Data analysis

12/09/2023

Libraries

```
library(tidyverse)
library(readr)
library(boot)
library(table1)
library(gridExtra)
library(MASS)
library(car)
library(dplyr)
library(leaps)
library(corrplot)
```

Data Clean

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

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

```
summary(breastcancer_data)
```

```
##       age            race           marital_status       t_stage
##  Min.   :30.00   Length:4024        Length:4024        Length:4024
##  1st Qu.:47.00   Class :character   Class :character   Class :character
##  Median :54.00   Mode  :character   Mode  :character   Mode  :character
##  Mean   :53.97
##  3rd Qu.:61.00
##  Max.   :69.00
##    n_stage           x6th_stage        differentiate         grade
##  Length:4024        Length:4024        Length:4024        Length:4024
```

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

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

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

Descriptive statistics for all variables

```
summary(bc)
```

```
##       age             race       marital_status     t_stage
##  Min.   :30.00   Min.   :1.000   Min.   :1.000   Min.   :1.000
##  1st Qu.:47.00   1st Qu.:1.000   1st Qu.:1.000   1st Qu.:1.000
##  Median :54.00   Median :1.000   Median :1.000   Median :2.000
##  Mean   :53.97   Mean   :1.231   Mean   :1.646   Mean   :1.785
##  3rd Qu.:61.00   3rd Qu.:1.000   3rd Qu.:2.000   3rd Qu.:2.000
##  Max.   :69.00   Max.   :3.000   Max.   :5.000   Max.   :4.000
##     n_stage        x6th_stage    differentiate       grade
##  Min.   :1.000   Min.   :1.000   Min.   :1.000   Min.   :1.000
##  1st Qu.:1.000   1st Qu.:1.000   1st Qu.:1.000   1st Qu.:2.000
##  Median :1.000   Median :2.000   Median :2.000   Median :2.000
##  Mean   :1.438   Mean   :2.405   Mean   :1.868   Mean   :2.151
##  3rd Qu.:2.000   3rd Qu.:4.000   3rd Qu.:2.000   3rd Qu.:3.000
##  Max.   :3.000   Max.   :5.000   Max.   :4.000   Max.   :4.000
##     a_stage         tumor_size     estrogen_status  progesterone_status
##  Min.   :0.0000   Min.   :  1.00   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:1.0000   1st Qu.: 16.00   1st Qu.:1.0000   1st Qu.:1.0000
##  Median :1.0000   Median : 25.00   Median :1.0000   Median :1.0000
##  Mean   :0.9771   Mean   : 30.47   Mean   :0.9332   Mean   :0.8265
##  3rd Qu.:1.0000   3rd Qu.: 38.00   3rd Qu.:1.0000   3rd Qu.:1.0000
##  Max.   :1.0000   Max.   :140.00   Max.   :1.0000   Max.   :1.0000
##  regional_node_examined reginol_node_positive survival_months     status
##  Min.   : 1.00          Min.   : 1.000        Min.   :  1.0   Min.   :0.0000
```

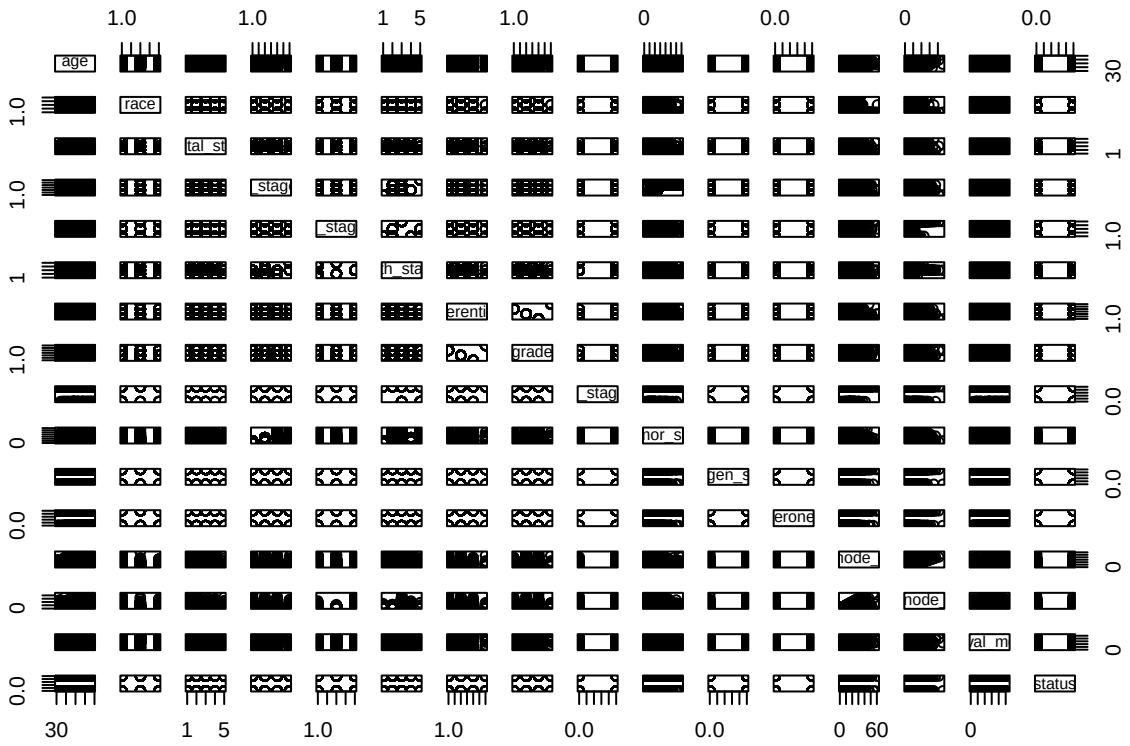
```
##  1st Qu.: 9.00          1st Qu.: 1.000        1st Qu.: 56.0   1st Qu.:1.0000
##  Median :14.00          Median : 2.000        Median : 73.0   Median :1.0000
##  Mean   :14.36          Mean   : 4.158        Mean   : 71.3   Mean   :0.8469
##  3rd Qu.:19.00          3rd Qu.: 5.000        3rd Qu.: 90.0   3rd Qu.:1.0000
##  Max.   :61.00          Max.   :46.000        Max.   :107.0   Max.   :1.0000
```

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

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

Covariance and Correlation

```
plot(bc)
```



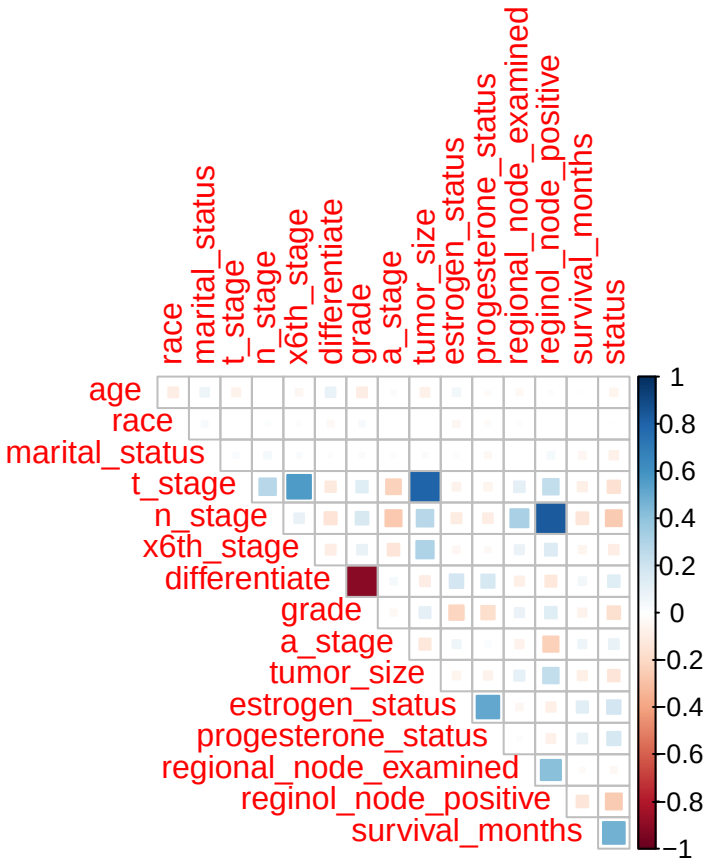

```
cor(bc) |>
  knitr::kable(digits=4,caption="Correlation for all variables")
```

