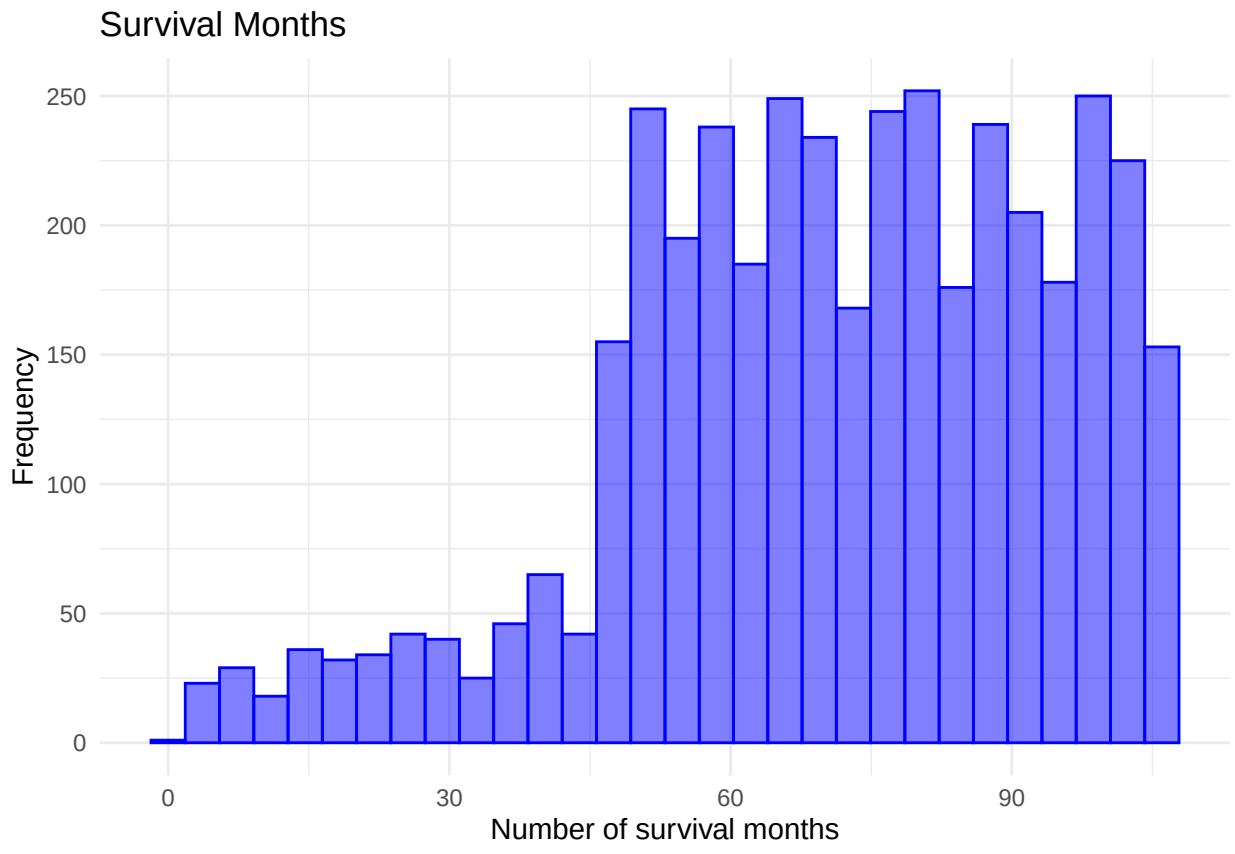
```r
plot14nodepositive =
  breastcancer_data|>
  ggplot(aes(x = reginol_node_positive)) +
  geom_histogram(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Regional Node Positive Distribution",
    x = "Positive Reginol Node",
    y = "Frequency"
  )

#plot14nodepositive
```

Y1 = survive months; (numeric)

Y2 = status; (binary)

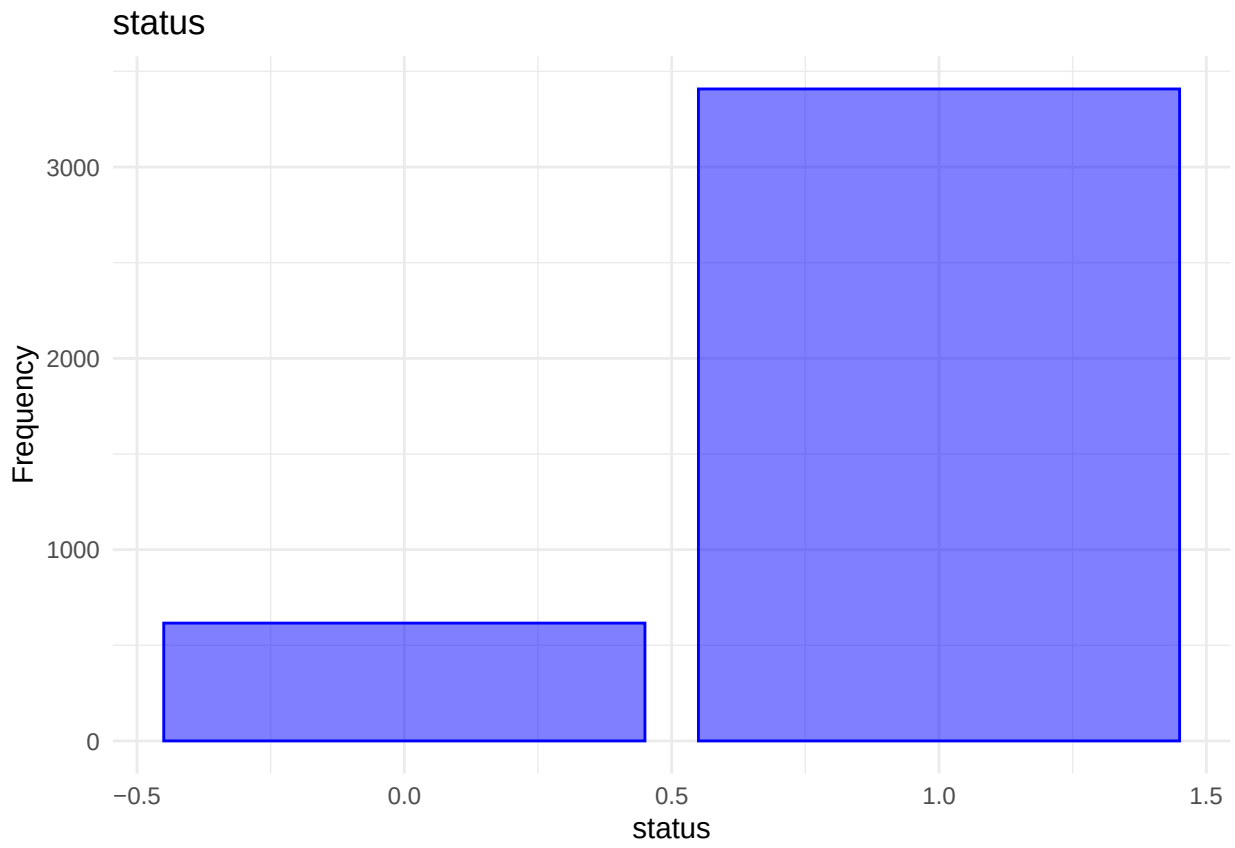
```
plot15survivalmonths =
  breastcancer_data|>
  ggplot(aes(x = survival_months)) +
  geom_histogram(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Survival Months",
    x = "Number of survival months",
    y = "Frequency"
  )

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(
```

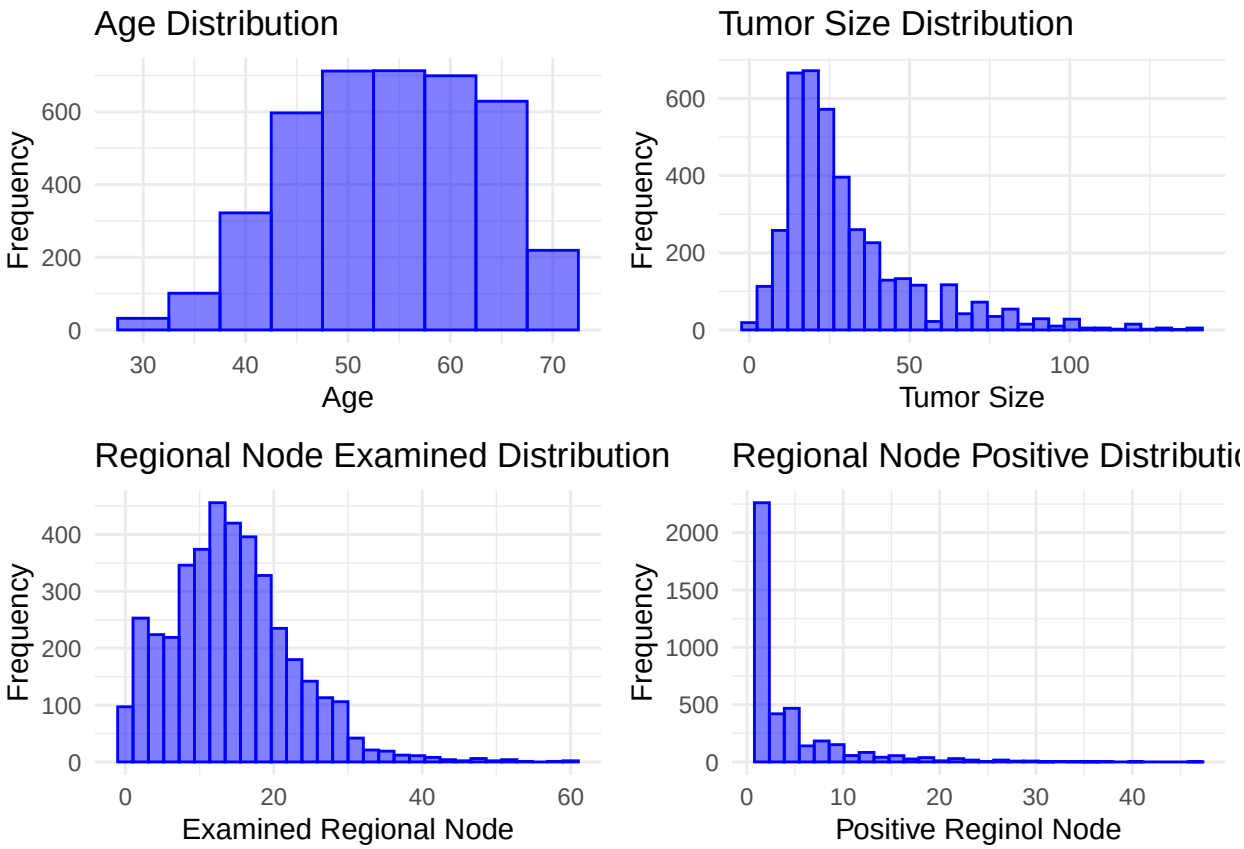
```
    title = "status",
    x = "status",
    y = "Frequency"
  )

plot16status
```



Summarized plots for covariates

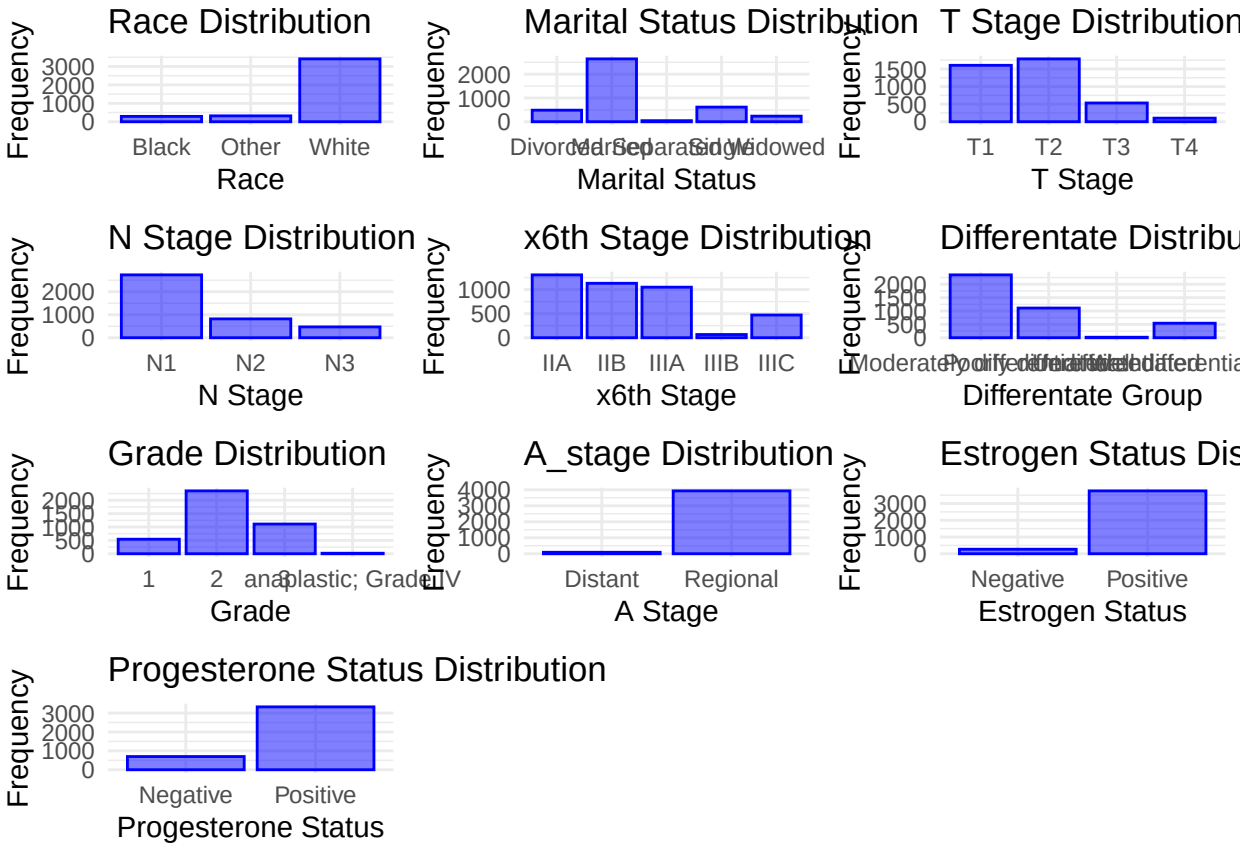
```
grid.arrange(plot1age, plot10tumorsize, plot13nodeexamined,
             plot14nodepositive, ncol = 2)
```

```
## `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`.
```



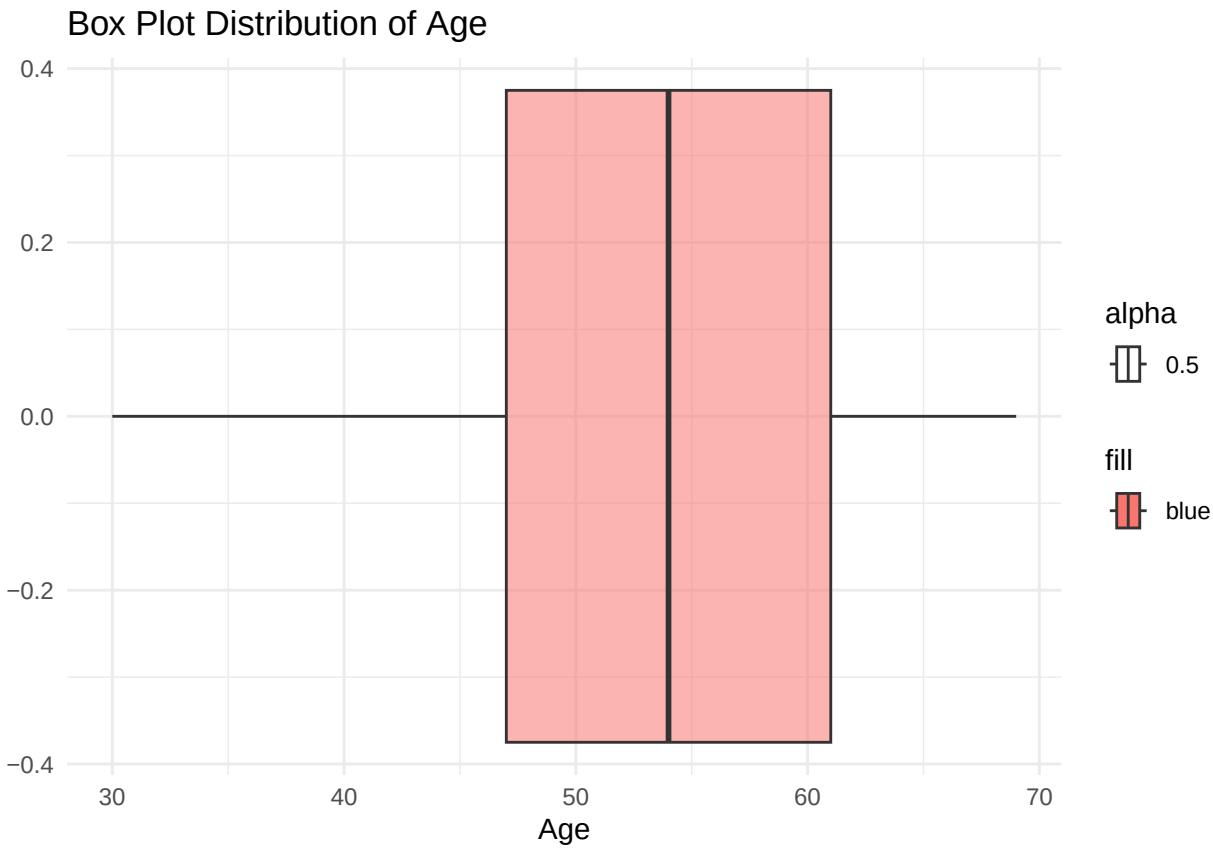
We can see that age is approximately normal, while tumor size, regional node examined, and regional node positive are skewed.

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

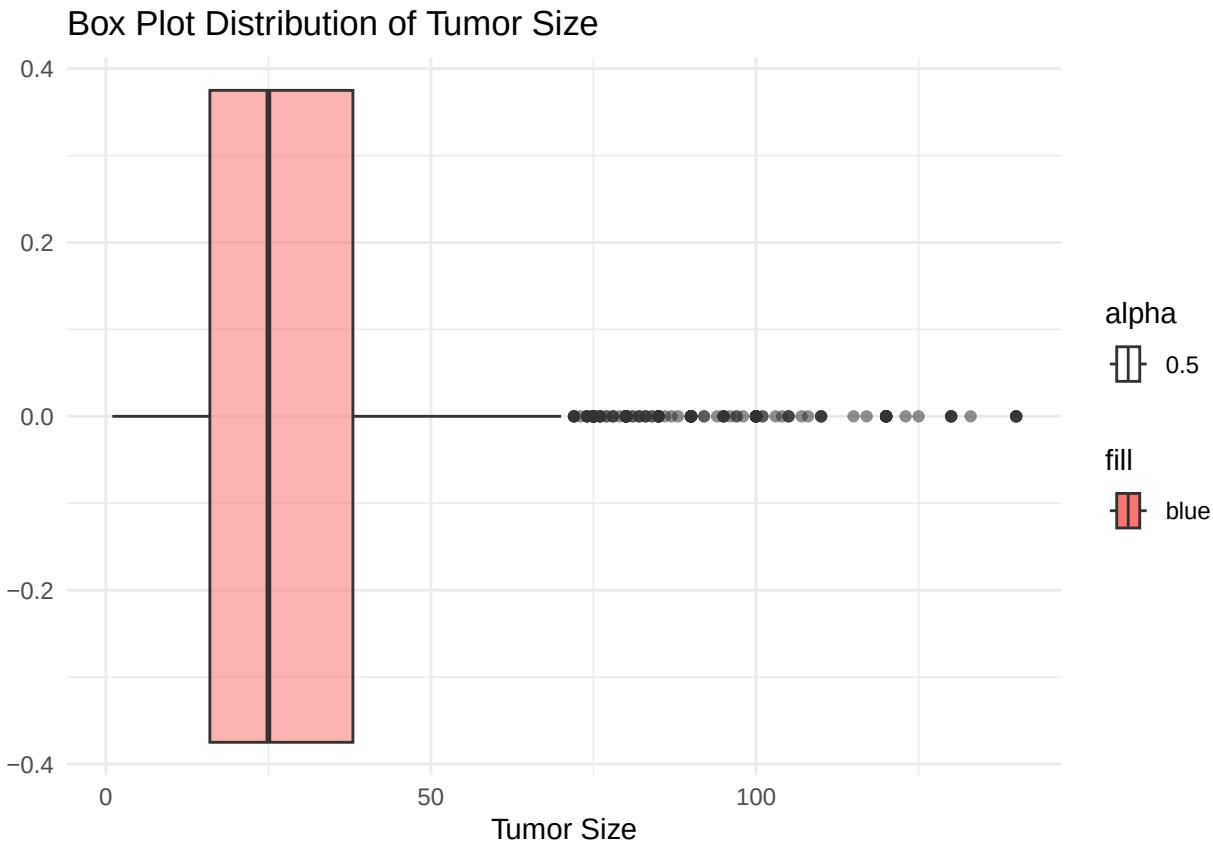


Boxplot visualissation to look for outliers

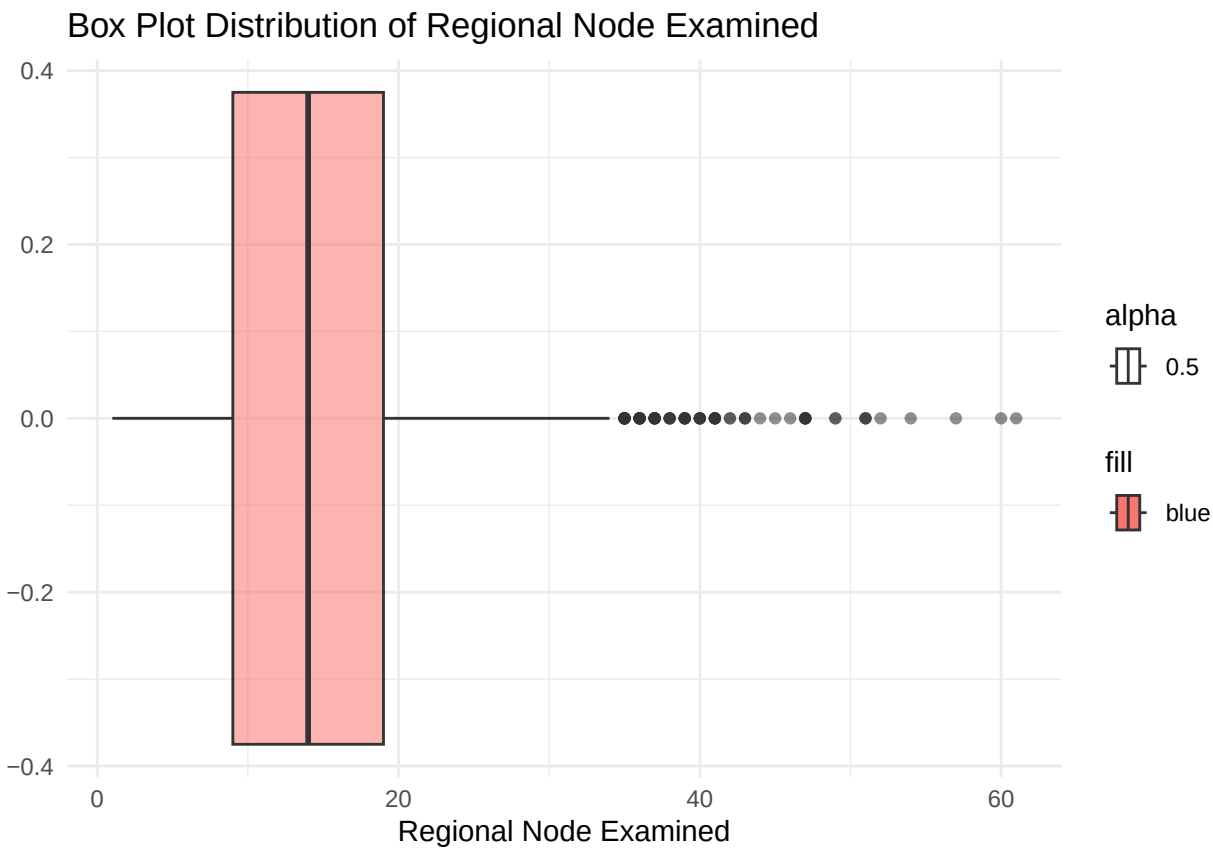
```
box_age = ggplot(bc, aes(x = age, fill = "blue", alpha = 0.5))+
        geom_boxplot() +
        theme(legend.position = 'none') +
        xlab("Age") +
        ggtitle("Box Plot Distribution of Age") +
        theme_minimal()

box_age
```