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

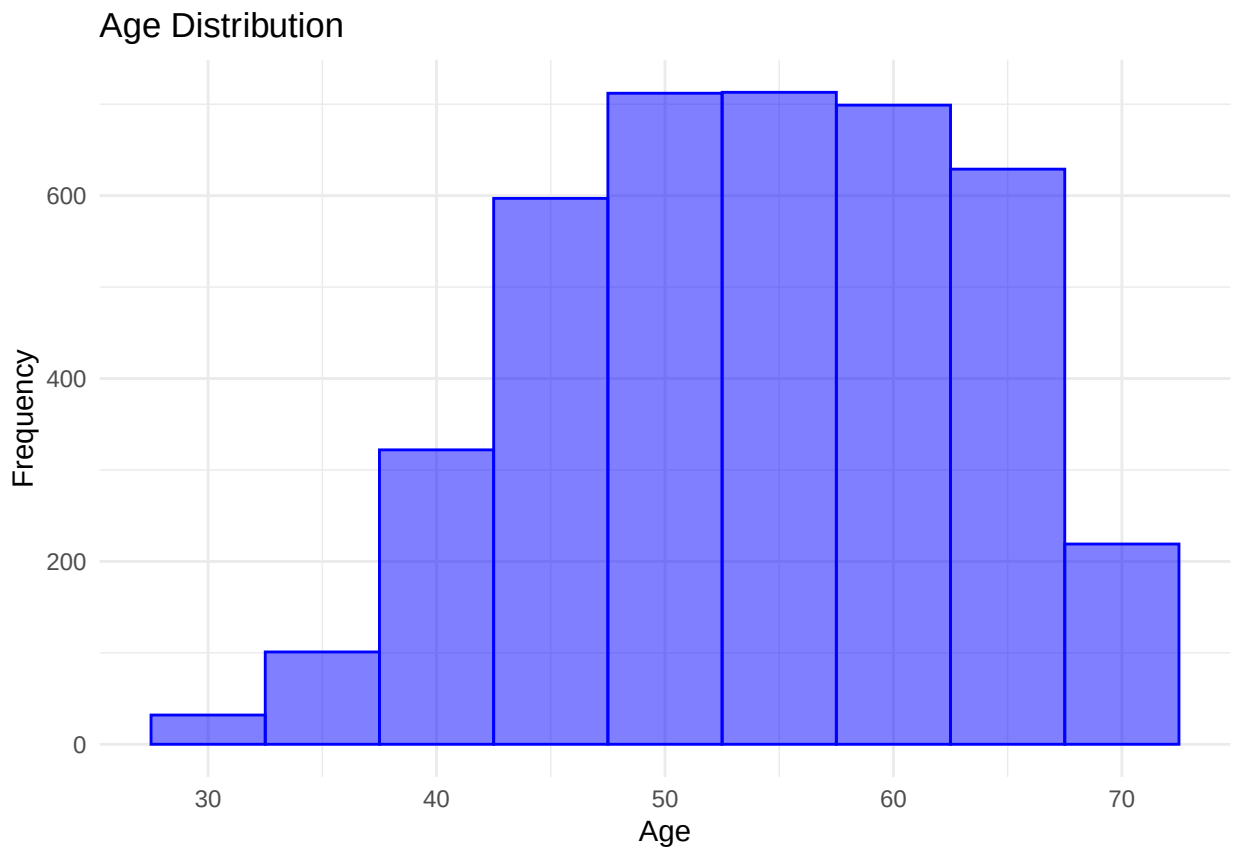
Another plot for correlation

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

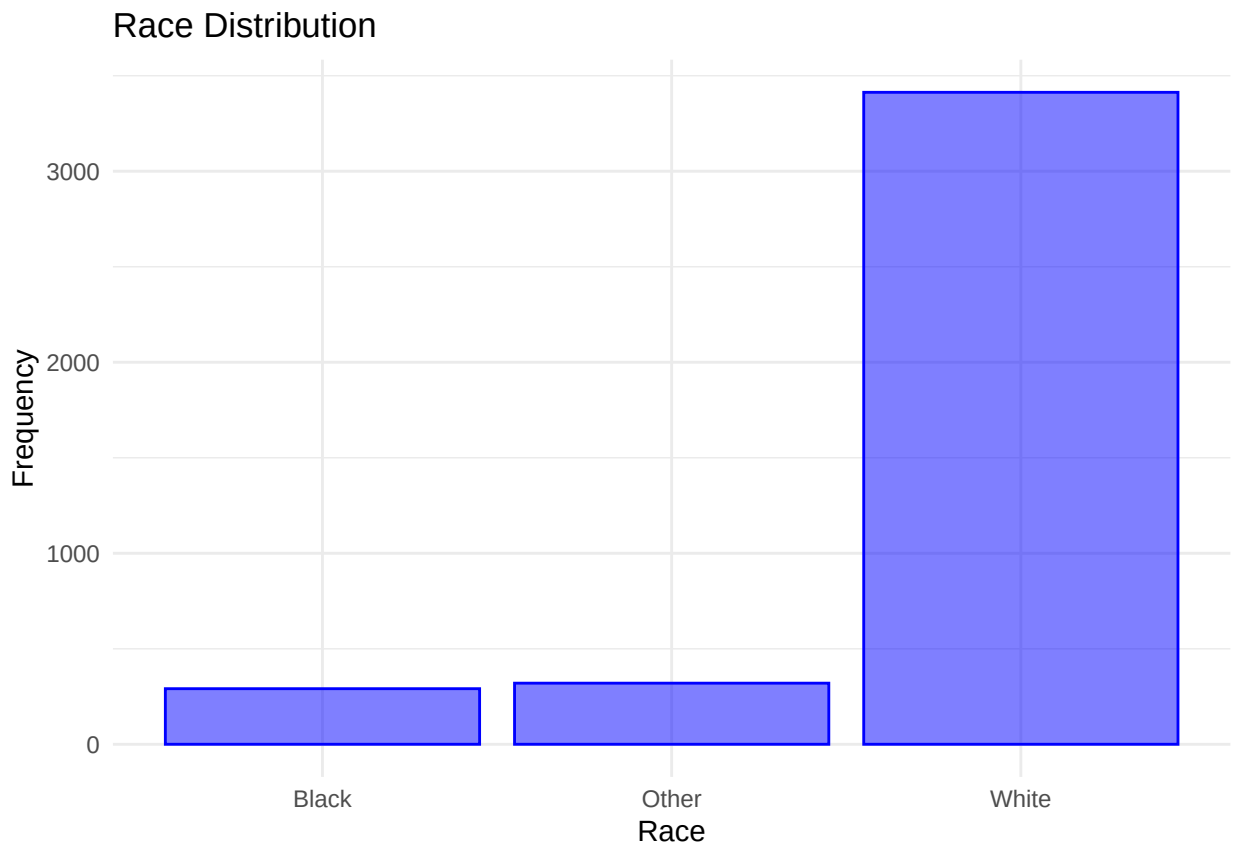


Exploratory visualisation

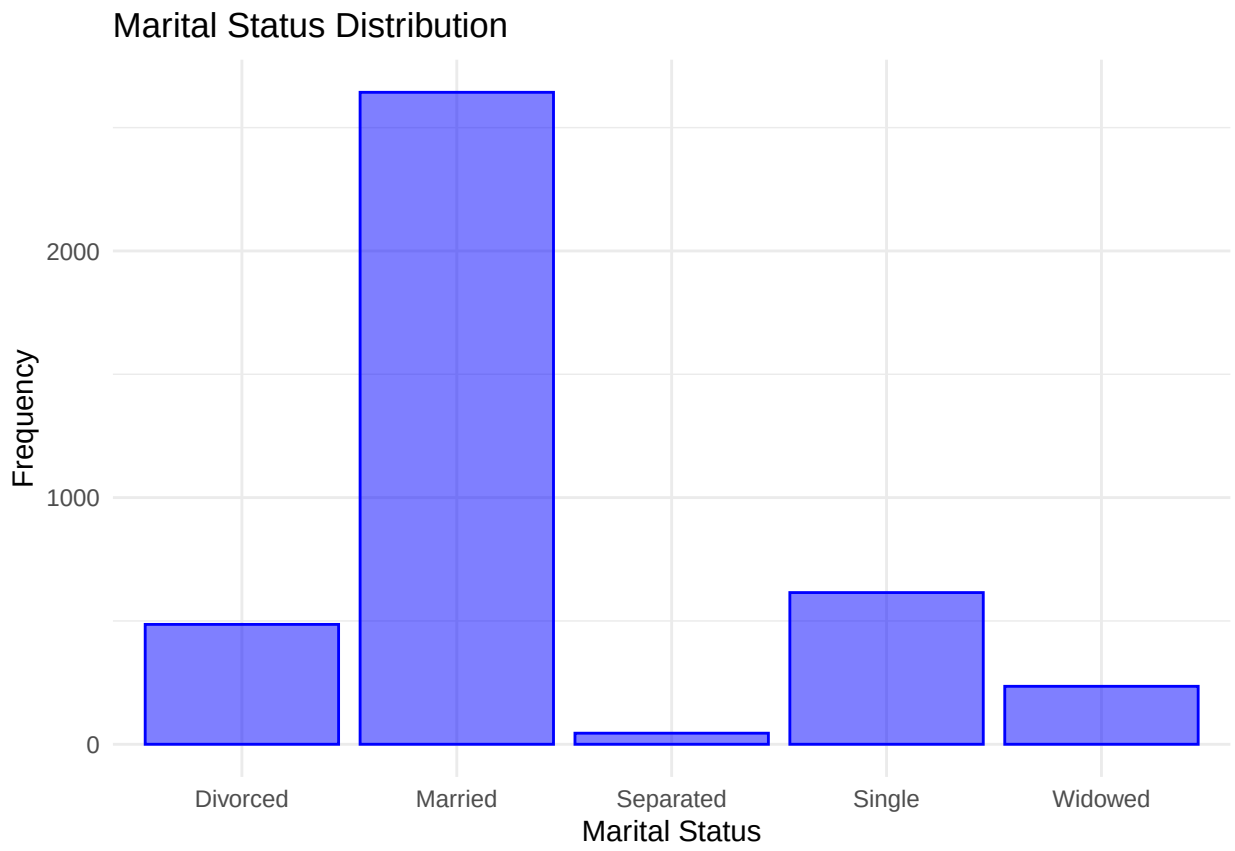
```
plot1age =
  breastcancer_data|>
  ggplot(aes(x = age)) +
  geom_histogram(color = "blue", fill = alpha("blue", 0.5), binwidth = 5) +
  theme_minimal() +
  labs(
    title = "Age Distribution",
    x = "Age",
    y = "Frequency"
  )
plot1age
```



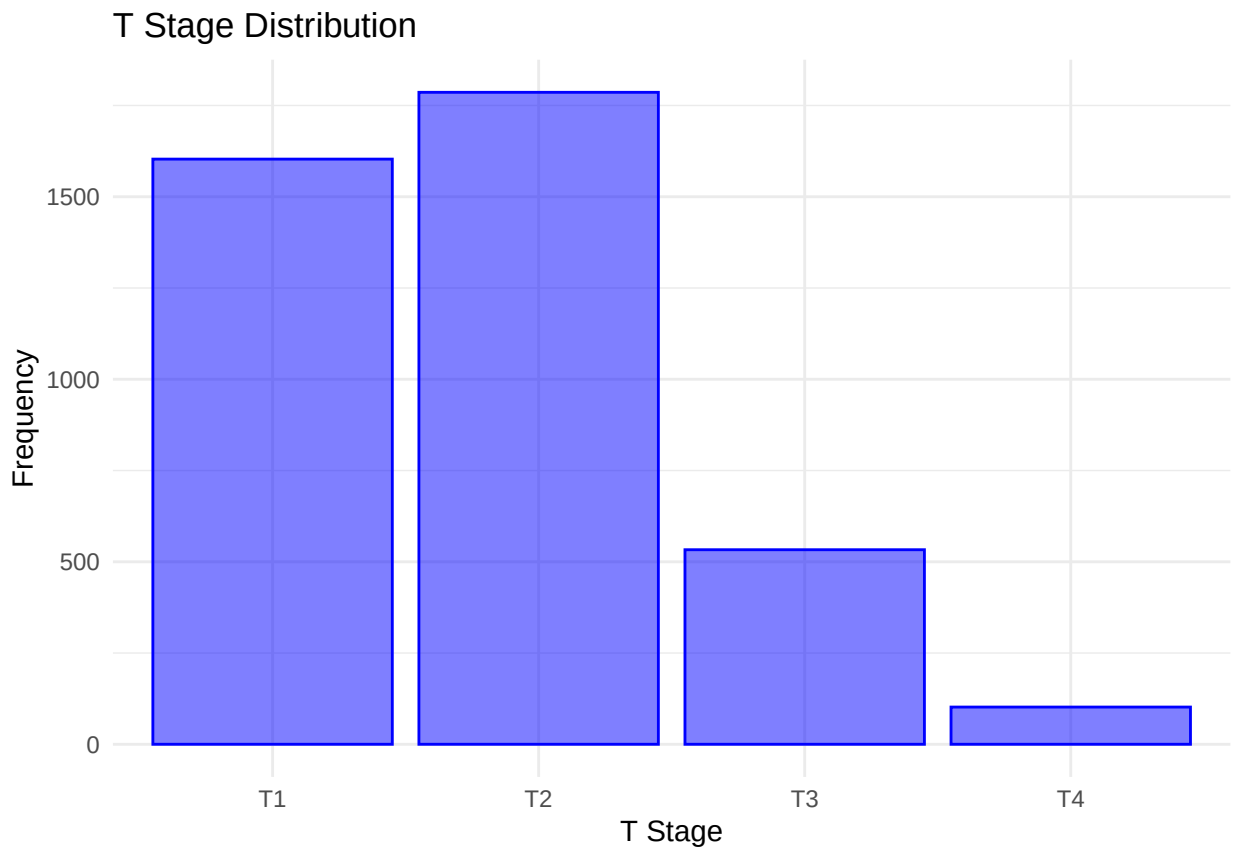

```
plot2race =
  breastcancer_data|>
  ggplot(aes(x = race)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Race Distribution",
    x = "Race",
    y = "Frequency"
  )
plot2race
```



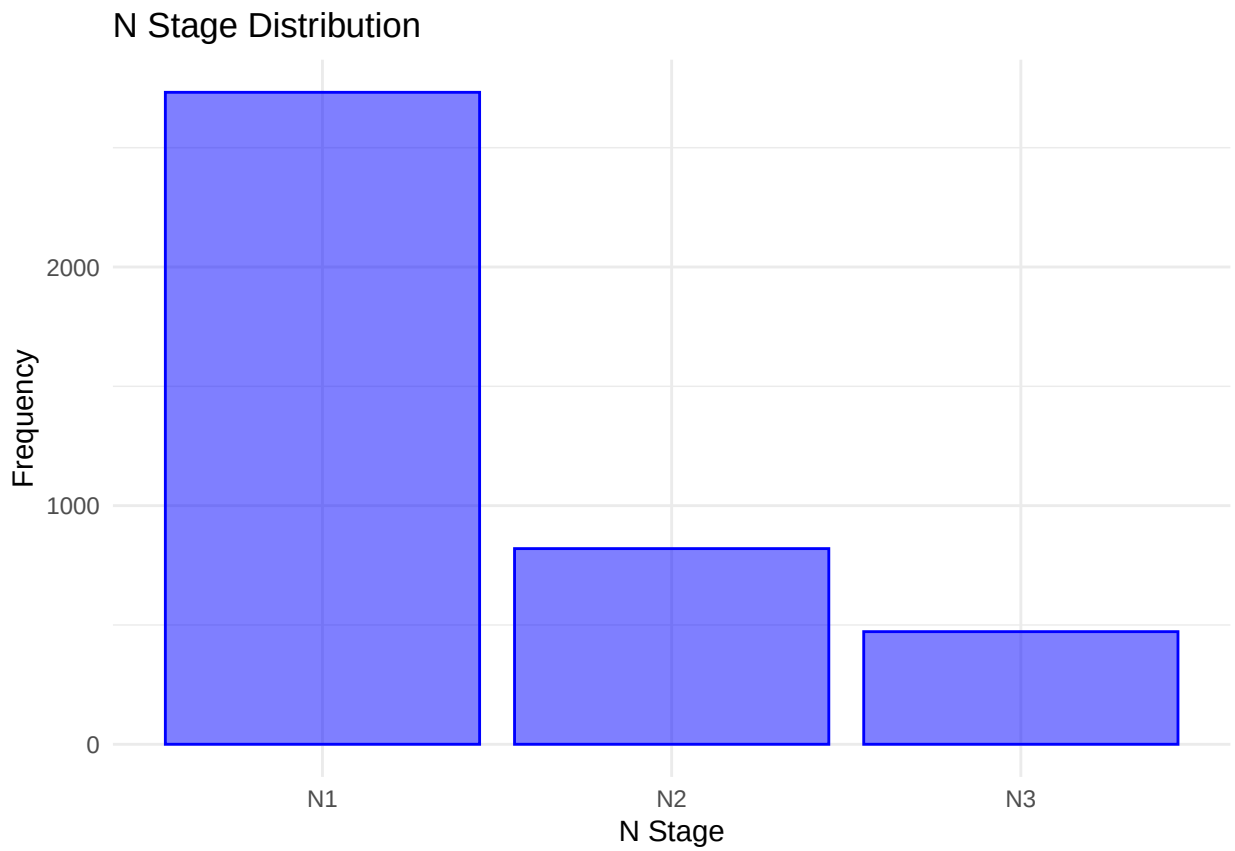

```
plot3marital =
  breastcancer_data|>
  ggplot(aes(x = marital_status)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Marital Status Distribution",
    x = "Marital Status",
    y = "Frequency"
  )

plot3marital
```



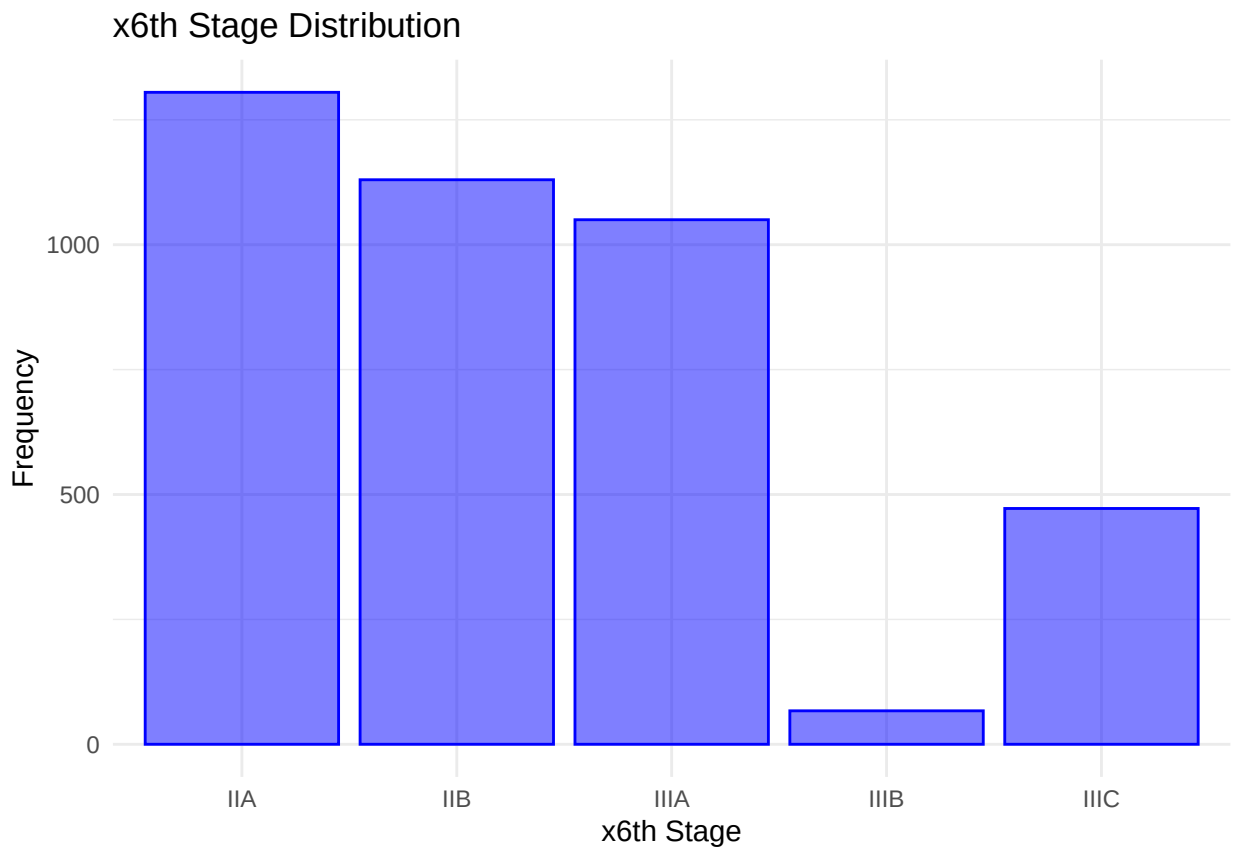

```
plot4tstage =
  breastcancer_data|>
  ggplot(aes(x = t_stage)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "T Stage Distribution",
    x = "T Stage",
    y = "Frequency"
  )

plot4tstage
```