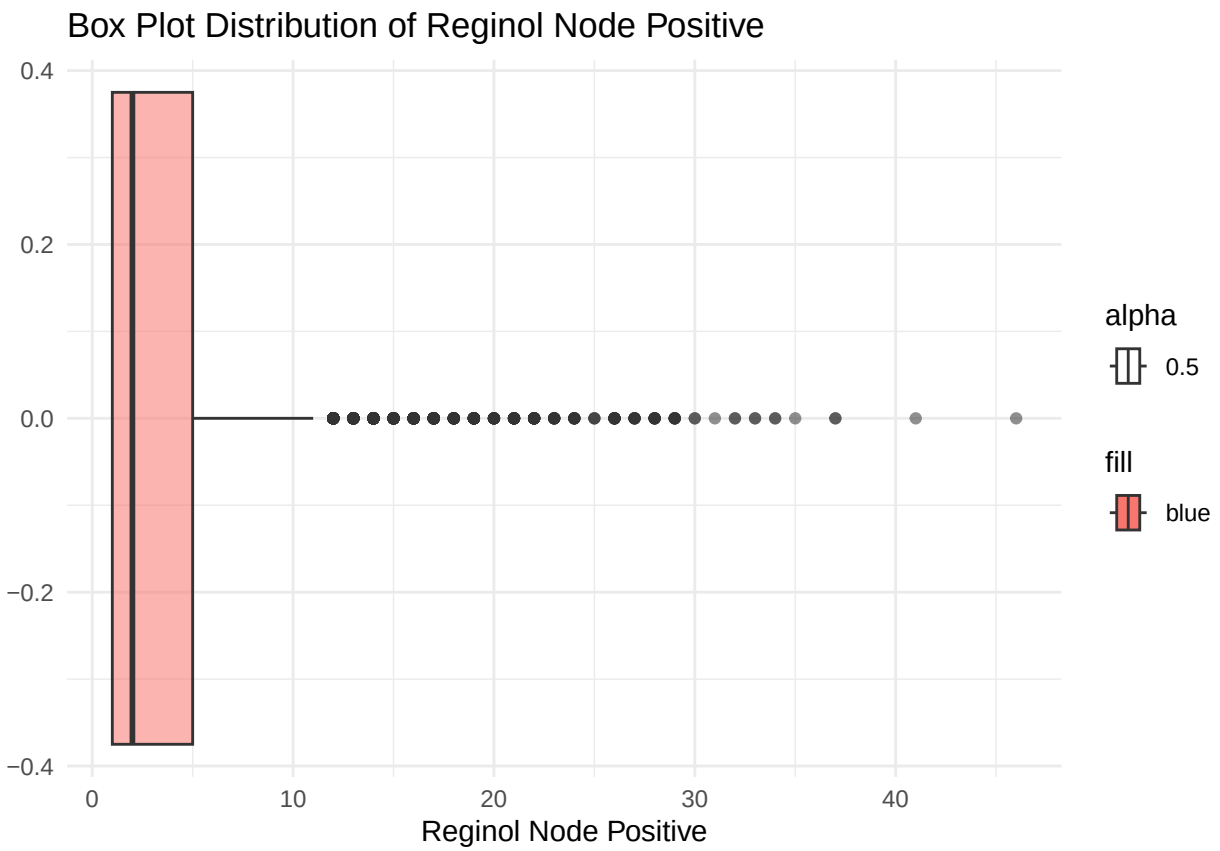

```
box_tumor = ggplot(bc, aes(x = tumor_size, fill = "blue", alpha = 0.5))+
        geom_boxplot() +
        theme(legend.position = 'none') +
        xlab("Tumor Size") +
        ggtitle("Box Plot Distribution of Tumor Size") +
        theme_minimal()

box_tumor
```




```
box_examined = ggplot(bc, aes(x = regional_node_examined, fill = "blue", alpha = 0.5))+
        geom_boxplot() +
        theme(legend.position = 'none') +
        xlab("Regional Node Examined") +
        ggtitle("Box Plot Distribution of Regional Node Examined") +
        theme_minimal()

box_examined
```




```
box_positive = ggplot(bc, aes(x = reginol_node_positive, fill = "blue", alpha = 0.5))+
        geom_boxplot() +
        theme(legend.position = 'none') +
        xlab("Reginol Node Positive") +
        ggtitle("Box Plot Distribution of Reginol Node Positive") +
        theme_minimal()

box_positive
```



- From the boxplots, we discover there are outliers in all the boxplots except the age distribution, so we will remove the outliers in our next step.

Outliers Remove

```
# Find the quantile
q1 = quantile(bc$tumor_size, probs = c(0.25, 0.75), na.rm = FALSE)
iqr1 = IQR(bc$tumor_size)
upper1 = q1[2] + 1.5*iqr1
lower1 = q1[1] - 1.5*iqr1

q2 = quantile(bc$regional_node_examined, probs = c(0.25, 0.75), na.rm = FALSE)
iqr2 = IQR(bc$regional_node_examined)
upper2 = q2[2] + 1.5*iqr2
lower2 = q2[1] - 1.5*iqr2

q3 = quantile(bc$reginol_node_positive, probs = c(0.25, 0.75), na.rm = FALSE)
iqr3 = IQR(bc$reginol_node_positive)
upper3 = q3[2] + 1.5*iqr3
lower3 = q3[1] - 1.5*iqr3

bc = bc|>
  filter(
    tumor_size <= upper1 & tumor_size >= lower1
  ) |>
```

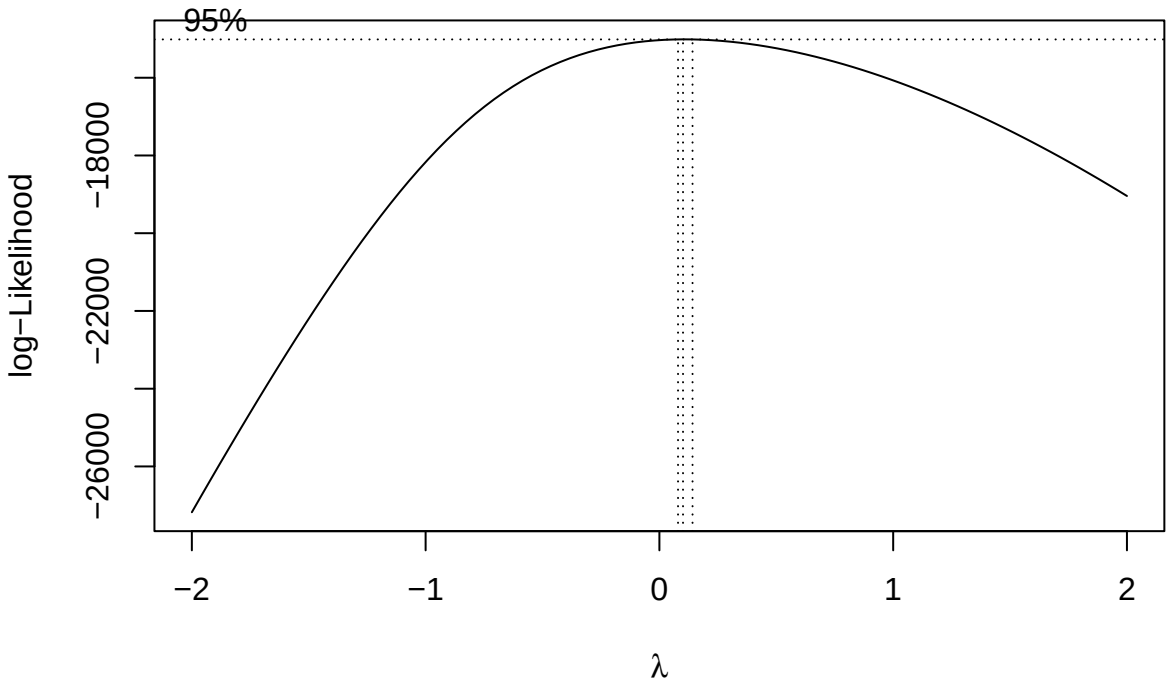
```
  filter(
    regional_node_examined <= upper2 & regional_node_examined >= lower2
  ) |>
  filter(
    reginol_node_positive <= upper3 & reginol_node_positive >= lower3
  )
bc
```

```
## # A tibble: 3,461 x 16
##      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    68     1              4       1       1          1              2     2
## 10    46     1              1       3       1          2              1     3
## # i 3,451 more rows
## # i 8 more variables: a_stage <dbl>, tumor_size <dbl>, estrogen_status <dbl>,
## #   progesterone_status <dbl>, regional_node_examined <dbl>,
## #   reginol_node_positive <dbl>, survival_months <dbl>, status <dbl>
```

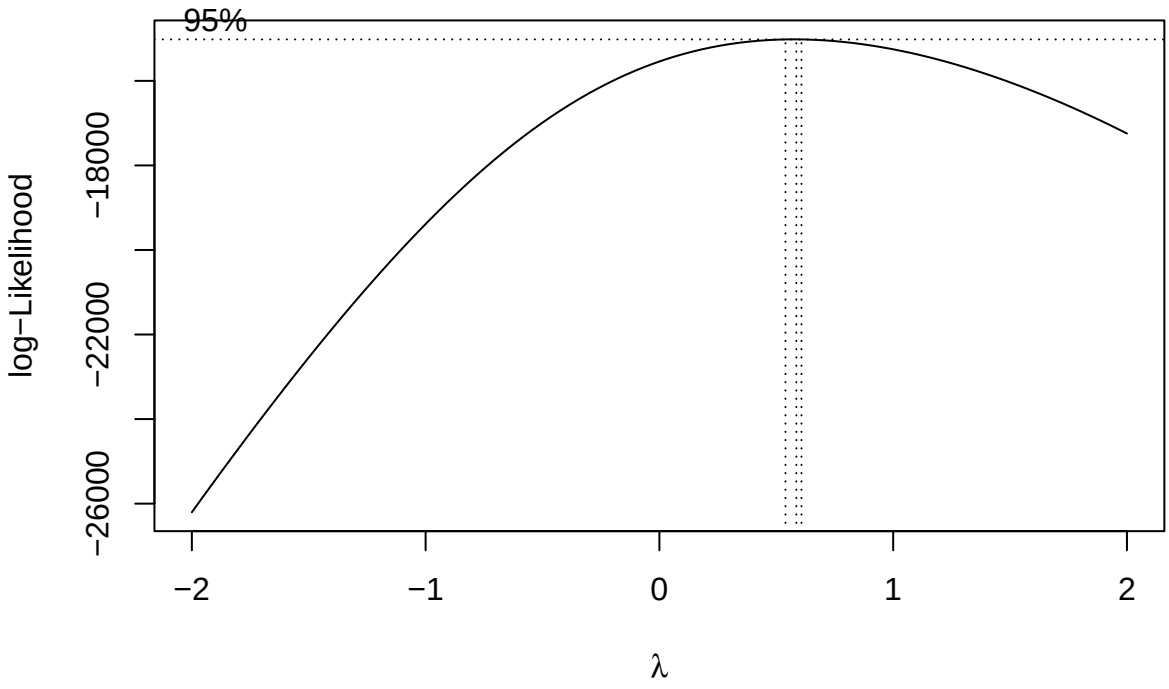
Transformation

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.

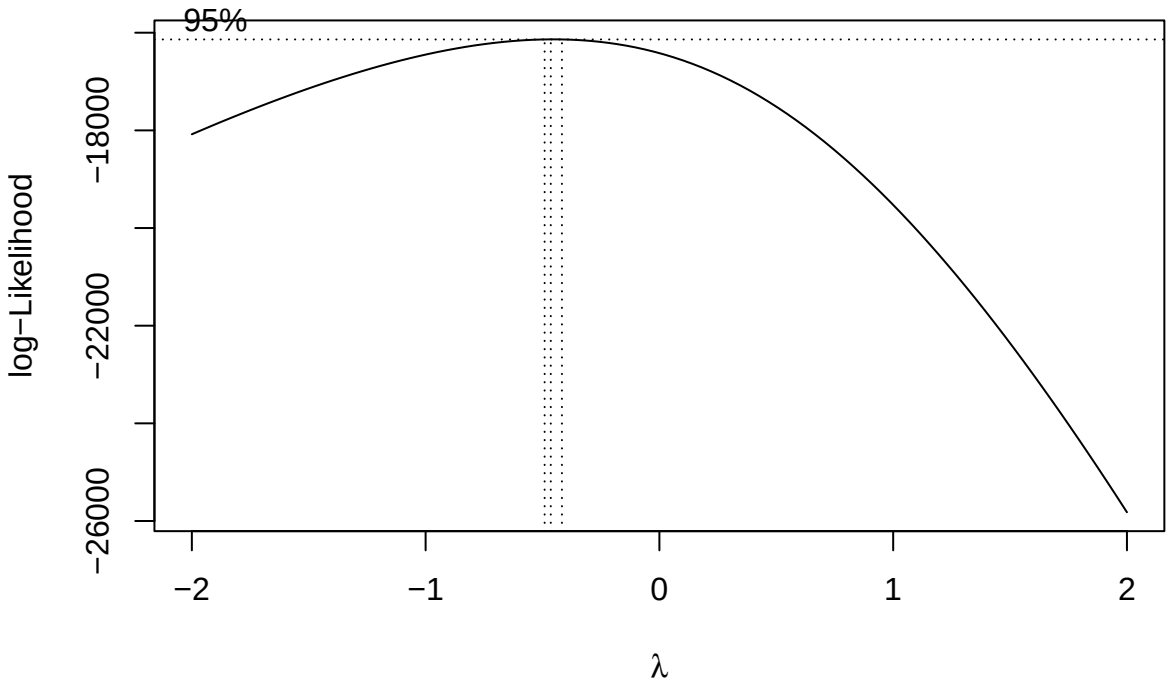
```
bc_transform_tumorsize <- boxcox(breastcancer_data$tumor_size ~ 1, lambda = seq(-2, 2, by=0.1))
```




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

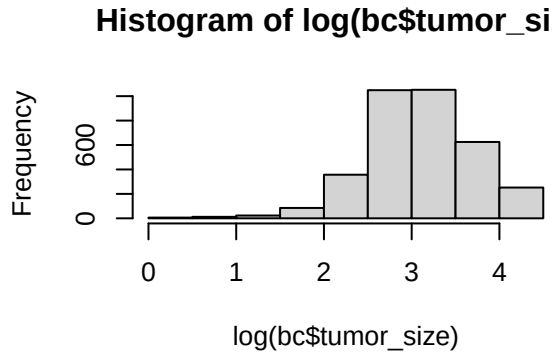


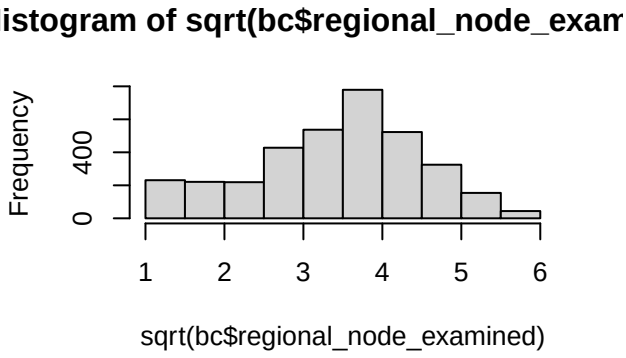

```
bc_transform_regionalnode_pos <- boxcox(breastcancer_data$reginol_node_positive ~ 1, lambda = seq(-2, 2
```

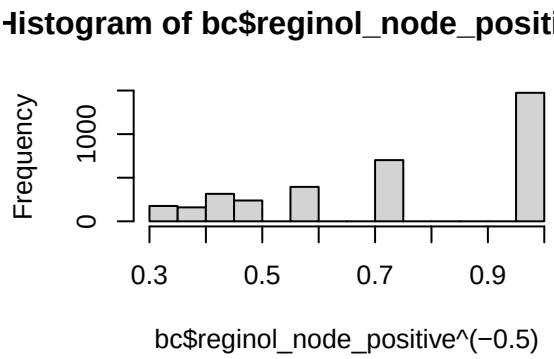


The lambda value of tumor size is close to 0, so we should use log transformation, while the lambda value of regional node examined is around 0.5, we should take a square root to the value, and the lambda value of regional node positive is around -0.5, so we should take a take square root and take an (-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: 3,461 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    68     1              4       1       1          1             2     2
## 10    46     1              1       3       1          2             1     3
## # i 3,451 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  65.86697 4.562572e-03
## X-squared1                   race  21.99791 1.671917e-05
## X-squared2         marital_status  15.09341 4.511343e-03
## X-squared3                t_stage  41.69011 4.667993e-09
## X-squared4                n_stage  86.19222 1.921313e-19
## X-squared5             x6th_stage  99.91678 1.024621e-20
```

```
## X-squared6          differentiate  49.08702 1.249981e-10
## X-squared7                  grade  49.08702 1.249981e-10
## X-squared8                a_stage  20.66537 5.469634e-06
## X-squared9        estrogen_status  43.52930 4.176585e-11
## X-squared10   progesterone_status  72.53788 1.638562e-17
## X-squared11 reginol_node_positive  89.47869 6.794837e-15
## X-squared12               ln_tumor  99.46257 7.706226e-03
## X-squared13         sqrt_examined  37.24307 2.800207e-01
```

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)           1.801100   0.749312   2.404 0.016231 *
## race2                -0.481824   0.181257  -2.658 0.007855 **
## race3                 0.546052   0.241766   2.259 0.023909 *
## marital_status2      -0.288991   0.160997  -1.795 0.072654 .
## marital_status3      -0.146541   0.151637  -0.966 0.333847
## marital_status4      -0.152521   0.222968  -0.684 0.493943
## marital_status5      -0.964852   0.426814  -2.261 0.023785 *
## t_stage2             -0.156440   0.257180  -0.608 0.542996
## t_stage3             -0.206208   0.379434  -0.543 0.586811
## t_stage4              0.200107   0.883657   0.226 0.820849
## n_stage2             -0.361974   0.342189  -1.058 0.290138
## n_stage3             -0.741041   0.429719  -1.724 0.084621 .
## x6th_stage2          -0.150844   0.372970  -0.404 0.685890
## x6th_stage3                 NA         NA      NA       NA
## x6th_stage4          -0.276250   0.261285  -1.057 0.290386
```

```
## x6th_stage5           -0.915541   0.958406  -0.955 0.339439
## differentiate2         0.296285   0.120380   2.461 0.013845 *
## differentiate3         0.879937   0.216335   4.067 4.75e-05 ***
## differentiate4        -0.933081   0.640835  -1.456 0.145382
## grade2                       NA         NA      NA       NA
## grade3                       NA         NA      NA       NA
## grade4                       NA         NA      NA       NA
## a_stage1               0.768184   0.437966   1.754 0.079434 .
## estrogen_status1       0.523089   0.209118   2.501 0.012370 *
## progesterone_status1   0.644165   0.140918   4.571 4.85e-06 ***
## ln_tumor              -0.099185   0.165585  -0.599 0.549175
## sqrt_examined          0.210107   0.054403   3.862 0.000112 ***
## reginol_node_positive -0.086809   0.037939  -2.288 0.022131 *
## age                   -0.027971   0.006466  -4.326 1.52e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2372.5  on 3436  degrees of freedom
## AIC: 2422.5
##
## 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

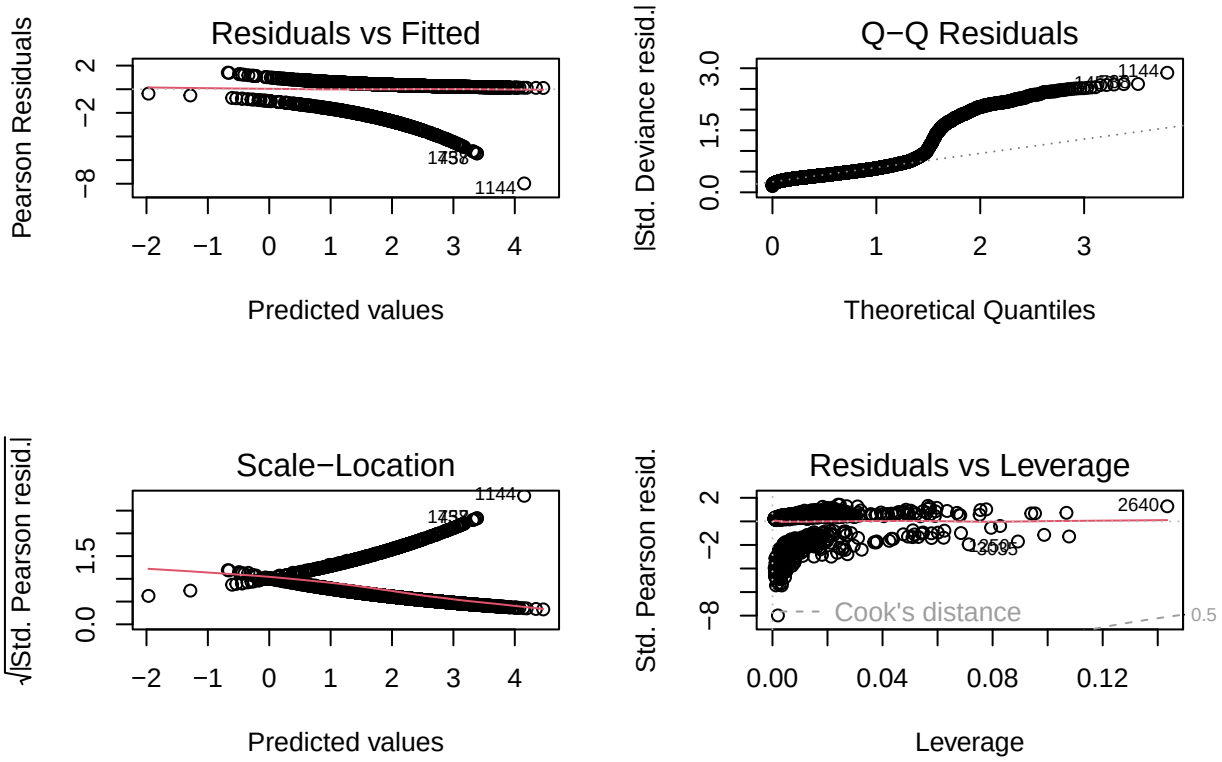
Initial Model

```
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)            1.669820   0.742257   2.250 0.024471 *
## race2                 -0.483041   0.181268  -2.665 0.007704 **
## race3                  0.545443   0.241632   2.257 0.023988 *
## marital_status2       -0.288452   0.161039  -1.791 0.073262 .
```

```
## marital_status3       -0.143745   0.151333  -0.950 0.342186
## marital_status4       -0.144722   0.223020  -0.649 0.516391
## marital_status5       -0.955754   0.428220  -2.232 0.025620 *
## t_stage2              -0.359156   0.178939  -2.007 0.044734 *
## t_stage3              -0.347678   0.306686  -1.134 0.256936
## t_stage4              -0.542171   0.429395  -1.263 0.206719
## n_stage2              -0.316154   0.195060  -1.621 0.105060
## n_stage3              -0.469552   0.371061  -1.265 0.205716
## differentiate2         0.301445   0.120242   2.507 0.012177 *
## differentiate3         0.883056   0.215825   4.092 4.29e-05 ***
## differentiate4        -0.832225   0.643368  -1.294 0.195823
## a_stage1               0.810269   0.437436   1.852 0.063981 .
## estrogen_status1       0.527199   0.209068   2.522 0.011680 *
## progesterone_status1   0.645038   0.140768   4.582 4.60e-06 ***
## ln_tumor              -0.087583   0.164874  -0.531 0.595272
## sqrt_examined          0.208411   0.054319   3.837 0.000125 ***
## reginol_node_positive -0.090653   0.037884  -2.393 0.016716 *
## age                   -0.027706   0.006456  -4.292 1.77e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2374.3  on 3439  degrees of freedom
## AIC: 2418.3
##
## 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)   1.9636     0.0562  34.936  < 2e-16 ***
## race2        -0.6265     0.1656  -3.782 0.000155 ***
## race3         0.5410     0.2338   2.314 0.020680 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2592.7  on 3458  degrees of freedom
## AIC: 2598.7
##
## Number of Fisher Scoring iterations: 5
```

```
## 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)              1.669820   0.742257   2.250 0.024471 *
## race2                   -0.483041   0.181268  -2.665 0.007704 **
## race3                    0.545443   0.241632   2.257 0.023988 *
## marital_status2         -0.288452   0.161039  -1.791 0.073262 .
## marital_status3         -0.143745   0.151333  -0.950 0.342186
## marital_status4         -0.144722   0.223020  -0.649 0.516391
## marital_status5         -0.955754   0.428220  -2.232 0.025620 *
## t_stage2                -0.359156   0.178939  -2.007 0.044734 *
## t_stage3                -0.347678   0.306686  -1.134 0.256936
## t_stage4                -0.542171   0.429395  -1.263 0.206719
## n_stage2                -0.316154   0.195060  -1.621 0.105060
## n_stage3                -0.469552   0.371061  -1.265 0.205716
## differentiate2           0.301445   0.120242   2.507 0.012177 *
## differentiate3           0.883056   0.215825   4.092 4.29e-05 ***
## differentiate4          -0.832225   0.643368  -1.294 0.195823
## a_stage1                 0.810269   0.437436   1.852 0.063981 .
## estrogen_status1         0.527199   0.209068   2.522 0.011680 *
## progesterone_status1     0.645038   0.140768   4.582 4.60e-06 ***
## reginol_node_positive -0.090653   0.037884  -2.393 0.016716 *
## ln_tumor                -0.087583   0.164874  -0.531 0.595272
```