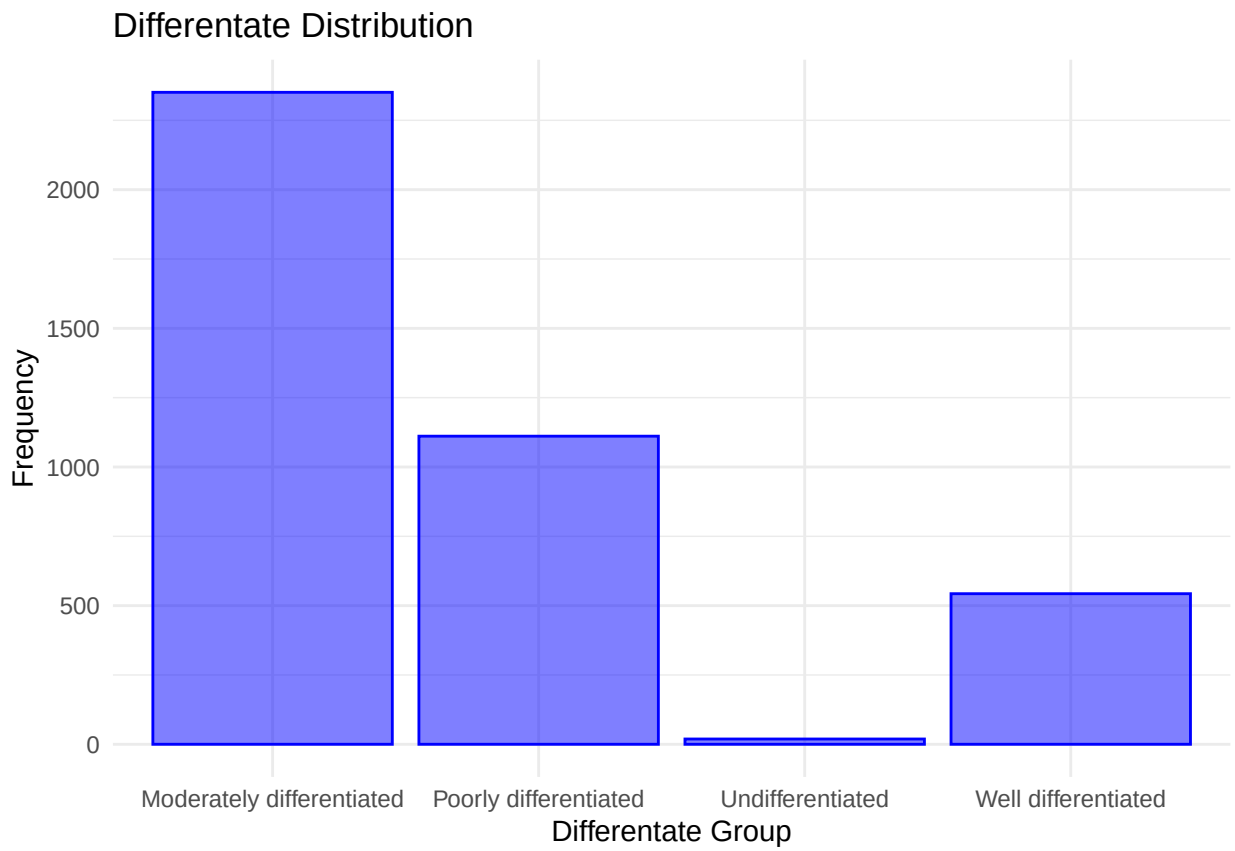

```
plot5nstage =
  breastcancer_data|>
  ggplot(aes(x = n_stage)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "N Stage Distribution",
    x = "N Stage",
    y = "Frequency"
  )

plot5nstage
```



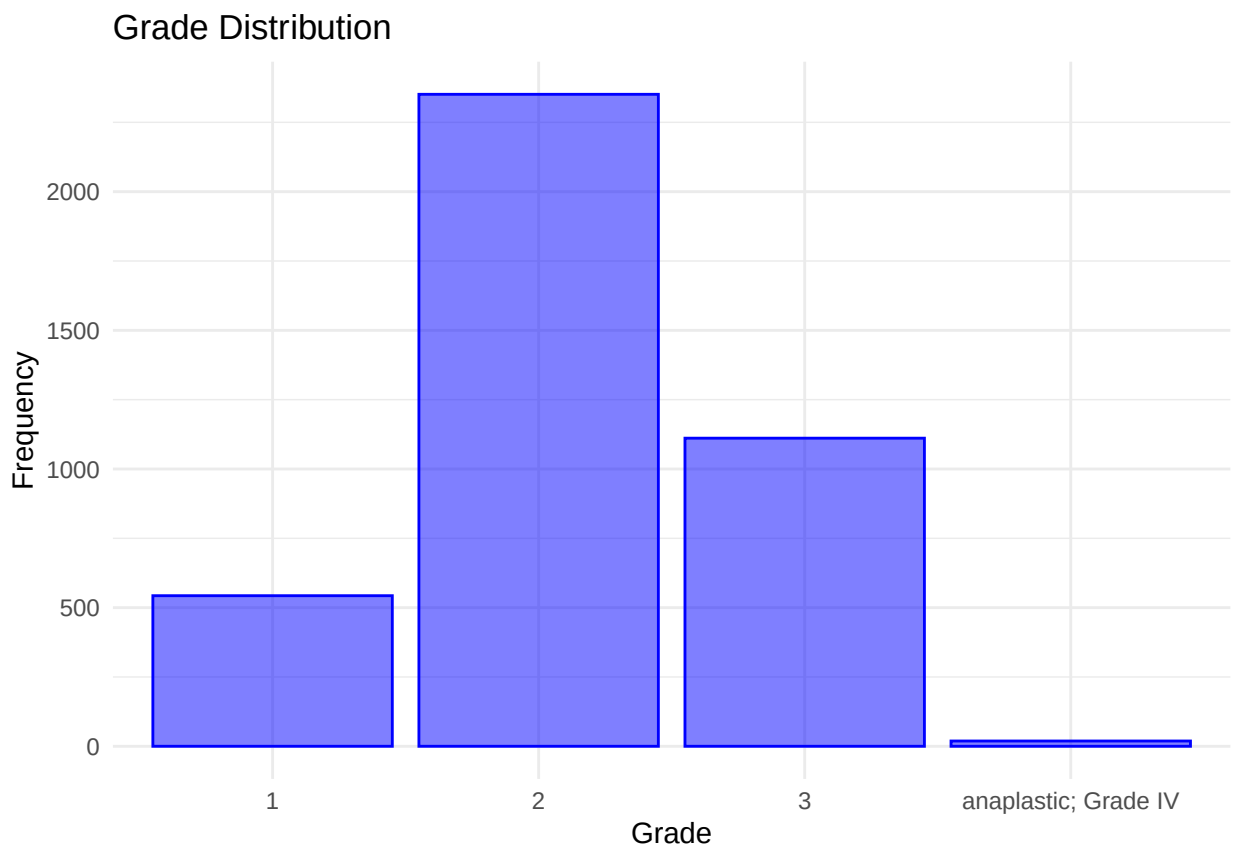

```
plot6x6thstage =
  breastcancer_data|>
  ggplot(aes(x = x6th_stage)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "x6th Stage Distribution",
    x = "x6th Stage",
    y = "Frequency"
  )

plot6x6thstage
```



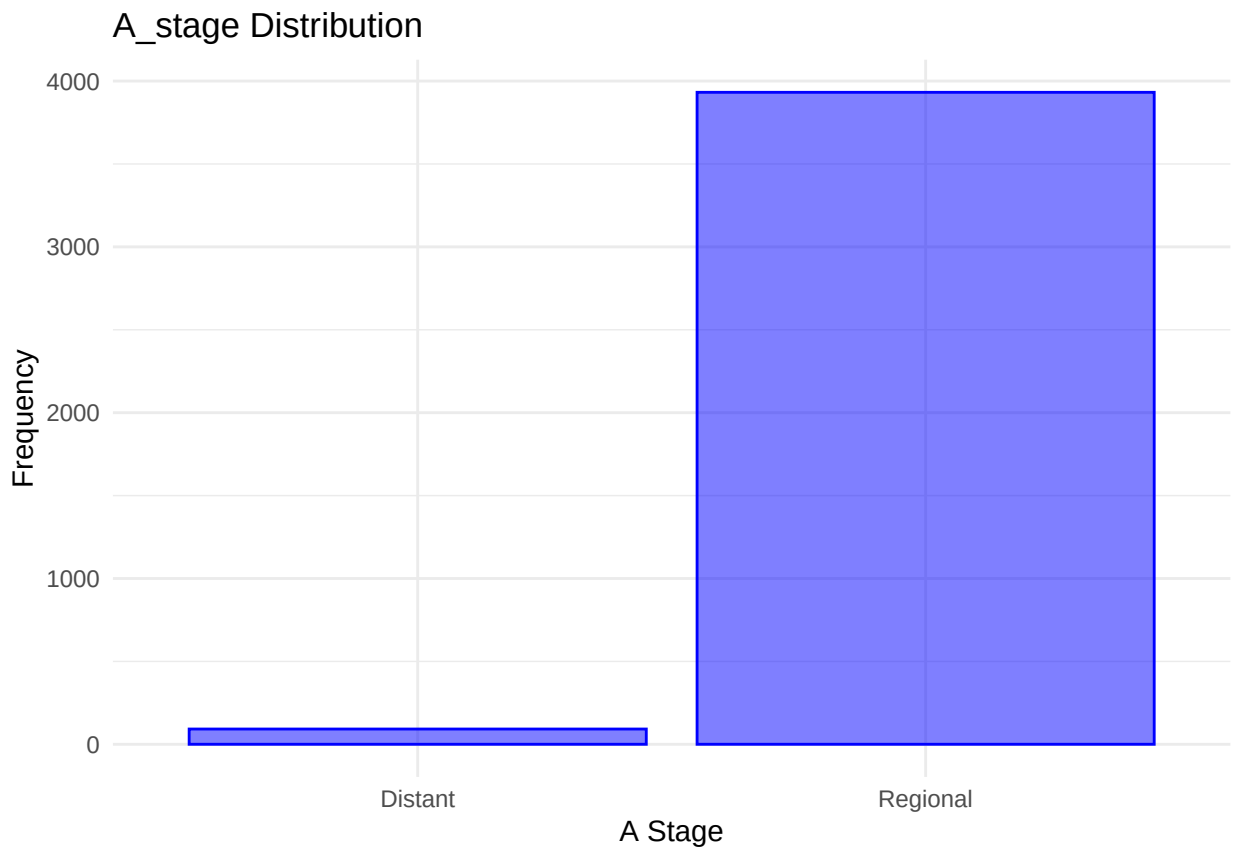

```
plot7differentate =
  breastcancer_data|>
  ggplot(aes(x = differentiate)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Differentate Distribution",
    x = "Differentate Group",
    y = "Frequency"
  )

plot7differentate
```




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

plot8grade
```

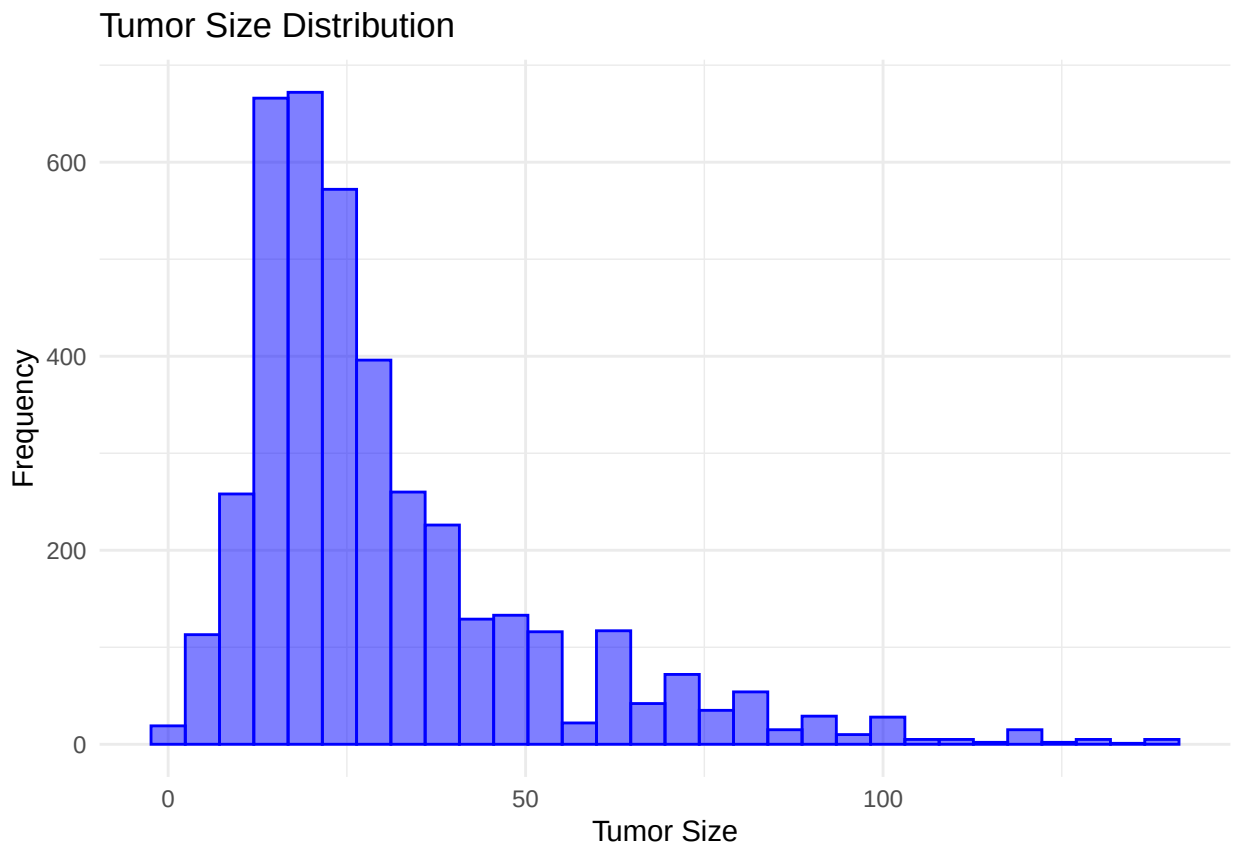



```
plot9astage =
  breastcancer_data|>
  ggplot(aes(x = a_stage)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "A_stage Distribution",
    x = "A Stage",
    y = "Frequency"
  )

plot9astage
```

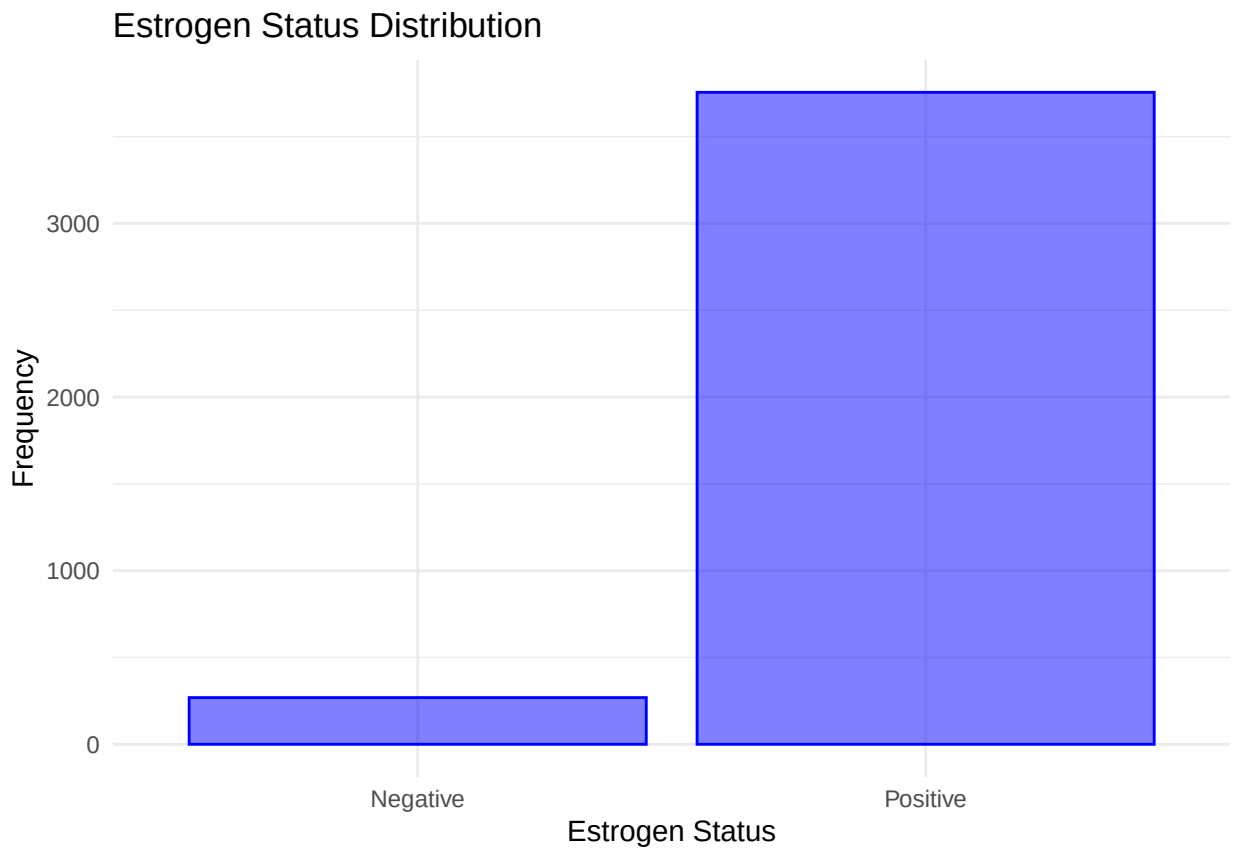



```
plot10tumorsize =
  breastcancer_data|>
  ggplot(aes(x = tumor_size)) +
  geom_histogram(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Tumor Size Distribution",
    x = "Tumor Size",
    y = "Frequency"
  )

plot10tumorsize
```

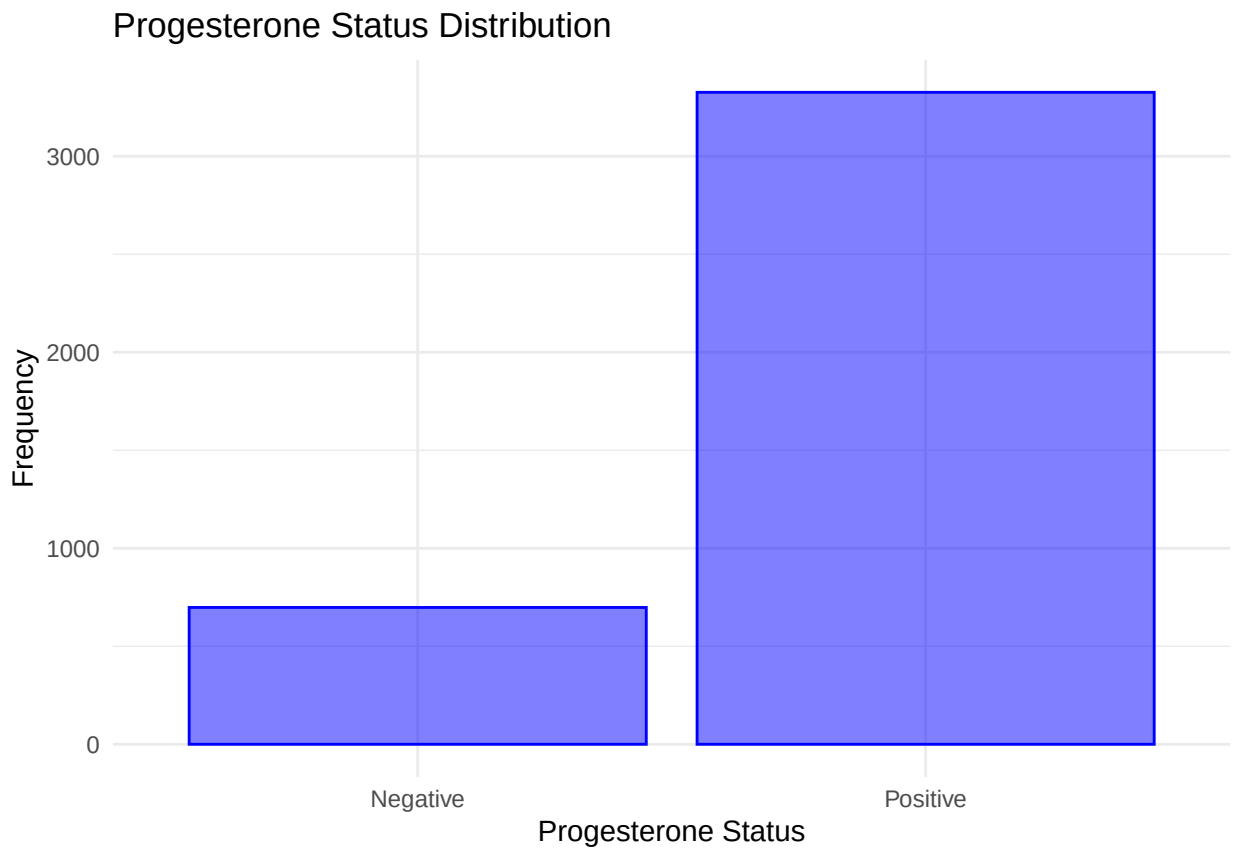
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




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

plot11estrogen
```

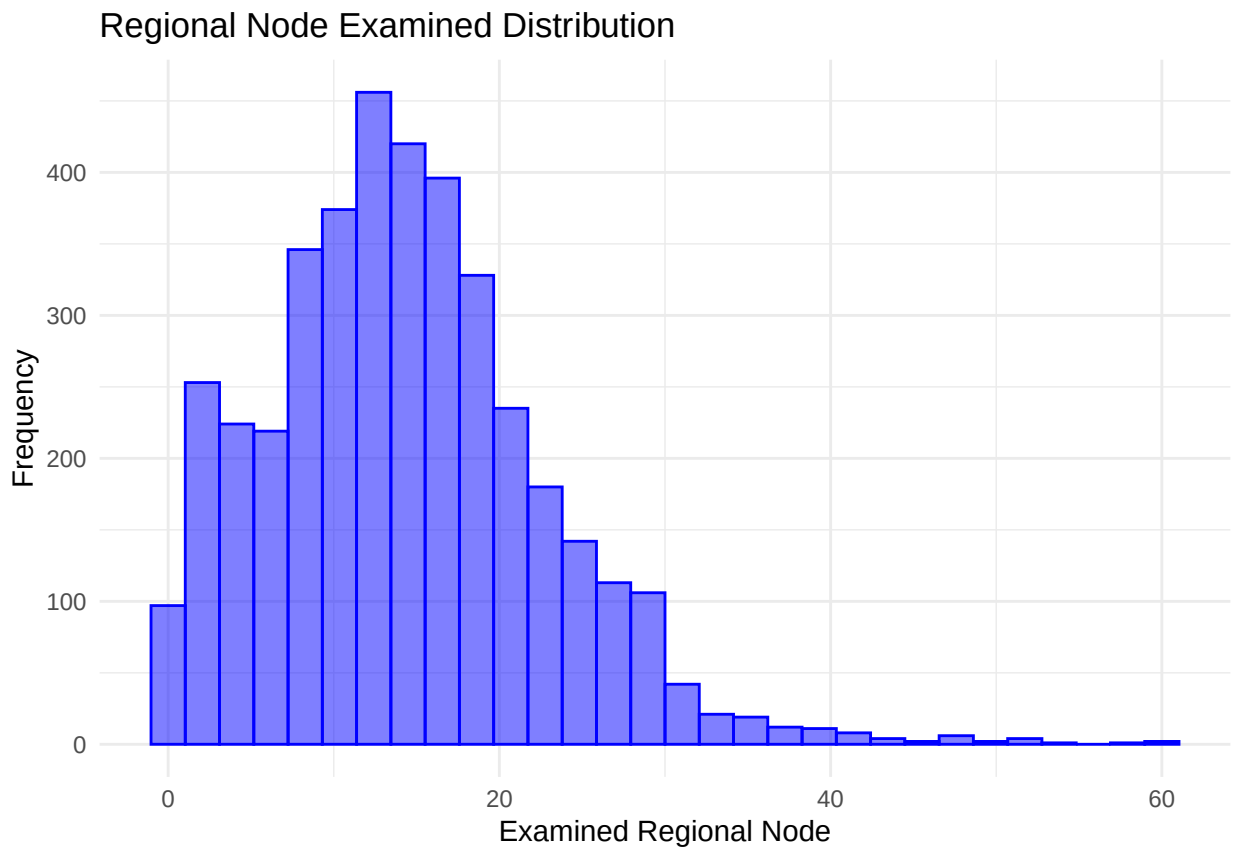



```
plot12progesterone =
  breastcancer_data|>
  ggplot(aes(x = progesterone_status)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Progesterone Status Distribution",
    x = "Progesterone Status",
    y = "Frequency"
  )

plot12progesterone
```



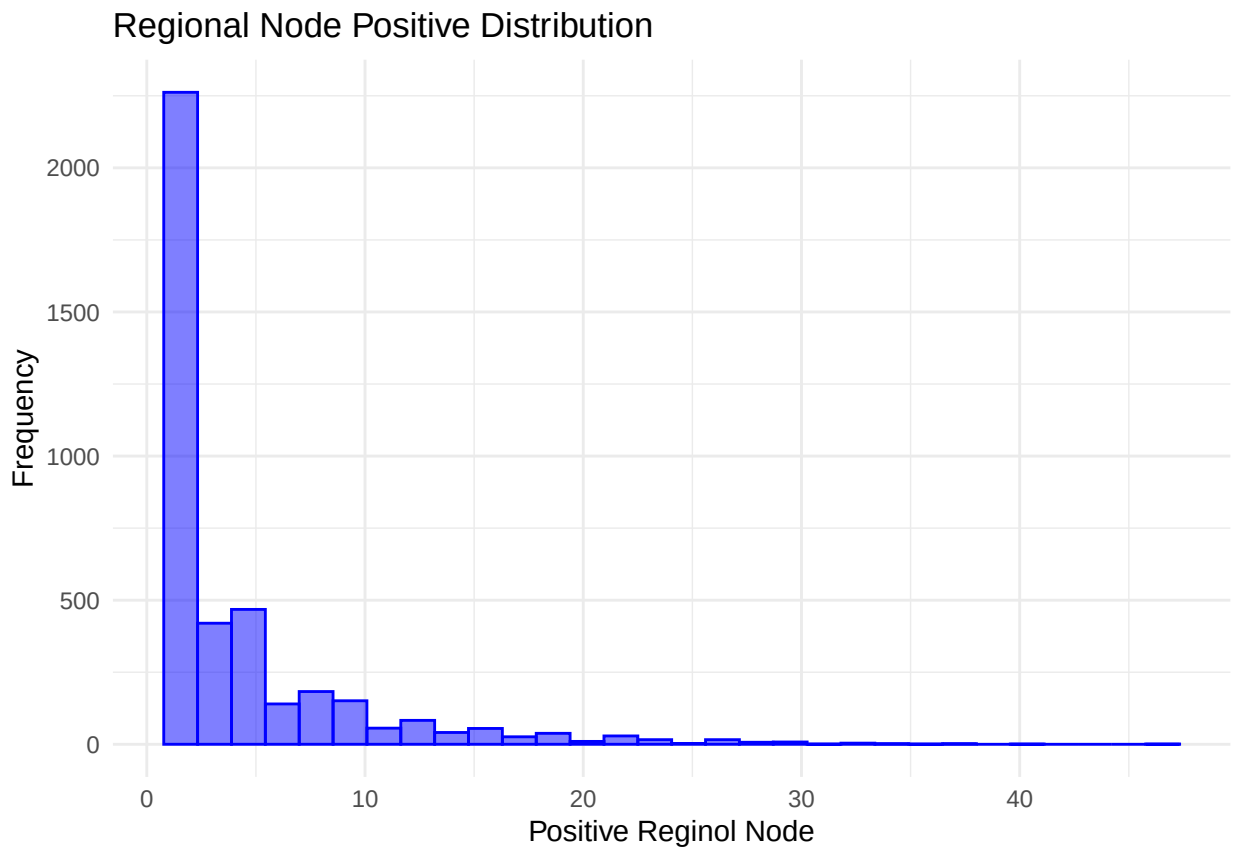

```
plot13nodeexamined =
  breastcancer_data|>
  ggplot(aes(x = regional_node_examined)) +
  geom_histogram(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "Regional Node Examined Distribution",
    x = "Examined Regional Node",
    y = "Frequency"
  )

plot13nodeexamined
```