```
## sqrt_examined          0.208411   0.054319   3.837 0.000125 ***
## age                   -0.027706   0.006456  -4.292 1.77e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2374.3  on 3439  degrees of freedom
## AIC: 2418.3
##
## 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)                   2.522726   0.860067   2.933  0.00336 **
## race2                        -3.939061   2.157982  -1.825  0.06795 .
## race3                         1.317146 678.517674   0.002  0.99845
## marital_status2              -0.301688   0.172130  -1.753  0.07966 .
## marital_status3               0.089754   0.179356   0.500  0.61678
## marital_status4               0.116965   0.266131   0.440  0.66030
## marital_status5              -1.052417   0.507443  -2.074  0.03808 *
## t_stage2                     -0.126953   0.202998  -0.625  0.53171
## t_stage3                     -0.011254   0.349032  -0.032  0.97428
## t_stage4                     -0.506856   0.471242  -1.076  0.28212
## n_stage2                     -0.274458   0.212721  -1.290  0.19697
## n_stage3                     -0.610550   0.400474  -1.525  0.12737
## differentiate2                0.373032   0.132103   2.824  0.00475 **
## differentiate3                0.937682   0.239446   3.916 9.00e-05 ***
## differentiate4               -0.788704   0.700348  -1.126  0.26010
## a_stage1                      0.537213   0.490992   1.094  0.27389
## estrogen_status1              0.710380   0.229623   3.094  0.00198 **
## progesterone_status1          0.686130   0.153912   4.458 8.28e-06 ***
## reginol_node_positive        -0.114888   0.041361  -2.778  0.00547 **
```

```
## ln_tumor                      -0.320751   0.197355  -1.625  0.10411
## sqrt_examined                  0.233912   0.060035   3.896 9.77e-05 ***
## age                           -0.032821   0.007161  -4.583 4.58e-06 ***
## race2:marital_status2          0.339341   0.666379   0.509  0.61059
## race3:marital_status2         -0.618404   0.742461  -0.833  0.40489
## race2:marital_status3         -1.022641   0.455715  -2.244  0.02483 *
## race3:marital_status3         -1.148739   0.757200  -1.517  0.12924
## race2:marital_status4         -0.664439   0.674543  -0.985  0.32461
## race3:marital_status4         -2.740426   0.934062  -2.934  0.00335 **
## race2:marital_status5          0.481739   1.217288   0.396  0.69229
## race3:marital_status5         -0.514287   1.442682  -0.356  0.72148
## race2:t_stage2                -0.955300   0.556300  -1.717  0.08594 .
## race3:t_stage2                -0.477768   0.883906  -0.541  0.58884
## race2:t_stage3                -0.719097   1.016740  -0.707  0.47941
## race3:t_stage3                -0.161734   1.597388  -0.101  0.91935
## race2:t_stage4                -0.235932   1.521925  -0.155  0.87680
## race3:t_stage4                12.153048 494.949345   0.025  0.98041
## race2:n_stage2                -0.420316   0.709835  -0.592  0.55376
## race3:n_stage2                -0.708345   1.163541  -0.609  0.54267
## race2:n_stage3                 0.819883   1.469222   0.558  0.57682
## race3:n_stage3                11.205380 371.150096   0.030  0.97591
## race2:differentiate2          -0.360661   0.414282  -0.871  0.38399
## race3:differentiate2          -0.083304   0.561563  -0.148  0.88207
## race2:differentiate3          -0.512976   0.713404  -0.719  0.47211
## race3:differentiate3           0.241208   0.939878   0.257  0.79746
## race2:differentiate4          -1.643613   1.930490  -0.851  0.39455
## race3:differentiate4                 NA         NA      NA       NA
## race2:a_stage1                 2.112209   1.460836   1.446  0.14821
## race3:a_stage1                -1.623707 678.510625  -0.002  0.99809
## race2:estrogen_status1        -1.214026   0.728330  -1.667  0.09554 .
## race3:estrogen_status1         0.706925   1.505458   0.470  0.63866
## race2:progesterone_status1     0.102737   0.484289   0.212  0.83200
## race3:progesterone_status1    -2.883793   1.439992  -2.003  0.04522 *
## race2:reginol_node_positive    0.090546   0.136732   0.662  0.50783
## race3:reginol_node_positive    0.262504   0.244971   1.072  0.28391
## race2:ln_tumor                 0.935650   0.410084   2.282  0.02251 *
## race3:ln_tumor                 0.142697   0.888872   0.161  0.87246
## race2:sqrt_examined           -0.101194   0.183537  -0.551  0.58139
## race3:sqrt_examined           -0.230949   0.248429  -0.930  0.35256
## race2:age                      0.013711   0.021734   0.631  0.52812
## race3:age                      0.059960   0.029658   2.022  0.04320 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2315.3  on 3402  degrees of freedom
## AIC: 2433.3
##
## Number of Fisher Scoring iterations: 13
```

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

```r
              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)                  1.922110   0.782570   2.456  0.01404 *
## race2                       -1.440245   0.876932  -1.642  0.10051
## race3                        3.446428   1.895159   1.819  0.06898 .
## marital_status2             -0.298533   0.171246  -1.743  0.08128 .
## marital_status3              0.098378   0.178370   0.552  0.58127
## marital_status4              0.101948   0.264810   0.385  0.70025
## marital_status5             -1.020923   0.506070  -2.017  0.04366 *
## t_stage2                    -0.303545   0.181316  -1.674  0.09411 .
## t_stage3                    -0.212548   0.313484  -0.678  0.49776
## t_stage4                    -0.491297   0.430386  -1.142  0.25365
## n_stage2                    -0.299767   0.196352  -1.527  0.12684
## n_stage3                    -0.487390   0.372179  -1.310  0.19035
## differentiate2               0.326891   0.121192   2.697  0.00699 **
## differentiate3               0.909188   0.217906   4.172 3.01e-05 ***
## differentiate4              -0.908342   0.643389  -1.412  0.15801
## a_stage1                     0.793932   0.439372   1.807  0.07077 .
## estrogen_status1             0.558580   0.213342   2.618  0.00884 **
## progesterone_status1         0.740140   0.149420   4.953 7.29e-07 ***
## reginol_node_positive       -0.100577   0.038138  -2.637  0.00836 **
## ln_tumor                    -0.208507   0.179779  -1.160  0.24613
## sqrt_examined                0.209221   0.054680   3.826  0.00013 ***
## age                         -0.028142   0.006513  -4.321 1.55e-05 ***
## race2:marital_status2        0.430857   0.658348   0.654  0.51282
## race3:marital_status2       -0.637648   0.730974  -0.872  0.38303
## race2:marital_status3       -1.109678   0.432964  -2.563  0.01038 *
## race3:marital_status3       -1.381856   0.739709  -1.868  0.06175 .
## race2:marital_status4       -0.739699   0.620023  -1.193  0.23286
## race3:marital_status4       -1.861138   0.742128  -2.508  0.01215 *
## race2:marital_status5        0.209062   1.171629   0.178  0.85838
## race3:marital_status5       -1.325019   1.402146  -0.945  0.34466
## race2:progesterone_status1  -0.428380   0.396952  -1.079  0.28051
## race3:progesterone_status1  -2.822455   1.083674  -2.605  0.00920 **
## race2:ln_tumor               0.534411   0.266071   2.009  0.04459 *
## race3:ln_tumor              -0.016804   0.473176  -0.036  0.97167
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2339.4  on 3427  degrees of freedom
## AIC: 2407.4
##
## Number of Fisher Scoring iterations: 6
```

- 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 +
##     age + t_stage + race + sqrt_examined + estrogen_status +
##     reginol_node_positive + a_stage, family = binomial, data = newbc)
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)            1.36855    0.60035   2.280 0.022631 *
## n_stage2              -0.31915    0.19476  -1.639 0.101284
## n_stage3              -0.47891    0.36906  -1.298 0.194412
## progesterone_status1   0.66437    0.14040   4.732 2.22e-06 ***
## differentiate2         0.29970    0.11986   2.500 0.012404 *
## differentiate3         0.86923    0.21430   4.056 4.99e-05 ***
## differentiate4        -0.87777    0.62808  -1.398 0.162254
## age                   -0.02735    0.00626  -4.370 1.24e-05 ***
## t_stage2              -0.44097    0.12077  -3.651 0.000261 ***
## t_stage3              -0.46596    0.19454  -2.395 0.016613 *
## t_stage4              -0.64519    0.39984  -1.614 0.106611
## race2                 -0.53578    0.17667  -3.033 0.002424 **
## race3                  0.54901    0.24094   2.279 0.022691 *
## sqrt_examined          0.21147    0.05425   3.898 9.69e-05 ***
## estrogen_status1       0.49587    0.20826   2.381 0.017268 *
## reginol_node_positive -0.09091    0.03777  -2.407 0.016085 *
## a_stage1               0.79915    0.43703   1.829 0.067459 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2382.1  on 3444  degrees of freedom
## AIC: 2416.1
##
## Number of Fisher Scoring iterations: 5
```

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

```
##
## Call:
## glm(formula = status ~ race + t_stage + differentiate + a_stage +
##     estrogen_status + progesterone_status + reginol_node_positive +
##     sqrt_examined + age, family = binomial, data = newbc)
##
## Coefficients:
##                        Estimate Std. Error z value Pr(>|z|)
## (Intercept)            1.267444   0.589918   2.149 0.031673 *
## race2                 -0.541906   0.176208  -3.075 0.002102 **
## race3                  0.553919   0.241076   2.298 0.021579 *
## t_stage2              -0.444318   0.120572  -3.685 0.000229 ***
## t_stage3              -0.464382   0.194620  -2.386 0.017028 *
## t_stage4              -0.593001   0.401139  -1.478 0.139330
## differentiate2         0.308150   0.119585   2.577 0.009972 **
```

```
## differentiate3         0.882129   0.214053   4.121 3.77e-05 ***
## differentiate4        -0.827385   0.626277  -1.321 0.186462
## a_stage1               0.922690   0.418529   2.205 0.027482 *
## estrogen_status1       0.513420   0.207524   2.474 0.013360 *
## progesterone_status1   0.662321   0.140178   4.725 2.30e-06 ***
## reginol_node_positive -0.141365   0.020450  -6.913 4.75e-12 ***
## sqrt_examined          0.211194   0.054041   3.908 9.31e-05 ***
## age                   -0.027140   0.006247  -4.345 1.40e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2384.8  on 3446  degrees of freedom
## AIC: 2414.8
##
## Number of Fisher Scoring iterations: 5
```

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

```
##
## Call:
## glm(formula = status ~ progesterone_status + differentiate +
##     age + t_stage + race + sqrt_examined + estrogen_status +
##     reginol_node_positive + a_stage, family = binomial, data = newbc)
##
## Coefficients:
##                        Estimate Std. Error z value Pr(>|z|)
## (Intercept)            1.267444   0.589918   2.149 0.031673 *
## progesterone_status1   0.662321   0.140178   4.725 2.30e-06 ***
## differentiate2         0.308150   0.119585   2.577 0.009972 **
## differentiate3         0.882129   0.214053   4.121 3.77e-05 ***
## differentiate4        -0.827385   0.626277  -1.321 0.186462
## age                   -0.027140   0.006247  -4.345 1.40e-05 ***
## t_stage2              -0.444318   0.120572  -3.685 0.000229 ***
## t_stage3              -0.464382   0.194620  -2.386 0.017028 *
## t_stage4              -0.593001   0.401139  -1.478 0.139330
## race2                 -0.541906   0.176208  -3.075 0.002102 **
## race3                  0.553919   0.241076   2.298 0.021579 *
## sqrt_examined          0.211194   0.054041   3.908 9.31e-05 ***
## estrogen_status1       0.513420   0.207524   2.474 0.013360 *
## reginol_node_positive -0.141365   0.020450  -6.913 4.75e-12 ***
## a_stage1               0.922690   0.418529   2.205 0.027482 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2384.8  on 3446  degrees of freedom
## AIC: 2414.8
##
```

```
## 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 ~ progesterone_status + differentiate +
##     age + t_stage + race + sqrt_examined + estrogen_status +
##     reginol_node_positive + a_stage + progesterone_status:race,
##     family = binomial, data = bc_ref)
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                   1.191869   0.590708   2.018 0.043623 *
## progesterone_status1          0.764857   0.148235   5.160 2.47e-07 ***
## differentiate2                0.315147   0.119838   2.630 0.008544 **
## differentiate3                0.889821   0.214405   4.150 3.32e-05 ***
## differentiate4               -0.821679   0.630015  -1.304 0.192158
## age                          -0.027579   0.006257  -4.407 1.05e-05 ***
## t_stage2                     -0.428258   0.121159  -3.535 0.000408 ***
## t_stage3                     -0.457069   0.195515  -2.338 0.019399 *
## t_stage4                     -0.575844   0.401250  -1.435 0.151252
## race2                        -0.431506   0.323287  -1.335 0.181959
## race3                         2.868574   1.023458   2.803 0.005066 **
## sqrt_examined                 0.210406   0.054166   3.884 0.000103 ***
## estrogen_status1              0.556702   0.210236   2.648 0.008097 **
## reginol_node_positive        -0.144036   0.020556  -7.007 2.44e-12 ***
## a_stage1                      0.904782   0.418222   2.163 0.030510 *
## progesterone_status1:race2 -0.148944   0.384075  -0.388 0.698165
## progesterone_status1:race3 -2.779082   1.053072  -2.639 0.008315 **
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2370.7  on 3444  degrees of freedom
## AIC: 2404.7
##
## Number of Fisher Scoring iterations: 6
```

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      3445     2385.3
## 2      3431     2347.0 14   38.303 0.000467 ***
## ---
## 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).