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




```
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
```

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

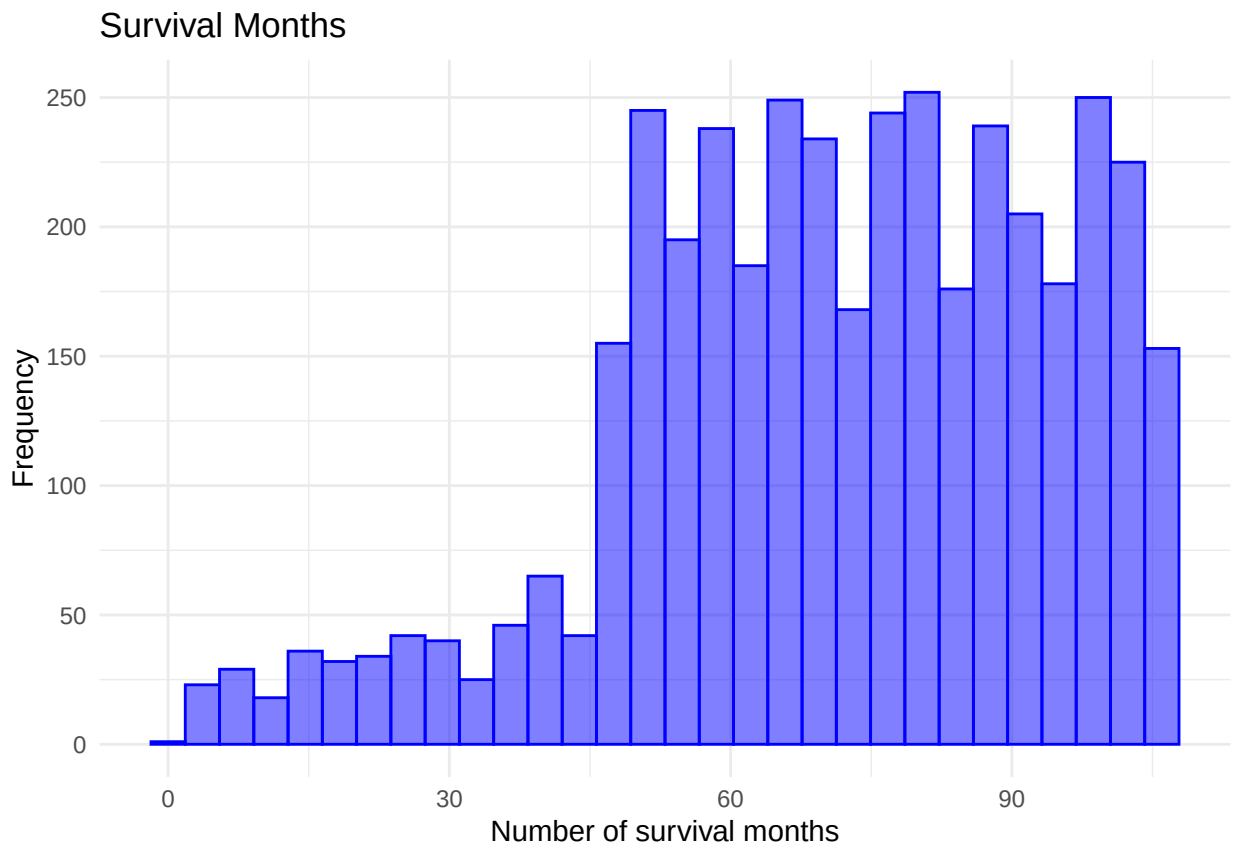


Y1 = survive months; (numeric)

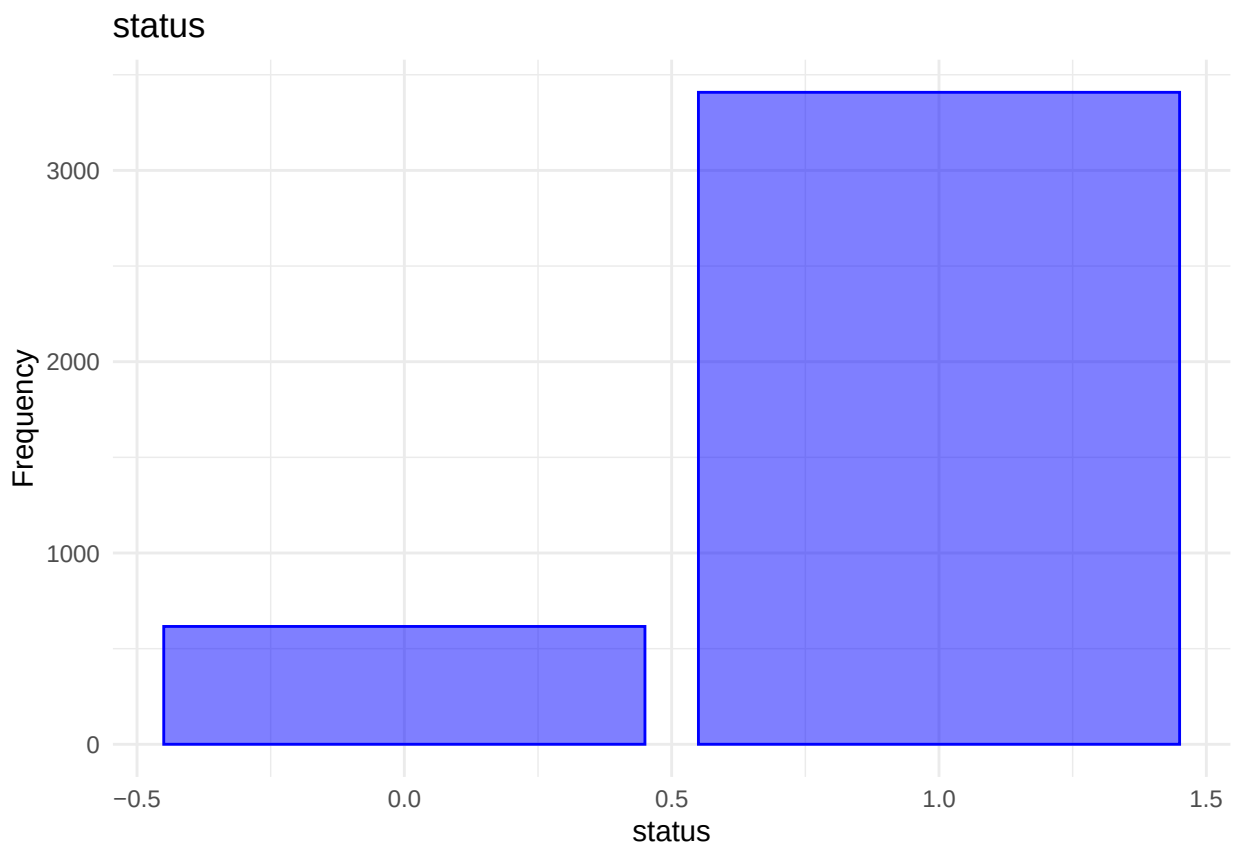
Y2 = status; (binary)

```
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`.
```



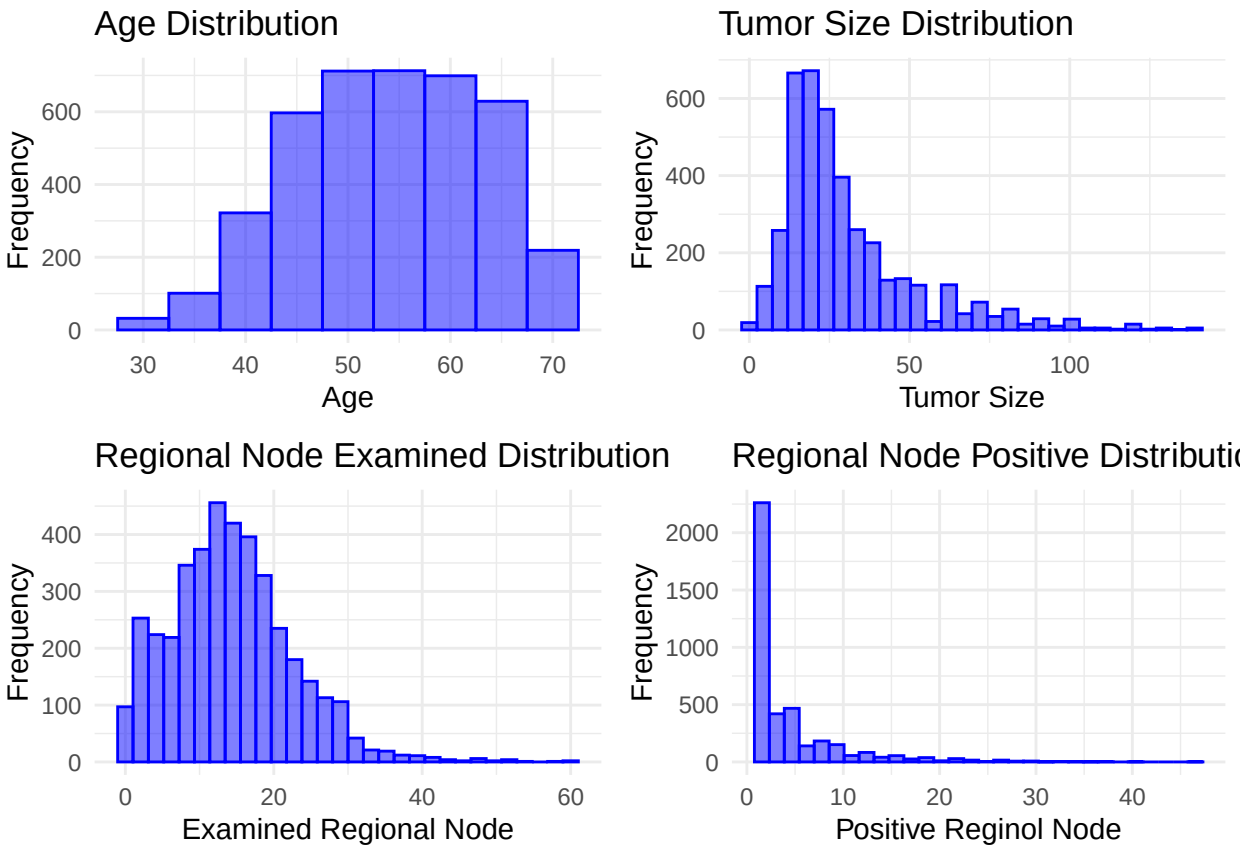

```
plot16status =
  bc|>
  ggplot(aes(x = status)) +
  geom_bar(color = "blue", fill = alpha("blue", 0.5))+
  theme_minimal() +
  labs(
    title = "status",
    x = "status",
    y = "Frequency"
  )

plot16status
```



Summarized plots

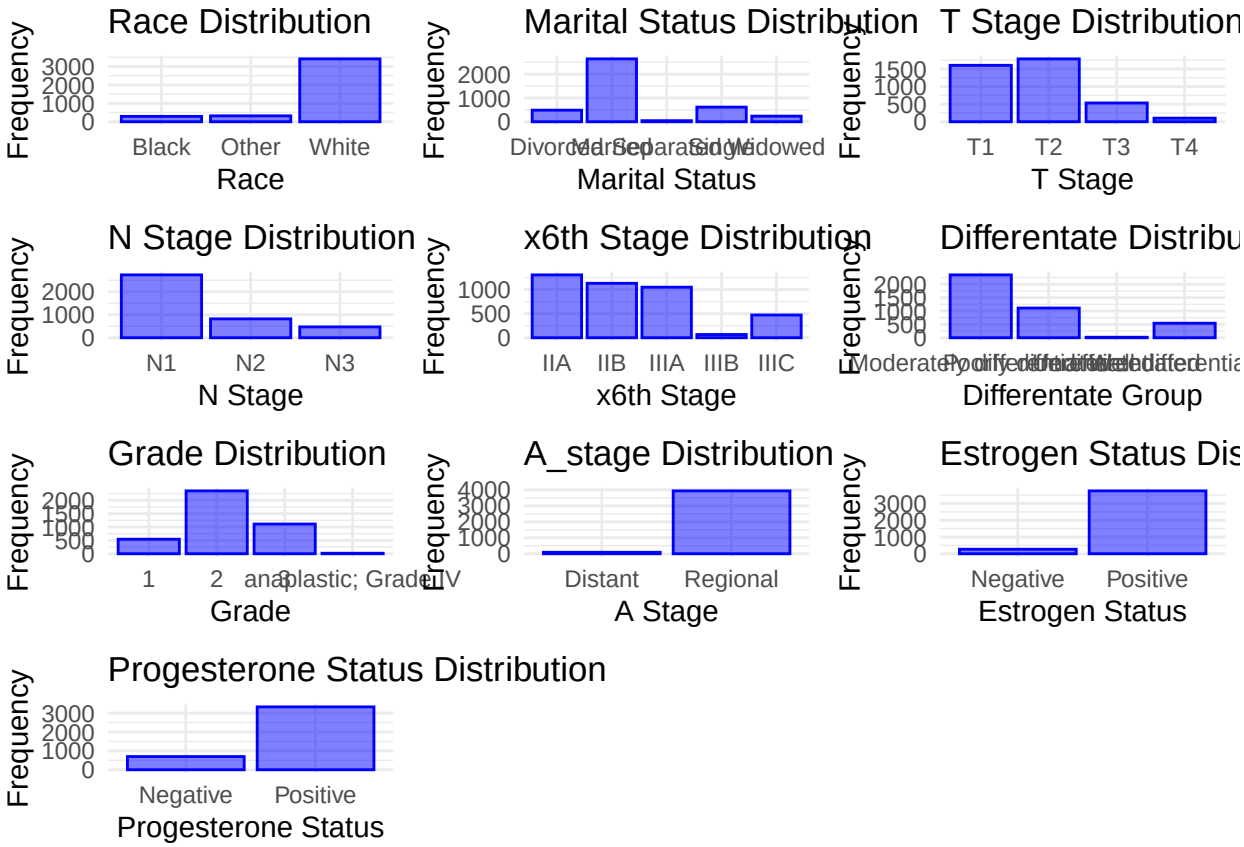
```
grid.arrange(plot1age, plot10tumorsize, plot13nodeexamined,
             plot14nodepositive, ncol = 2)
```

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



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

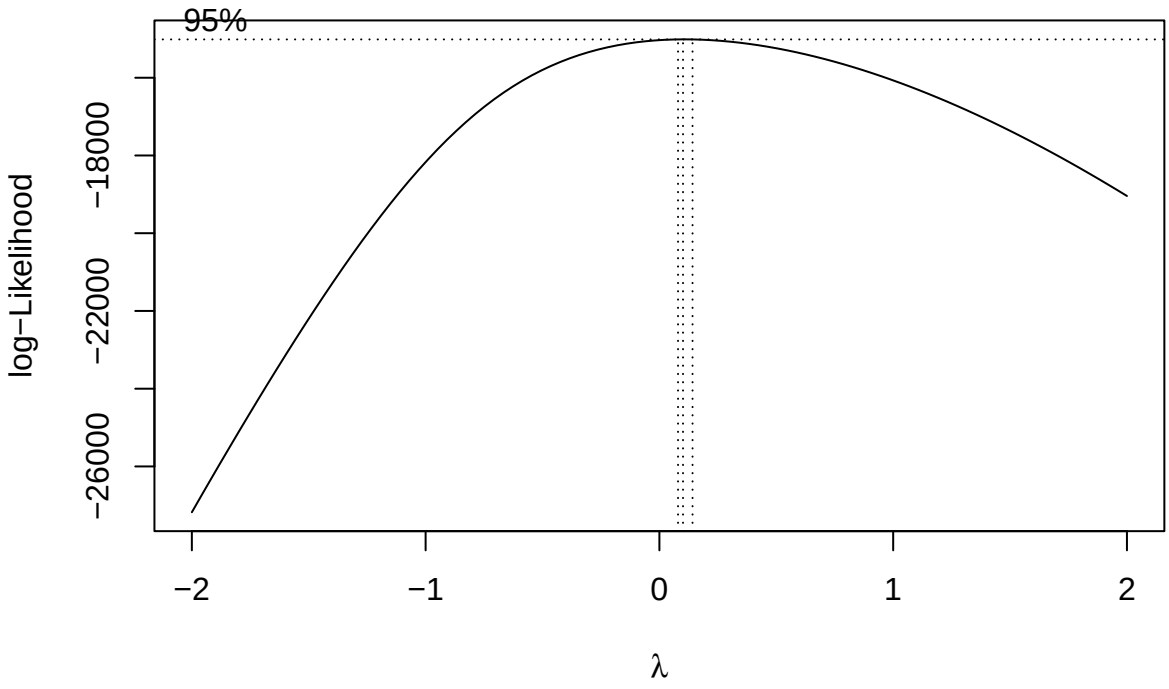
```
grid.arrange(plot2race, plot3marital,plot4tstage,
             plot5nstage, plot6x6thstage,plot7differentate,
             plot8grade,plot9astage,plot11estrogen,plot12progesterone, ncol = 3)
```



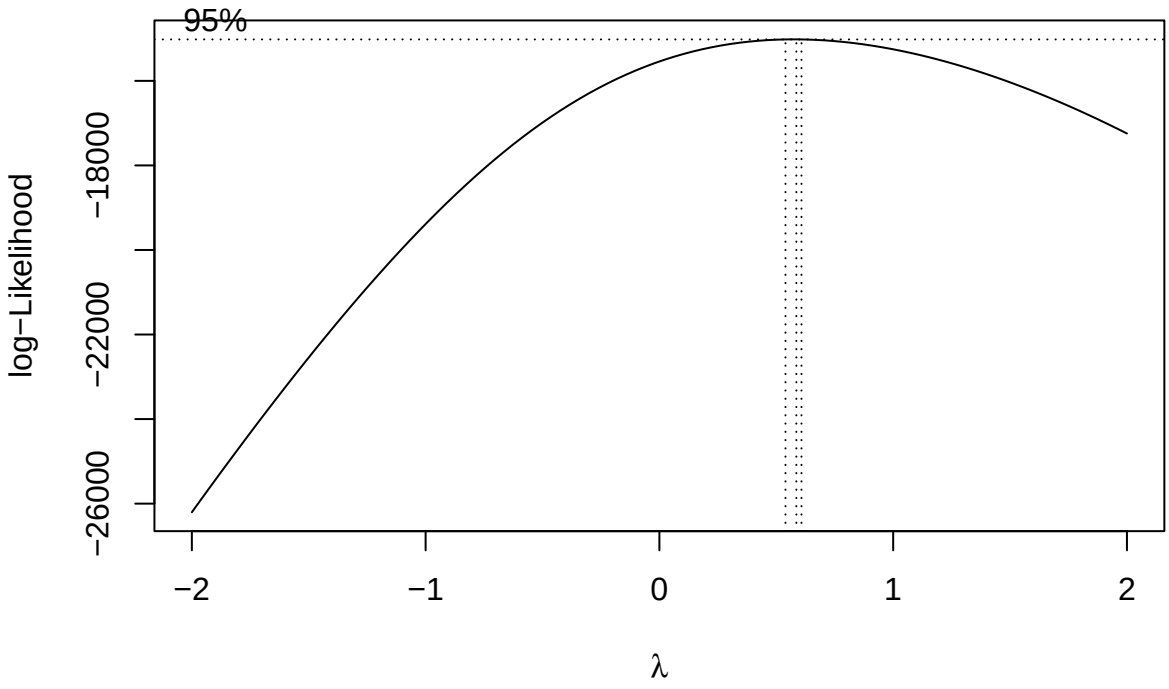
Transformation

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

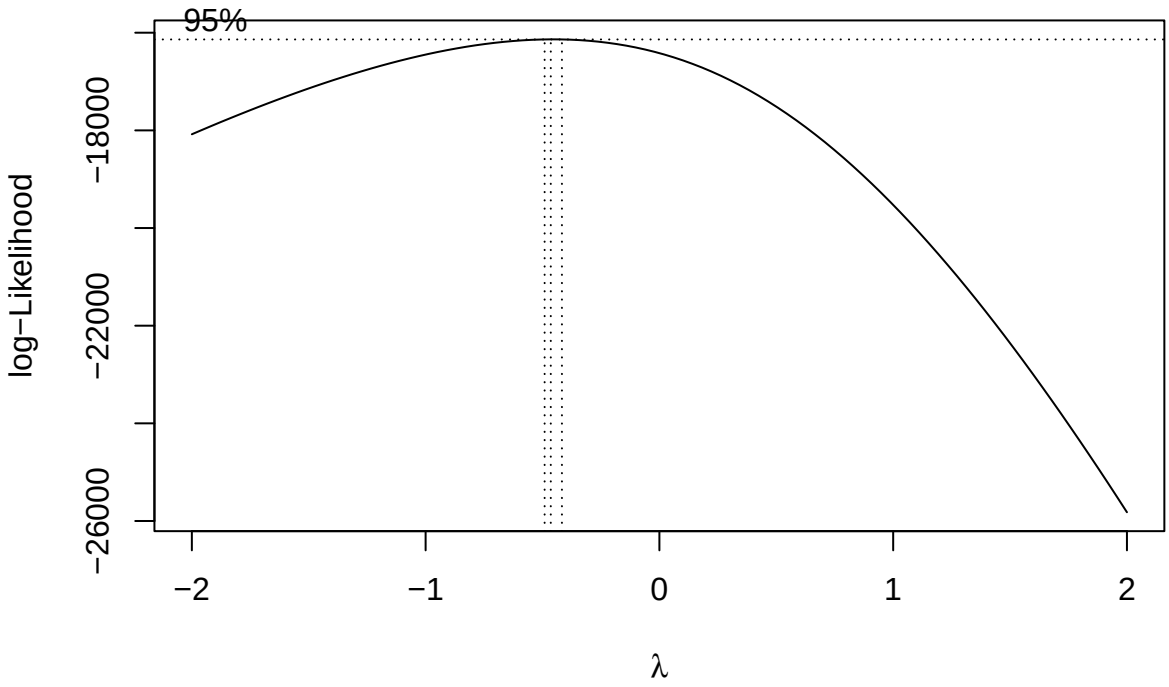
```
bc_transform_tumorsize <- boxcox(breastcancer_data$tumor_size ~ 1, lambda = seq(-2, 2, by=0.1))
```




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

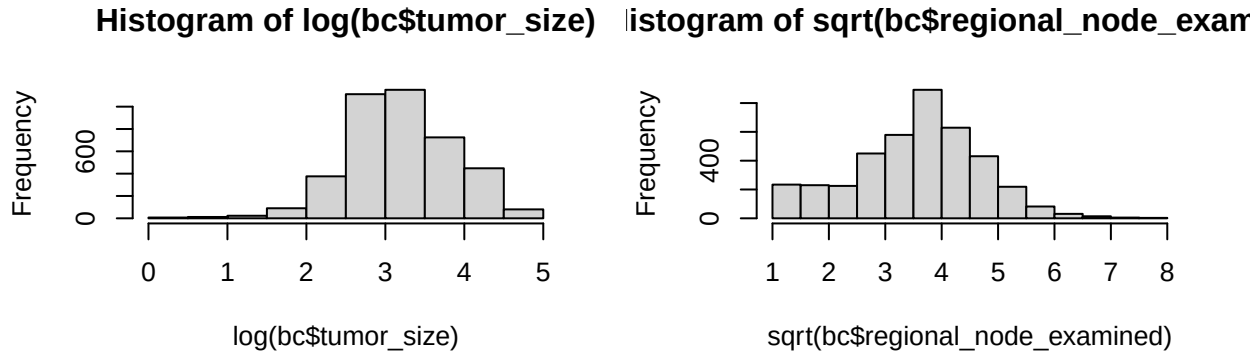


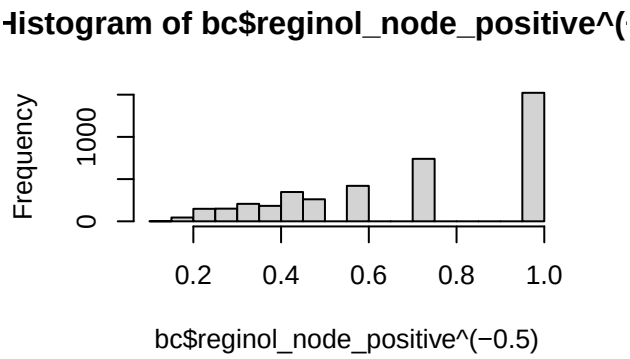

```
bc_transform_regionalnode_pos <- boxcox(breastcancer_data$reginol_node_positive ~ 1, lambda = seq(-2, 2
```



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

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





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

Transformation model

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

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

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

Indicator Test

When y is status

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

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

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

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

summary(model)
```

```
##
## Call:
## glm(formula = formula, family = binomial(), data = newbc)
##
## Coefficients: (4 not defined because of singularities)
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)           1.826084   0.591231   3.089  0.00201 **
## race2                -0.517829   0.161866  -3.199  0.00138 **
## race3                 0.412988   0.202323   2.041  0.04123 *
## marital_status2      -0.208737   0.141798  -1.472  0.14100
## marital_status3      -0.137065   0.134860  -1.016  0.30946
## marital_status4      -0.226852   0.192395  -1.179  0.23836
## marital_status5      -0.870139   0.369406  -2.356  0.01850 *
## t_stage2             -0.241275   0.214882  -1.123  0.26151
## t_stage3             -0.463184   0.308144  -1.503  0.13280
## t_stage4             -0.911657   0.451201  -2.021  0.04333 *
## n_stage2             -0.652606   0.238058  -2.741  0.00612 **
## n_stage3             -0.757283   0.301072  -2.515  0.01189 *
## x6th_stage2           0.069464   0.294083   0.236  0.81327
## x6th_stage3                 NA         NA      NA       NA
## x6th_stage4          -0.226947   0.231875  -0.979  0.32771
## x6th_stage5          -0.085418   0.528445  -0.162  0.87159
## differentiate2        0.387813   0.104972   3.694  0.00022 ***
## differentiate3        0.922456   0.193026   4.779 1.76e-06 ***
## differentiate4       -0.970582   0.533726  -1.819  0.06899 .
## grade2                      NA         NA      NA       NA
```

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

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

Model Fitting

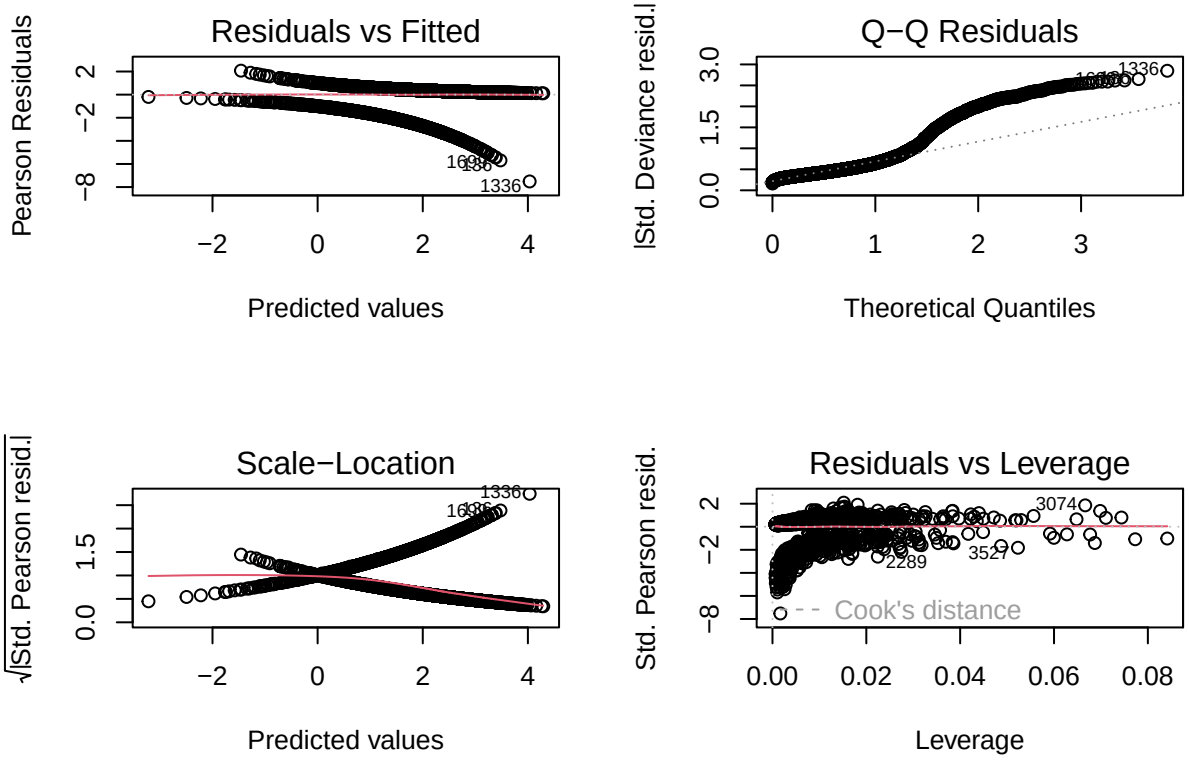
Initial Model

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