Criterion procedures

Model with Interaction terms

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

```
## Start:  AIC=2407.04
## 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
## - n_stage                    2   2350.9 2406.9
## <none>                           2347.0 2407.0
## - race:marital_status        8   2363.9 2407.9
## - reginol_node_positive      1   2352.7 2410.7
## - estrogen_status            1   2353.8 2411.8
## - progesterone_status:race   2   2360.5 2416.5
## - t_stage                    3   2363.2 2417.2
## - sqrt_examined              1   2361.6 2419.6
## - age                        1   2365.4 2423.4
## - differentiate              3   2369.9 2423.9
##
## Step:  AIC=2406.95
## status ~ 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>                           2350.9 2406.9
## + n_stage                    2   2347.0 2407.0
## - race:marital_status        8   2367.6 2407.6
## - estrogen_status            1   2358.3 2412.3
## - progesterone_status:race   2   2364.8 2416.8
## - t_stage                    3   2367.4 2417.4
## - sqrt_examined              1   2365.9 2419.9
## - age                        1   2368.9 2422.9
## - differentiate              3   2374.2 2424.2
## - reginol_node_positive      1   2405.2 2459.2
```

```
summary(aic_selected_bin_model1)
```

```
##
## Call:
## glm(formula = status ~ 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)                 2.112234   0.441696   4.782 1.73e-06 ***
```

```
## progesterone_status1        0.742211   0.148885   4.985 6.19e-07 ***
## differentiate2              0.335116   0.120301   2.786 0.005342 **
## differentiate3              0.917027   0.216672   4.232 2.31e-05 ***
## differentiate4             -0.749826   0.651454  -1.151 0.249731
## t_stage2                   -0.420982   0.121960  -3.452 0.000557 ***
## t_stage3                   -0.466637   0.195381  -2.388 0.016924 *
## t_stage4                   -0.913598   0.349981  -2.610 0.009043 **
## age                        -0.027164   0.006477  -4.194 2.74e-05 ***
## race2                       0.077486   0.430182   0.180 0.857056
## race3                       3.427965   1.082813   3.166 0.001547 **
## estrogen_status1            0.582737   0.212177   2.746 0.006024 **
## sqrt_examined               0.210595   0.054402   3.871 0.000108 ***
## reginol_node_positive      -0.155179   0.020597  -7.534 4.92e-14 ***
## marital_status2            -0.304240   0.170592  -1.783 0.074515 .
## marital_status3             0.088802   0.177395   0.501 0.616659
## marital_status4             0.080912   0.263254   0.307 0.758574
## marital_status5            -0.989818   0.504665  -1.961 0.049840 *
## progesterone_status1:race2 -0.318614   0.393475  -0.810 0.418087
## progesterone_status1:race3 -2.874920   1.084662  -2.651 0.008037 **
## race2:marital_status2       0.642112   0.660739   0.972 0.331146
## race3:marital_status2      -0.602688   0.727758  -0.828 0.407590
## race2:marital_status3      -0.999914   0.429491  -2.328 0.019905 *
## race3:marital_status3      -1.306519   0.737359  -1.772 0.076413 .
## race2:marital_status4      -0.686535   0.621456  -1.105 0.269281
## race3:marital_status4      -1.811568   0.740454  -2.447 0.014423 *
## race2:marital_status5       0.167040   1.185987   0.141 0.887993
## race3:marital_status5      -1.411976   1.399396  -1.009 0.312979
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2350.9  on 3433  degrees of freedom
## AIC: 2406.9
##
## Number of Fisher Scoring iterations: 6
```

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

```
## Start:  AIC=2591.52
## 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   2363.9 2543.2
## - n_stage                   2   2350.9 2579.1
## - t_stage                   3   2363.2 2583.3
## - progesterone_status:race  2   2360.5 2588.7
## - reginol_node_positive     1   2352.7 2589.1
## - differentiate             3   2369.9 2590.0
## - estrogen_status           1   2353.8 2590.2
## <none>                          2347.0 2591.5
```

```
## - sqrt_examined             1   2361.6 2597.9
## - age                        1   2365.4 2601.7
##
## Step:  AIC=2543.2
## 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   2371.5 2518.2
## - n_stage                    2   2367.6 2530.6
## - t_stage                    3   2380.4 2535.2
## - reginol_node_positive      1   2369.2 2540.3
## - progesterone_status:race   2   2377.9 2540.9
## - differentiate              3   2386.1 2540.9
## - estrogen_status            1   2370.8 2542.0
## <none>                           2363.9 2543.2
## - sqrt_examined              1   2378.2 2549.3
## - age                        1   2382.8 2554.0
## + race:marital_status        8   2347.0 2591.5
##
## Step:  AIC=2518.22
## status ~ n_stage + progesterone_status + differentiate + t_stage +
##     age + race + estrogen_status + sqrt_examined + reginol_node_positive +
##     progesterone_status:race
##
##                             Df Deviance    AIC
## - n_stage                    2   2375.2 2505.6
## - t_stage                    3   2388.7 2510.9
## - reginol_node_positive      1   2376.8 2515.3
## - differentiate              3   2393.2 2515.4
## - progesterone_status:race   2   2385.3 2515.7
## - estrogen_status            1   2377.8 2516.3
## <none>                           2371.5 2518.2
## - sqrt_examined              1   2386.5 2525.0
## - age                        1   2391.2 2529.7
## + marital_status             4   2363.9 2543.2
##
## Step:  AIC=2505.63
## status ~ progesterone_status + differentiate + t_stage + age +
##     race + estrogen_status + sqrt_examined + reginol_node_positive +
##     progesterone_status:race
##
##                             Df Deviance    AIC
## - t_stage                    3   2392.6 2498.6
## - differentiate              3   2397.3 2503.2
## - progesterone_status:race   2   2389.5 2503.6
## - estrogen_status            1   2382.0 2504.3
## <none>                           2375.2 2505.6
## - sqrt_examined              1   2390.5 2512.7
## - age                        1   2394.6 2516.8
## + n_stage                    2   2371.5 2518.2
## + marital_status             4   2367.6 2530.6
## - reginol_node_positive      1   2425.7 2547.9
```

```
##
## Step:  AIC=2498.57
## status ~ progesterone_status + differentiate + age + race + estrogen_status +
##     sqrt_examined + reginol_node_positive + progesterone_status:race
##
##                             Df Deviance    AIC
## - estrogen_status            1   2399.1 2496.9
## - progesterone_status:race   2   2408.1 2497.8
## <none>                           2392.6 2498.6
## - differentiate              3   2418.5 2500.0
## - sqrt_examined              1   2406.7 2504.5
## + t_stage                    3   2375.2 2505.6
## - age                        1   2410.6 2508.4
## + n_stage                    2   2388.7 2510.9
## + marital_status             4   2384.3 2522.8
## - reginol_node_positive      1   2459.1 2556.9
##
## Step:  AIC=2496.88
## status ~ progesterone_status + differentiate + age + race + sqrt_examined +
##     reginol_node_positive + progesterone_status:race
##
##                             Df Deviance    AIC
## - progesterone_status:race   2   2413.7 2495.2
## <none>                           2399.1 2496.9
## + estrogen_status            1   2392.6 2498.6
## - differentiate              3   2428.6 2501.9
## - sqrt_examined              1   2412.7 2502.3
## + t_stage                    3   2382.0 2504.3
## - age                        1   2415.3 2505.0
## + n_stage                    2   2394.6 2508.7
## + marital_status             4   2391.4 2521.8
## - reginol_node_positive      1   2464.3 2554.0
##
## Step:  AIC=2495.15
## status ~ progesterone_status + differentiate + age + race + sqrt_examined +
##     reginol_node_positive
##
##                             Df Deviance    AIC
## <none>                           2413.7 2495.2
## - race                       2   2430.1 2495.3
## + progesterone_status:race   2   2399.1 2496.9
## + estrogen_status            1   2408.1 2497.8
## - differentiate              3   2442.7 2499.7
## - sqrt_examined              1   2427.5 2500.8
## + t_stage                    3   2395.4 2501.3
## - age                        1   2429.4 2502.7
## + n_stage                    2   2408.8 2506.5
## + marital_status             4   2406.0 2520.1
## - progesterone_status        1   2456.0 2529.3
## - reginol_node_positive      1   2478.0 2551.3
```

```
summary(bic_selected_bin_model1)
```

```
##
```

```
## Call:
## glm(formula = status ~ progesterone_status + differentiate +
##     age + race + sqrt_examined + reginol_node_positive, family = binomial,
##     data = bc_ref)
##
## Coefficients:
##                         Estimate Std. Error z value Pr(>|z|)
## (Intercept)             2.131645   0.407669   5.229 1.71e-07 ***
## progesterone_status1    0.821413   0.122031   6.731 1.68e-11 ***
## differentiate2          0.383320   0.117279   3.268  0.00108 **
## differentiate3          0.970160   0.211839   4.580 4.66e-06 ***
## differentiate4         -0.889032   0.605519  -1.468  0.14205
## age                    -0.024176   0.006164  -3.922 8.77e-05 ***
## race2                  -0.537937   0.174653  -3.080  0.00207 **
## race3                   0.560248   0.241010   2.325  0.02009 *
## sqrt_examined           0.199883   0.053753   3.719  0.00020 ***
## reginol_node_positive -0.162239   0.019701  -8.235  < 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: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2413.7  on 3451  degrees of freedom
## AIC: 2433.7
##
## 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=2417.34
## status ~ n_stage + progesterone_status + differentiate + t_stage +
##     age + race + estrogen_status + sqrt_examined + reginol_node_positive
##
##                         Df Deviance    AIC
## <none>                       2385.3 2417.3
## - n_stage                2   2389.5 2417.5
## - reginol_node_positive  1   2389.9 2419.9
## - estrogen_status        1   2390.8 2420.8
## - race                   2   2401.2 2429.2
## - t_stage                3   2403.7 2429.7
## - sqrt_examined          1   2400.4 2430.4
## - differentiate          3   2406.7 2432.7
```

```
## - age                    1   2404.4 2434.4
## - progesterone_status    1   2406.3 2436.3
```

```
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)              2.138220   0.428713   4.988 6.12e-07 ***
## n_stage2                -0.363094   0.194354  -1.868 0.061733 .
## n_stage3                -0.673870   0.356822  -1.889 0.058954 .
## progesterone_status1     0.663852   0.140389   4.729 2.26e-06 ***
## differentiate2           0.305799   0.119618   2.556 0.010574 *
## differentiate3           0.864405   0.214039   4.039 5.38e-05 ***
## differentiate4          -0.812407   0.638610  -1.272 0.203320
## t_stage2                -0.442975   0.120767  -3.668 0.000244 ***
## t_stage3                -0.481292   0.193867  -2.483 0.013043 *
## t_stage4                -0.958209   0.349481  -2.742 0.006110 **
## age                     -0.027013   0.006254  -4.320 1.56e-05 ***
## race2                   -0.534532   0.176578  -3.027 0.002469 **
## race3                    0.552329   0.241117   2.291 0.021980 *
## estrogen_status1         0.491848   0.208508   2.359 0.018330 *
## sqrt_examined            0.210528   0.054200   3.884 0.000103 ***
## reginol_node_positive -0.081054   0.037808  -2.144 0.032043 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2385.3  on 3445  degrees of freedom
## AIC: 2417.3
##
## Number of Fisher Scoring iterations: 5
```