```
##
## Call:
## glm(formula = status ~ race + marital_status + t_stage + n_stage +
##     differentiate + a_stage + estrogen_status + progesterone_status +
##     ln_tumor + sqrt_examined + reginol_node_positive + age, family = binomial,
##     data = newbc)
##
## Coefficients:
##                        Estimate Std. Error z value Pr(>|z|)
## (Intercept)            1.775787   0.587386   3.023 0.002501 **
## race2                 -0.522765   0.161744  -3.232 0.001229 **
## race3                  0.419131   0.202312   2.072 0.038293 *
## marital_status2       -0.209325   0.141735  -1.477 0.139709
## marital_status3       -0.140584   0.134542  -1.045 0.296064
## marital_status4       -0.222113   0.192496  -1.154 0.248558
## marital_status5       -0.867369   0.370116  -2.344 0.019104 *
## t_stage2              -0.372488   0.159129  -2.341 0.019243 *
## t_stage3              -0.471905   0.266764  -1.769 0.076894 .
```

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

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



Indicator Variables categorize by Race

```
# According to our data formating in the upper procedure, in Race:
# 1 represents "white"
# 2 represents "black"
# 3 represents "others"
## A newdataset with "white" as reference
bc_ref =
  newbc |>
  mutate(
     race= relevel(
       race, ref = 1
     )
     )

bc_ref
```

```
## # A tibble: 4,024 x 15
##      age race  marital_status t_stage n_stage x6th_stage differentiate grade
##    <dbl> <fct> <fct>          <fct>   <fct>   <fct>      <fct>          <fct>
##  1    68 1     1              1       1       1          1              3
##  2    50 1     1              2       2       2          2              2
##  3    58 1     2              3       3       3          2              2
##  4    58 1     1              1       1       1          1              3
##  5    47 1     1              2       1       4          1              3
##  6    51 1     3              1       1       1          2              2
##  7    51 1     1              1       1       1          3              1
##  8    40 1     1              2       1       4          2              2
##  9    40 1     2              4       3       3          1              3
## 10    69 1     1              4       3       3          3              1
## # i 4,014 more rows
## # i 7 more variables: a_stage <fct>, estrogen_status <fct>,
## #   progesterone_status <fct>, reginol_node_positive <dbl>, status <dbl>,
## #   ln_tumor <dbl>, sqrt_examined <dbl>
```

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

summary(single_race)
```

```
##
## Call:
## glm(formula = status ~ race, family = binomial, data = bc_ref)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.73909    0.04801  36.221  < 2e-16 ***
## race2       -0.64505    0.14350  -4.495 6.95e-06 ***
## race3        0.42389    0.18997   2.231   0.0257 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
```

```
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 3418.9  on 4021  degrees of freedom
## AIC: 3424.9
##
## Number of Fisher Scoring iterations: 4
```

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

```
##
## 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:
##           (Intercept)                 race2                 race3
##               1.77579              -0.52276               0.41913
##       marital_status2       marital_status3       marital_status4
##              -0.20933              -0.14058              -0.22211
##       marital_status5             t_stage2              t_stage3
##              -0.86737              -0.37249              -0.47191
##              t_stage4             n_stage2              n_stage3
##              -1.02596              -0.47409              -0.63710
##        differentiate2        differentiate3        differentiate4
##               0.38603               0.91746              -0.94709
##              a_stage1      estrogen_status1  progesterone_status1
##               0.04521               0.73783               0.58838
## reginol_node_positive             ln_tumor         sqrt_examined
##              -0.07496              -0.05527               0.25600
##                   age
##              -0.02365
##
## Degrees of Freedom: 4023 Total (i.e. Null);  4002 Residual
## Null Deviance:       3445
## Residual Deviance: 2953  AIC: 2997
```

```
summary(model_ref)
```

```
##
## Call:
## glm(formula = status ~ race + marital_status + t_stage + n_stage +
##     differentiate + a_stage + estrogen_status + progesterone_status +
##     reginol_node_positive + ln_tumor + sqrt_examined + age, family = binomial,
##     data = bc_ref)
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)            1.775787   0.587386   3.023 0.002501 **
## race2                 -0.522765   0.161744  -3.232 0.001229 **
## race3                  0.419131   0.202312   2.072 0.038293 *
## marital_status2       -0.209325   0.141735  -1.477 0.139709
## marital_status3       -0.140584   0.134542  -1.045 0.296064
## marital_status4       -0.222113   0.192496  -1.154 0.248558
## marital_status5       -0.867369   0.370116  -2.344 0.019104 *
## t_stage2              -0.372488   0.159129  -2.341 0.019243 *
## t_stage3              -0.471905   0.266764  -1.769 0.076894 .
## t_stage4              -1.025962   0.313035  -3.277 0.001047 **
## n_stage2              -0.474091   0.129288  -3.667 0.000245 ***
## n_stage3              -0.637101   0.237639  -2.681 0.007341 **
## differentiate2         0.386027   0.104898   3.680 0.000233 ***
## differentiate3         0.917457   0.192668   4.762 1.92e-06 ***
## differentiate4        -0.947095   0.531127  -1.783 0.074557 .
## a_stage1               0.045211   0.265718   0.170 0.864894
## estrogen_status1       0.737828   0.177538   4.156 3.24e-05 ***
## progesterone_status1   0.588385   0.127499   4.615 3.93e-06 ***
## reginol_node_positive -0.074961   0.014984  -5.003 5.65e-07 ***
## ln_tumor              -0.055274   0.138631  -0.399 0.690103
## sqrt_examined          0.255997   0.049654   5.156 2.53e-07 ***
## age                   -0.023647   0.005618  -4.209 2.56e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2953.4  on 4002  degrees of freedom
## AIC: 2997.4
##
## Number of Fisher Scoring iterations: 5
```

```
## Run a MLR 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
```

```
##
## 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:
##                 (Intercept)                        race2
##                    2.143663                   -3.268199
```

```
##                      race3              marital_status2
##                   5.514563                    -0.183704
##             marital_status3              marital_status4
##                   0.085036                    -0.055626
##             marital_status5                     t_stage2
##                  -0.799662                    -0.275236
##                     t_stage3                     t_stage4
##                  -0.295508                    -0.940666
##                     n_stage2                     n_stage3
##                  -0.567320                    -0.843987
##              differentiate2               differentiate3
##                   0.436042                     1.011119
##              differentiate4                     a_stage1
##                  -0.948202                    -0.060677
##            estrogen_status1         progesterone_status1
##                   0.806235                     0.660775
##       reginol_node_positive                     ln_tumor
##                  -0.065841                    -0.165689
##               sqrt_examined                          age
##                   0.278198                    -0.027956
##       race2:marital_status2        race3:marital_status2
##                  -0.231457                    -0.493298
##       race2:marital_status3        race3:marital_status3
##                  -1.145440                    -1.209396
##       race2:marital_status4        race3:marital_status4
##                  -0.440236                    -2.132622
##       race2:marital_status5        race3:marital_status5
##                   0.098692                    -0.880739
##              race2:t_stage2               race3:t_stage2
##                  -0.465403                     0.437497
##              race2:t_stage3               race3:t_stage3
##                  -0.703756                     1.603080
##              race2:t_stage4               race3:t_stage4
##                   0.014416                    -0.127448
##              race2:n_stage2               race3:n_stage2
##                   0.484228                     1.082513
##              race2:n_stage3               race3:n_stage3
##                   1.463405                     2.525936
##        race2:differentiate2         race3:differentiate2
##                  -0.208584                    -0.109563
##        race2:differentiate3         race3:differentiate3
##                  -0.381274                    -0.140078
##        race2:differentiate4         race3:differentiate4
##                  -0.724327                           NA
##              race2:a_stage1               race3:a_stage1
##                   1.903928                    -1.581496
##      race2:estrogen_status1       race3:estrogen_status1
##                  -0.686042                     1.820519
##  race2:progesterone_status1   race3:progesterone_status1
##                  -0.050826                    -2.784800
## race2:reginol_node_positive  race3:reginol_node_positive
##                  -0.121505                    -0.153094
##              race2:ln_tumor               race3:ln_tumor
##                   0.776264                    -1.194039
```

```
##         race2:sqrt_examined          race3:sqrt_examined
##                   -0.085330                    -0.162959
##                   race2:age                    race3:age
##                    0.008341                     0.035269
##
## Degrees of Freedom: 4023 Total (i.e. Null);  3965 Residual
## Null Deviance:       3445
## Residual Deviance: 2898  AIC: 3016
```

```
summary(model_refinter)
```

```
##
## Call:
## glm(formula = status ~ race + marital_status + t_stage + n_stage +
##     differentiate + a_stage + estrogen_status + progesterone_status +
##     reginol_node_positive + ln_tumor + sqrt_examined + age +
##     race * (marital_status + t_stage + n_stage + differentiate +
##         a_stage + estrogen_status + progesterone_status + reginol_node_positive +
##         ln_tumor + sqrt_examined + age), family = binomial, data = bc_ref)
##
## Coefficients: (1 not defined because of singularities)
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                  2.143663   0.663026   3.233 0.001224 **
## race2                       -3.268199   1.771947  -1.844 0.065123 .
## race3                        5.514563   3.122929   1.766 0.077424 .
## marital_status2             -0.183704   0.152054  -1.208 0.226988
## marital_status3              0.085036   0.158426   0.537 0.591437
## marital_status4             -0.055626   0.220307  -0.252 0.800660
## marital_status5             -0.799662   0.435399  -1.837 0.066266 .
## t_stage2                    -0.275236   0.176881  -1.556 0.119696
## t_stage3                    -0.295508   0.299330  -0.987 0.323529
## t_stage4                    -0.940666   0.342650  -2.745 0.006046 **
## n_stage2                    -0.567320   0.141733  -4.003 6.26e-05 ***
## n_stage3                    -0.843987   0.258302  -3.267 0.001085 **
## differentiate2               0.436042   0.115677   3.769 0.000164 ***
## differentiate3               1.011119   0.214291   4.718 2.38e-06 ***
## differentiate4              -0.948202   0.577004  -1.643 0.100317
## a_stage1                    -0.060677   0.293299  -0.207 0.836106
## estrogen_status1             0.806235   0.196393   4.105 4.04e-05 ***
## progesterone_status1         0.660775   0.138367   4.776 1.79e-06 ***
## reginol_node_positive       -0.065841   0.016154  -4.076 4.59e-05 ***
## ln_tumor                    -0.165689   0.159061  -1.042 0.297566
## sqrt_examined                0.278198   0.054658   5.090 3.58e-07 ***
## age                         -0.027956   0.006220  -4.495 6.97e-06 ***
## race2:marital_status2       -0.231457   0.537505  -0.431 0.666750
## race3:marital_status2       -0.493298   0.712072  -0.693 0.488458
## race2:marital_status3       -1.145440   0.409405  -2.798 0.005145 **
## race3:marital_status3       -1.209396   0.612332  -1.975 0.048261 *
## race2:marital_status4       -0.440236   0.601871  -0.731 0.464507
## race3:marital_status4       -2.132622   0.838528  -2.543 0.010981 *
## race2:marital_status5        0.098692   1.175316   0.084 0.933080
## race3:marital_status5       -0.880739   1.347639  -0.654 0.513407
## race2:t_stage2              -0.465403   0.502263  -0.927 0.354128
## race3:t_stage2               0.437497   0.782923   0.559 0.576298
```

```
## race2:t_stage3              -0.703756   0.806589  -0.873 0.382931
## race3:t_stage3               1.603080   1.333557   1.202 0.229322
## race2:t_stage4               0.014416   1.193986   0.012 0.990367
## race3:t_stage4              -0.127448   1.726137  -0.074 0.941142
## race2:n_stage2               0.484228   0.476679   1.016 0.309707
## race3:n_stage2               1.082513   0.645862   1.676 0.093724 .
## race2:n_stage3               1.463405   0.897850   1.630 0.103123
## race3:n_stage3               2.525936   1.462710   1.727 0.084188 .
## race2:differentiate2        -0.208584   0.358607  -0.582 0.560802
## race3:differentiate2        -0.109563   0.465485  -0.235 0.813919
## race2:differentiate3        -0.381274   0.682640  -0.559 0.576483
## race3:differentiate3        -0.140078   0.835274  -0.168 0.866816
## race2:differentiate4        -0.724327   1.669867  -0.434 0.664460
## race3:differentiate4               NA         NA      NA       NA
## race2:a_stage1               1.903928   1.021605   1.864 0.062369 .
## race3:a_stage1              -1.581496   1.588021  -0.996 0.319303
## race2:estrogen_status1      -0.686042   0.595097  -1.153 0.248982
## race3:estrogen_status1       1.820519   0.981128   1.856 0.063520 .
## race2:progesterone_status1  -0.050826   0.451620  -0.113 0.910394
## race3:progesterone_status1  -2.784800   0.946246  -2.943 0.003251 **
## race2:reginol_node_positive -0.121505   0.064782  -1.876 0.060712 .
## race3:reginol_node_positive -0.153094   0.089011  -1.720 0.085442 .
## race2:ln_tumor               0.776264   0.361491   2.147 0.031762 *
## race3:ln_tumor              -1.194039   0.762242  -1.566 0.117236
## race2:sqrt_examined         -0.085330   0.168637  -0.506 0.612859
## race3:sqrt_examined         -0.162959   0.213679  -0.763 0.445681
## race2:age                    0.008341   0.019360   0.431 0.666599
## race3:age                    0.035269   0.024348   1.449 0.147466
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2898.0  on 3965  degrees of freedom
## AIC: 3016
##
## Number of Fisher Scoring iterations: 6
```