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

```
## Start:  AIC=2515.73
## status ~ n_stage + progesterone_status + differentiate + t_stage +
##     age + race + estrogen_status + sqrt_examined + reginol_node_positive
##
##                          Df Deviance    AIC
## - n_stage                 2   2389.5 2503.6
## - t_stage                 3   2403.7 2509.7
## - reginol_node_positive   1   2389.9 2512.2
## - differentiate           3   2406.7 2512.6
## - estrogen_status         1   2390.8 2513.0
## - race                    2   2401.2 2515.3
```

```
## <none>                       2385.3 2515.7
## - sqrt_examined          1   2400.4 2522.7
## - age                    1   2404.4 2526.7
## - progesterone_status    1   2406.3 2528.5
##
## Step:  AIC=2503.55
## status ~ progesterone_status + differentiate + t_stage + age +
##     race + estrogen_status + sqrt_examined + reginol_node_positive
##
##                         Df Deviance    AIC
## - t_stage                3   2408.1 2497.8
## - differentiate          3   2411.2 2500.9
## - estrogen_status        1   2395.4 2501.3
## <none>                       2389.5 2503.6
## - race                   2   2406.0 2503.8
## - sqrt_examined          1   2404.9 2510.8
## - age                    1   2408.2 2514.2
## + n_stage                2   2385.3 2515.7
## - progesterone_status    1   2410.5 2516.4
## - reginol_node_positive  1   2438.6 2544.6
##
## Step:  AIC=2497.75
## status ~ progesterone_status + differentiate + age + race + estrogen_status +
##     sqrt_examined + reginol_node_positive
##
##                         Df Deviance    AIC
## - estrogen_status        1   2413.7 2495.2
## <none>                       2408.1 2497.8
## - race                   2   2424.5 2497.9
## - differentiate          3   2433.7 2498.8
## + t_stage                3   2389.5 2503.6
## - sqrt_examined          1   2422.5 2504.0
## - age                    1   2425.3 2506.8
## + n_stage                2   2403.7 2509.7
## - progesterone_status    1   2429.8 2511.2
## - reginol_node_positive  1   2473.7 2555.2
##
## Step:  AIC=2495.15
## status ~ progesterone_status + differentiate + age + race + sqrt_examined +
##     reginol_node_positive
##
##                         Df Deviance    AIC
## <none>                       2413.7 2495.2
## - race                   2   2430.1 2495.3
## + estrogen_status        1   2408.1 2497.8
## - differentiate          3   2442.7 2499.7
## - sqrt_examined          1   2427.5 2500.8
## + t_stage                3   2395.4 2501.3
## - age                    1   2429.4 2502.7
## + n_stage                2   2408.8 2506.5
## - progesterone_status    1   2456.0 2529.3
## - reginol_node_positive  1   2478.0 2551.3
```

```r
summary(bic_selected_bin_model2)
```

```
##
## Call:
## glm(formula = status ~ progesterone_status + differentiate +
##     age + race + sqrt_examined + reginol_node_positive, family = binomial,
##     data = newbc)
##
## Coefficients:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)              2.131645   0.407669   5.229 1.71e-07 ***
## progesterone_status1     0.821413   0.122031   6.731 1.68e-11 ***
## differentiate2           0.383320   0.117279   3.268  0.00108 **
## differentiate3           0.970160   0.211839   4.580 4.66e-06 ***
## differentiate4          -0.889032   0.605519  -1.468  0.14205
## age                     -0.024176   0.006164  -3.922 8.77e-05 ***
## race2                   -0.537937   0.174653  -3.080  0.00207 **
## race3                    0.560248   0.241010   2.325  0.02009 *
## sqrt_examined            0.199883   0.053753   3.719  0.00020 ***
## reginol_node_positive -0.162239   0.019701  -8.235  < 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: 2613.3  on 3460  degrees of freedom
## Residual deviance: 2413.7  on 3451  degrees of freedom
## AIC: 2433.7
##
## 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.

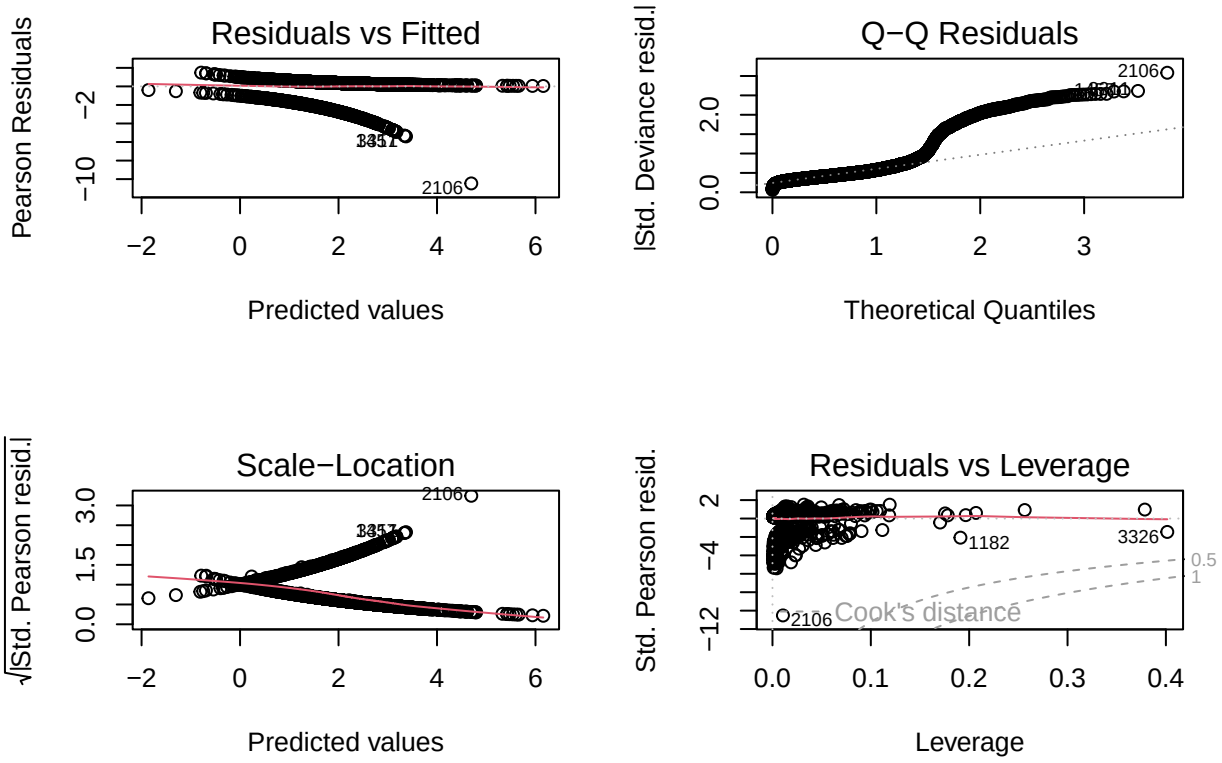
Plots to check the model assumptions for four candidate models:

```r
# model1 assumption check
model1 <- glm(status ~ 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)
# check multicollinearity
vif(model1)
```

```
## there are higher-order terms (interactions) in this model
## consider setting type = 'predictor'; see ?vif
```

```
##                                GVIF Df GVIF^(1/(2*Df))
## progesterone_status        1.474366  1        1.214235
## differentiate              1.123135  3        1.019542
## t_stage                    1.111721  3        1.017808
## age                        1.106325  1        1.051820
## race                     116.751962  2        3.287124
## estrogen_status            1.376564  1        1.173271
## sqrt_examined              1.138660  1        1.067080
## reginol_node_positive      1.188240  1        1.090064
## marital_status             3.373595  4        1.164157
## progesterone_status:race  67.733208  2        2.868801
## race:marital_status       18.261521  8        1.199074
```

```
# Model diagnostics - Plotting to check for influential outliers, equal variance
par(mfrow = c(2, 2))
plot(model1)
```




```
# Compute AUC for model1 assessment
roc_result1 <- roc(bc_ref$status, fitted(model1))
```

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

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

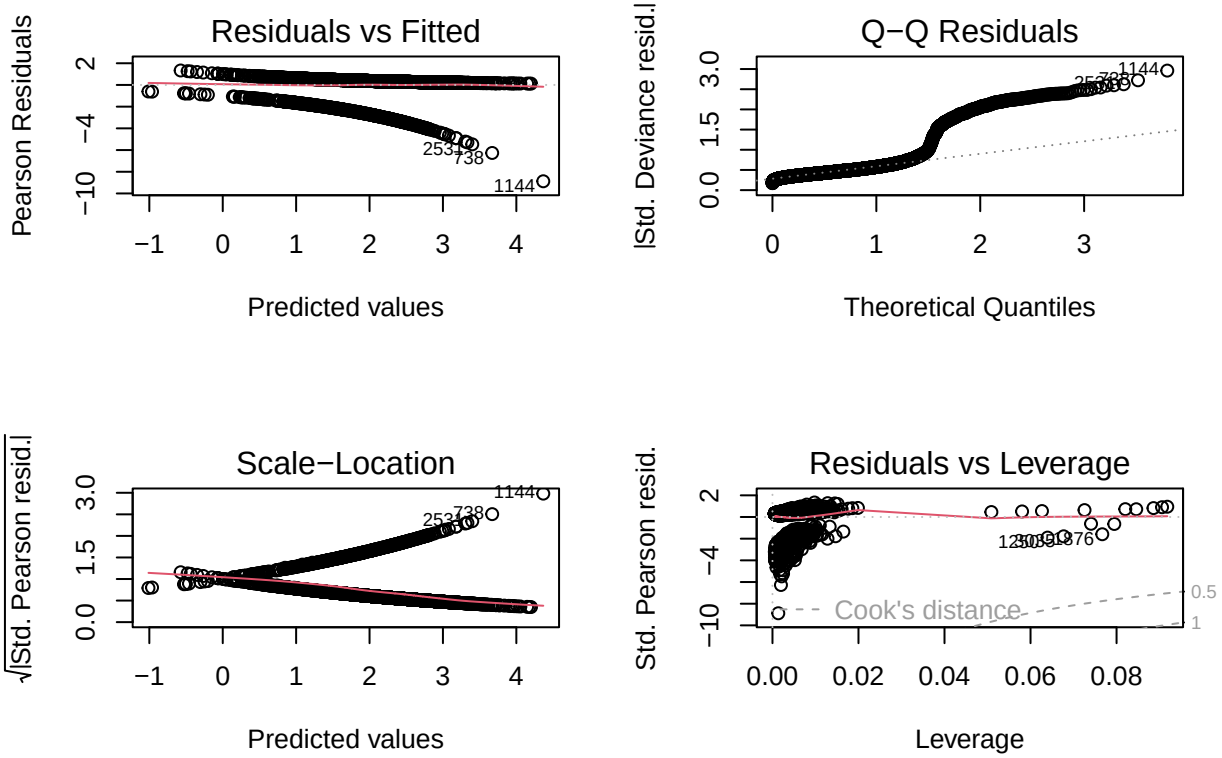
```r
auc_result1 <- auc(roc_result1)
print(auc_result1)
```

```
## Area under the curve: 0.7291
```

```r
# model2 assumption check
model2 <- glm(status ~ progesterone_status + differentiate + age + race + sqrt_examined +
    reginol_node_positive,
                  data=bc_ref, family=binomial)
# check multicollinearity
vif(model2)
```

```
##                            GVIF Df GVIF^(1/(2*Df))
## progesterone_status    1.030425  1        1.015099
## differentiate          1.060036  3        1.009765
## age                    1.021612  1        1.010748
## race                   1.019878  2        1.004933
## sqrt_examined          1.129211  1        1.062643
## reginol_node_positive 1.129159  1        1.062619
```

```r
# Model diagnostics - Plotting to check for influential outliers, equal variance
par(mfrow = c(2, 2))
plot(model2)
```



```r
# Compute AUC for model2 assessment
roc_result2 <- roc(bc_ref$status, fitted(model2))
```

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

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

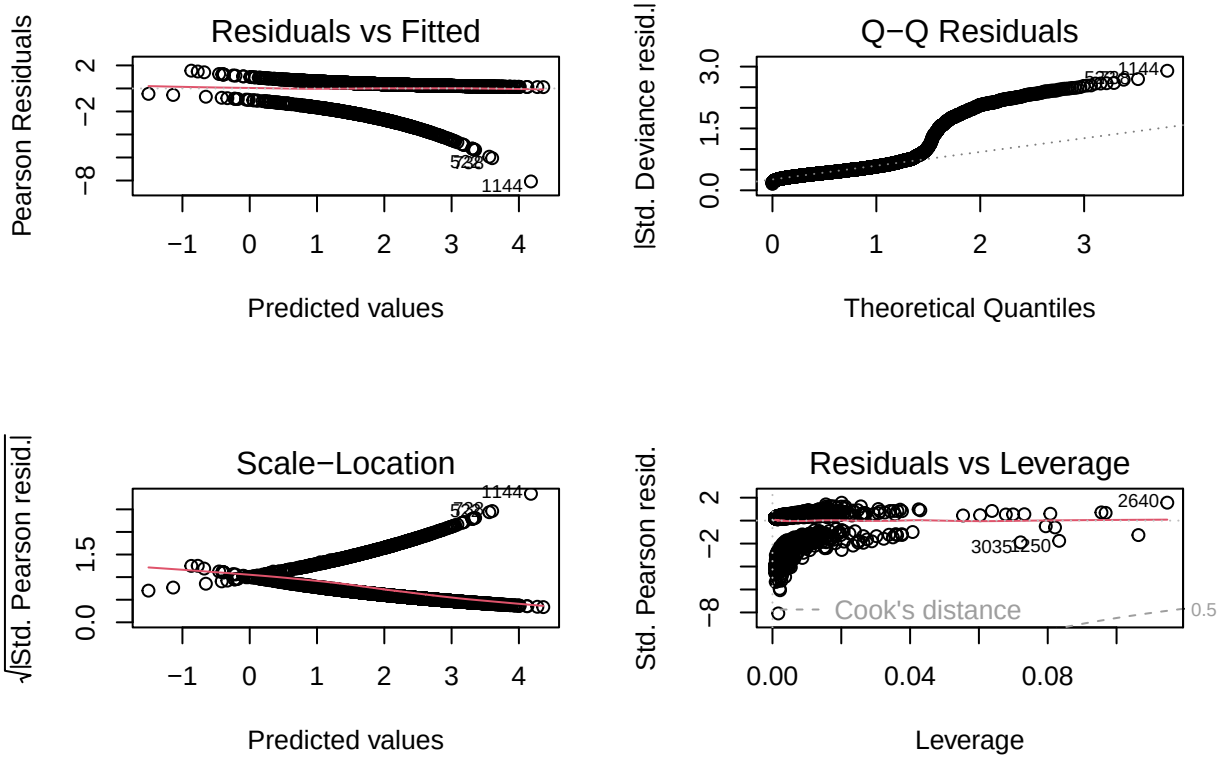
```r
auc_result2 <- auc(roc_result2)
print(auc_result2)
```

```
## Area under the curve: 0.7007
```

```r
# model3 assumption check
model3 <- glm(status ~ n_stage + progesterone_status + differentiate + t_stage +
    age + race + estrogen_status + sqrt_examined + reginol_node_positive,
                data=bc_ref, family=binomial)
# check multicollinearity
vif(model3)
```

```
##                           GVIF Df GVIF^(1/(2*Df))
## n_stage                3.936561  2        1.408573
## progesterone_status    1.342099  1        1.158490
## differentiate          1.110364  3        1.017601
## t_stage                1.097076  3        1.015561
## age                    1.036114  1        1.017897
## race                   1.025302  2        1.006266
## estrogen_status        1.379009  1        1.174312
## sqrt_examined          1.138065  1        1.066801
## reginol_node_positive 4.053773  1        2.013398
```

```r
# Model diagnostics - Plotting to check for influential outliers, equal variance
par(mfrow = c(2, 2))
plot(model3)
```




```
# Compute AUC for model3 assessment
roc_result3 <- roc(bc_ref$status, fitted(model3))
```

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

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

```
auc_result3 <- auc(roc_result3)
print(auc_result3)
```

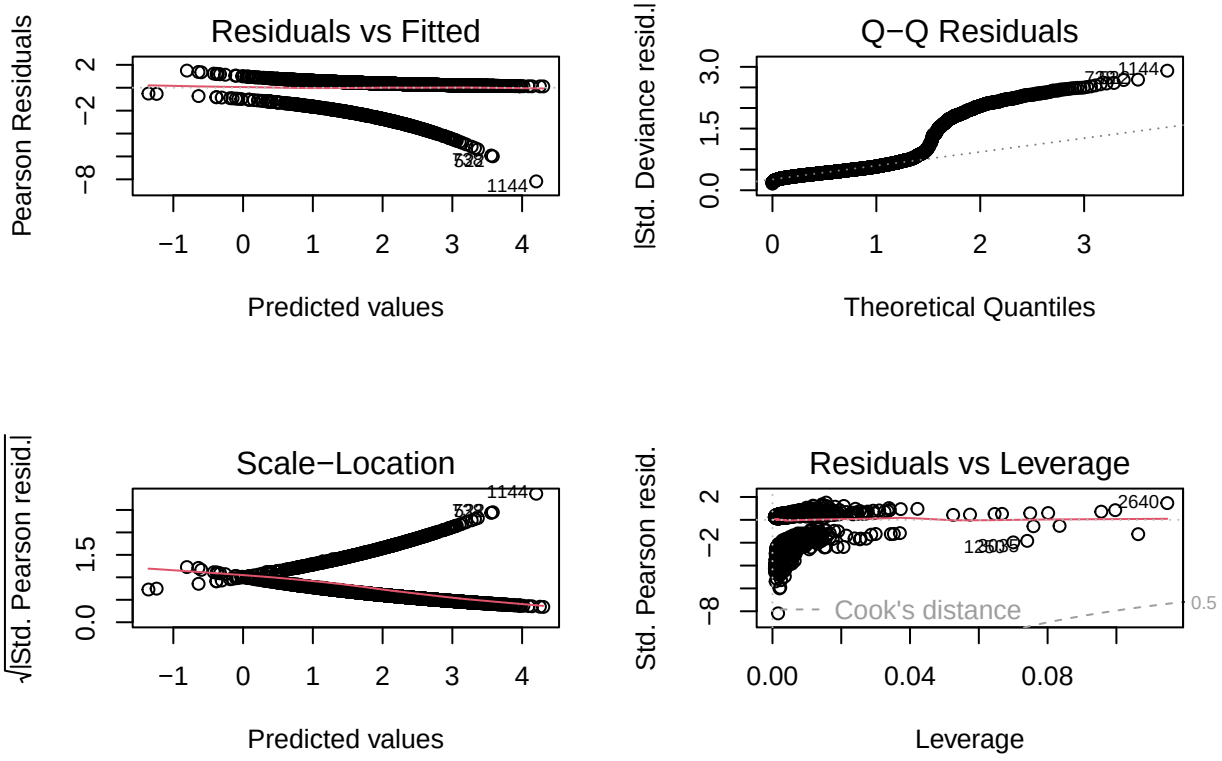
```
## Area under the curve: 0.7128
```

```
# model4 assumption check
model4 <- glm(status ~ progesterone_status + differentiate + t_stage + age +
                race + estrogen_status + sqrt_examined + reginol_node_positive,
                data=bc_ref, family=binomial)
# check multicollinearity
vif(model4)
```

```
##                          GVIF Df GVIF^(1/(2*Df))
## progesterone_status   1.341348  1        1.158166
## differentiate         1.103290  3        1.016518
## t_stage               1.093337  3        1.014984
## age                   1.034692  1        1.017198
```

```
## race                   1.024110  2        1.005974
## estrogen_status        1.376595  1        1.173284
## sqrt_examined          1.131523  1        1.063731
## reginol_node_positive 1.178496  1        1.085586
```

```
# Model diagnostics - Plotting to check for influential outliers, equal variance
par(mfrow = c(2, 2))
plot(model4)
```




```
# Compute AUC for model4 assessment
roc_result4 <- roc(bc_ref$status, fitted(model4))
```

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

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

```
auc_result4 <- auc(roc_result4)
print(auc_result4)
```

```
## Area under the curve: 0.7119
```

For the four candidate models: The diagnostic charts for logistic regression models imply that the assumptions are largely met. All residuals versus fitted values plot shows a pattern that could hint at some

non-linearity, but it's subtle. And there are bare outliers shown in the Q-Q plot. The scale-location plots suggest consistent variance across the data. VIF values also suggest that the predictors in these models are relatively independent of each other. An Area Under the Receiver Operating Characteristic (ROC) Curve (AUC) of around 0.7indicates 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>         <fct>
## 1    68 1     1              1       1       1          1             3
## 2    50 1     1              2       2       2          2             2
## 3    58 1     1              1       1       1          1             3
## 4    47 1     1              2       1       4          1             3
## 5    51 1     3              1       1       1          2             2
## 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)
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
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
print(cvmodel1)
```

```
## Generalized Linear Model
##
## 3115 samples
##    9 predictor
```

```
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 2803, 2803, 2804, 2804, 2803, 2804, ...
## Resampling results:
##
##   RMSE       Rsquared    MAE
##   0.3233196  0.06097161  0.2065152
```

```
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   2   1
##          1  35 308
##
##                Accuracy : 0.896
##                  95% CI : (0.8589, 0.9261)
##     No Information Rate : 0.8931
##     P-Value [Acc > NIR] : 0.4744
##
##                   Kappa : 0.0853
##
##  Mcnemar's Test P-Value : 3.798e-08
##
##             Sensitivity : 0.054054
##             Specificity : 0.996764
##          Pos Pred Value : 0.666667
##          Neg Pred Value : 0.897959
##              Prevalence : 0.106936
##          Detection Rate : 0.005780
##    Detection Prevalence : 0.008671
##       Balanced Accuracy : 0.525409
##
##        '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
##
## 3115 samples
##    6 predictor
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 2803, 2803, 2804, 2804, 2803, 2804, ...
## Resampling results:
##
##   RMSE       Rsquared    MAE
##   0.3227789  0.06145303  0.2086395
```

```
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   2   1
##          1  35 308
##
##                Accuracy : 0.896
##                  95% CI : (0.8589, 0.9261)
##     No Information Rate : 0.8931
##     P-Value [Acc > NIR] : 0.4744
##
##                   Kappa : 0.0853
##
##  Mcnemar's Test P-Value : 3.798e-08
##
##             Sensitivity : 0.054054
##             Specificity : 0.996764
##          Pos Pred Value : 0.666667
##          Neg Pred Value : 0.897959
##              Prevalence : 0.106936
##          Detection Rate : 0.005780
##    Detection Prevalence : 0.008671
##       Balanced Accuracy : 0.525409
##
##        '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
##
## 3115 samples
##    9 predictor
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 2803, 2803, 2804, 2804, 2803, 2804, ...
## Resampling results:
##
##   RMSE       Rsquared    MAE
##   0.3215198  0.06874745  0.2063091
```

```
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   2   2
##          1  35 307
##
##                Accuracy : 0.8931
##                  95% CI : (0.8556, 0.9236)
##     No Information Rate : 0.8931
##     P-Value [Acc > NIR] : 0.5436
##
##                   Kappa : 0.0783
##
##  Mcnemar's Test P-Value : 1.435e-07
```

```
##
##             Sensitivity : 0.05405
##             Specificity : 0.99353
##          Pos Pred Value : 0.50000
##          Neg Pred Value : 0.89766
##              Prevalence : 0.10694
##          Detection Rate : 0.00578
##    Detection Prevalence : 0.01156
##       Balanced Accuracy : 0.52379
##
##        '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
##
## 3115 samples
##    6 predictor
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 2803, 2803, 2804, 2804, 2803, 2804, ...
## Resampling results:
##
##   RMSE       Rsquared    MAE
##   0.3227789  0.06145303  0.2086395
```

```
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   1   2
##          1  36 307
##
##                Accuracy : 0.8902
##                  95% CI : (0.8524, 0.9211)
##     No Information Rate : 0.8931
##     P-Value [Acc > NIR] : 0.6111
##
##                   Kappa : 0.0345
##
##  Mcnemar's Test P-Value : 8.636e-08
##
##             Sensitivity : 0.027027
##             Specificity : 0.993528
##          Pos Pred Value : 0.333333
##          Neg Pred Value : 0.895044
##              Prevalence : 0.106936
##          Detection Rate : 0.002890
##    Detection Prevalence : 0.008671
##       Balanced Accuracy : 0.510277
##
##        '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