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

```
##
## 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:
##                (Intercept)                      race2
##                    1.88212                   -1.13148
##                      race3             marital_status2
##                    3.21416                   -0.18674
##            marital_status3             marital_status4
##                    0.08622                   -0.07674
##            marital_status5                    t_stage2
##                   -0.78065                   -0.33844
##                   t_stage3                    t_stage4
##                   -0.37530                   -0.97312
##                   n_stage2                    n_stage3
##                   -0.49529                   -0.66460
##             differentiate2              differentiate3
##                    0.40530                    0.94765
##             differentiate4                    a_stage1
##                   -0.99784                    0.05782
##           estrogen_status1        progesterone_status1
##                    0.76878                    0.68469
##      reginol_node_positive                    ln_tumor
##                   -0.07592                   -0.12537
##              sqrt_examined                         age
##                    0.25840                   -0.02485
##      race2:marital_status2       race3:marital_status2
##                   -0.12824                   -0.37328
##      race2:marital_status3       race3:marital_status3
##                   -1.10936                   -1.34977
##      race2:marital_status4       race3:marital_status4
##                   -0.42749                   -1.60036
##      race2:marital_status5       race3:marital_status5
##                   -0.54279                   -0.91116
## race2:progesterone_status1  race3:progesterone_status1
##                   -0.51665                   -1.64600
##             race2:ln_tumor              race3:ln_tumor
##                    0.43654                   -0.33627
##
## Degrees of Freedom: 4023 Total (i.e. Null);  3990 Residual
## Null Deviance:       3445
## Residual Deviance: 2922  AIC: 2990
```

```
summary(model_inter)
```

```
##
## Call:
## glm(formula = status ~ race + marital_status + t_stage + n_stage +
##     differentiate + a_stage + estrogen_status + progesterone_status +
##     reginol_node_positive + ln_tumor + sqrt_examined + age +
##     race * (marital_status + progesterone_status + ln_tumor),
##     family = binomial, data = bc_ref)
##
## Coefficients:
##                             Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 1.882124   0.611049   3.080 0.002069 **
## race2                      -1.131478   0.754804  -1.499 0.133864
```

```
## race3                       3.214161   1.374949   2.338 0.019405 *
## marital_status2            -0.186741   0.151851  -1.230 0.218785
## marital_status3             0.086222   0.158014   0.546 0.585299
## marital_status4            -0.076745   0.219242  -0.350 0.726303
## marital_status5            -0.780653   0.435332  -1.793 0.072935 .
## t_stage2                   -0.338441   0.160266  -2.112 0.034708 *
## t_stage3                   -0.375302   0.269563  -1.392 0.163844
## t_stage4                   -0.973119   0.315838  -3.081 0.002063 **
## n_stage2                   -0.495290   0.130427  -3.797 0.000146 ***
## n_stage3                   -0.664599   0.239253  -2.778 0.005473 **
## differentiate2              0.405297   0.105478   3.842 0.000122 ***
## differentiate3              0.947648   0.194613   4.869 1.12e-06 ***
## differentiate4             -0.997840   0.537651  -1.856 0.063464 .
## a_stage1                    0.057824   0.268010   0.216 0.829180
## estrogen_status1            0.768781   0.180131   4.268 1.97e-05 ***
## progesterone_status1        0.684689   0.134874   5.077 3.84e-07 ***
## reginol_node_positive      -0.075918   0.015092  -5.030 4.89e-07 ***
## ln_tumor                   -0.125372   0.146813  -0.854 0.393129
## sqrt_examined               0.258396   0.049886   5.180 2.22e-07 ***
## age                        -0.024851   0.005663  -4.389 1.14e-05 ***
## race2:marital_status2      -0.128238   0.518941  -0.247 0.804820
## race3:marital_status2      -0.373279   0.702629  -0.531 0.595238
## race2:marital_status3      -1.109358   0.385796  -2.876 0.004034 **
## race3:marital_status3      -1.349766   0.576548  -2.341 0.019226 *
## race2:marital_status4      -0.427490   0.551410  -0.775 0.438182
## race3:marital_status4      -1.600358   0.671688  -2.383 0.017191 *
## race2:marital_status5      -0.542786   1.006774  -0.539 0.589795
## race3:marital_status5      -0.911159   1.284113  -0.710 0.477975
## race2:progesterone_status1 -0.516652   0.357042  -1.447 0.147887
## race3:progesterone_status1 -1.646000   0.561267  -2.933 0.003361 **
## race2:ln_tumor              0.436542   0.213238   2.047 0.040638 *
## race3:ln_tumor             -0.336268   0.352855  -0.953 0.340594
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2922.3  on 3990  degrees of freedom
## AIC: 2990.3
##
## Number of Fisher Scoring iterations: 5
```

- From the SRL 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 MRL 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 MRL 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 MRL model with race interaction terms selected, and we get a model with

AIC of 2990.3 dropped sharply and the interaction term is included.

Partial Test

Partial Test for binary Y

```
# Our 1st global model for the predicts without colinearity and not normal predicts
model_global_bin = glm(status ~ race + marital_status + t_stage + n_stage +
                       differentiate + a_stage +estrogen_status + progesterone_status + ln_tumor + sqrt

summary(model_global_bin)
```

```
##
## Call:
## glm(formula = status ~ race + marital_status + t_stage + n_stage +
##     differentiate + a_stage + estrogen_status + progesterone_status +
##     ln_tumor + sqrt_examined + age, family = binomial, data = newbc)
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)           2.025431   0.583766   3.470 0.000521 ***
## race2                -0.490040   0.161448  -3.035 0.002403 **
## race3                 0.412102   0.201264   2.048 0.040602 *
## marital_status2      -0.213770   0.140919  -1.517 0.129273
## marital_status3      -0.149790   0.134179  -1.116 0.264275
## marital_status4      -0.220417   0.191076  -1.154 0.248681
## marital_status5      -0.936900   0.365551  -2.563 0.010378 *
## t_stage2             -0.355769   0.158618  -2.243 0.024902 *
## t_stage3             -0.450653   0.266574  -1.691 0.090925 .
## t_stage4             -1.044577   0.312476  -3.343 0.000829 ***
## n_stage2             -0.733552   0.117910  -6.221 4.93e-10 ***
## n_stage3             -1.575446   0.141592 -11.127  < 2e-16 ***
## differentiate2        0.375295   0.104473   3.592 0.000328 ***
## differentiate3        0.901142   0.192252   4.687 2.77e-06 ***
## differentiate4       -0.960780   0.535816  -1.793 0.072955 .
## a_stage1              0.002227   0.262767   0.008 0.993239
## estrogen_status1      0.730261   0.176959   4.127 3.68e-05 ***
## progesterone_status1  0.573254   0.127304   4.503 6.70e-06 ***
## ln_tumor             -0.065530   0.138852  -0.472 0.636966
## sqrt_examined         0.180931   0.046777   3.868 0.000110 ***
## age                  -0.024590   0.005591  -4.398 1.09e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2978.6  on 4003  degrees of freedom
## AIC: 3020.6
##
## Number of Fisher Scoring iterations: 5
```

From the summary of the global model, we can see that from the P-value of a_stage, ln_tumor, marital_status(2, 3, 4) have the p-value above 0.05 which is not significant. While differentiate has a 0.0729 p-value, and t_stage3 has a p-value of 0.0909, we may consider keep them. The covariates like t_stage, n_stage, race, estrogen_status, progesterone_status, sqrt_examined, age have a P-value smaller than 0.05 indicating significance. Therefore, our 1st partial test may include the significant covariates.

```
# 1st binary partial test with all significant covariates
# We will still keep marital_status because one group in this variable is significant
binmodel_partial_1 = glm(status ~ race + marital_status + t_stage + n_stage + differentiate + estrogen_

summary(binmodel_partial_1)
```

```
##
## Call:
## glm(formula = status ~ race + marital_status + t_stage + n_stage +
##     differentiate + estrogen_status + progesterone_status + sqrt_examined +
##     age, family = binomial, data = newbc)
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)           1.851463   0.377142   4.909 9.15e-07 ***
## race2                -0.488627   0.161358  -3.028 0.002460 **
## race3                 0.411208   0.201230   2.043 0.041006 *
## marital_status2      -0.215703   0.140825  -1.532 0.125594
## marital_status3      -0.151385   0.134089  -1.129 0.258903
## marital_status4      -0.221820   0.191055  -1.161 0.245631
## marital_status5      -0.938507   0.365357  -2.569 0.010207 *
## t_stage2             -0.408664   0.112638  -3.628 0.000285 ***
## t_stage3             -0.555367   0.148281  -3.745 0.000180 ***
## t_stage4             -1.125881   0.244474  -4.605 4.12e-06 ***
## n_stage2             -0.737853   0.117555  -6.277 3.46e-10 ***
## n_stage3             -1.581593   0.137038 -11.541  < 2e-16 ***
## differentiate2        0.377070   0.104385   3.612 0.000303 ***
## differentiate3        0.904754   0.191998   4.712 2.45e-06 ***
## differentiate4       -0.961568   0.535510  -1.796 0.072557 .
## estrogen_status1      0.730173   0.176789   4.130 3.62e-05 ***
## progesterone_status1  0.573495   0.127268   4.506 6.60e-06 ***
## sqrt_examined         0.181071   0.046740   3.874 0.000107 ***
## age                  -0.024489   0.005585  -4.385 1.16e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2978.9  on 4005  degrees of freedom
## AIC: 3016.9
##
## Number of Fisher Scoring iterations: 5
```

```
# 2nd binary partial test with all in-significant covariates
binmodel_partial_2 = glm(status ~ a_stage + ln_tumor, family = binomial, newbc)

summary(binmodel_partial_2)
```

```
##
## Call:
## glm(formula = status ~ a_stage + ln_tumor, family = binomial,
##     data = newbc)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.53355    0.34110   7.428 1.11e-13 ***
## a_stage1     1.02938    0.22401   4.595 4.32e-06 ***
## ln_tumor    -0.55245    0.07032  -7.856 3.97e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 3351.7  on 4021  degrees of freedom
## AIC: 3357.7
##
## Number of Fisher Scoring iterations: 4
```

```
# 3rd binary partial test with some significant in 2nd test added
binmodel_partial_3 = glm(status ~ marital_status + t_stage + n_stage + differentiate + estrogen_status +

summary(binmodel_partial_3)
```

```
##
## Call:
## glm(formula = status ~ marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age +
##     a_stage + ln_tumor, family = binomial, data = newbc)
##
## Coefficients:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)           1.985848   0.582219   3.411 0.000648 ***
## marital_status2      -0.247509   0.140237  -1.765 0.077575 .
## marital_status3      -0.231808   0.131581  -1.762 0.078119 .
## marital_status4      -0.281274   0.189215  -1.487 0.137138
## marital_status5      -0.986920   0.363073  -2.718 0.006563 **
## t_stage2             -0.346774   0.158600  -2.186 0.028781 *
## t_stage3             -0.450100   0.267133  -1.685 0.092003 .
## t_stage4             -1.056179   0.311620  -3.389 0.000701 ***
## n_stage2             -0.736774   0.117479  -6.272 3.57e-10 ***
## n_stage3             -1.584207   0.141279 -11.213  < 2e-16 ***
## differentiate2        0.390591   0.104008   3.755 0.000173 ***
## differentiate3        0.920784   0.191675   4.804 1.56e-06 ***
## differentiate4       -0.993288   0.534044  -1.860 0.062894 .
## estrogen_status1      0.731365   0.176189   4.151 3.31e-05 ***
## progesterone_status1  0.573479   0.126984   4.516 6.30e-06 ***
## sqrt_examined         0.183193   0.046609   3.930 8.48e-05 ***
## age                  -0.024564   0.005550  -4.426 9.60e-06 ***
## a_stage1             -0.004192   0.262185  -0.016 0.987243
## ln_tumor             -0.056204   0.139460  -0.403 0.686939
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2993.1  on 4005  degrees of freedom
## AIC: 3031.1
##
## Number of Fisher Scoring iterations: 5
```

- Our 1st partial test only include the significant predicts on global test, and then we also did a second partial test includes all the covariates that are non significant, and we can see the 1st partial model has an AIC at 3016.9. While the second model with all the non signifcant covraites only get an AIC at 3357.7, which is higher than the first model, so we will definitely not use the model 2 combination. However, we do discover some covariates are significant on the second model like a_stage, and ln_tumor, so we include these 2 again into the 1st model to get our 3rd model. However, our 3rd model has a higher AIC at 3031.1 than model 1, so we will continue to keep with model 1.

Step-wise: forward/backward/AiC

Step-wise for binary Y

```
binglobal_backward = stepAIC(model_global_bin, direction = "backward")
```

```
## Start:  AIC=3020.64
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     a_stage + estrogen_status + progesterone_status + ln_tumor +
##     sqrt_examined + age
##
##                       Df Deviance    AIC
## - a_stage              1   2978.6 3018.6
## - ln_tumor             1   2978.9 3018.9
## <none>                     2978.6 3020.6
## - marital_status       4   2987.5 3021.5
## - t_stage              3   2990.2 3026.2
## - race                 2   2993.1 3031.1
## - sqrt_examined        1   2993.7 3033.7
## - estrogen_status      1   2995.5 3035.5
## - progesterone_status  1   2997.9 3037.9
## - age                  1   2998.3 3038.3
## - differentiate        3   3011.0 3047.0
## - n_stage              2   3107.3 3145.3
##
## Step:  AIC=3018.64
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + ln_tumor + sqrt_examined +
##     age
##
##                       Df Deviance    AIC
## - ln_tumor             1   2978.9 3016.9
## <none>                     2978.6 3018.6
```

```
## - marital_status       4   2987.5 3019.5
## - t_stage              3   2991.2 3025.2
## - race                 2   2993.1 3029.1
## - sqrt_examined        1   2993.7 3031.7
## - estrogen_status      1   2995.5 3033.5
## - progesterone_status  1   2997.9 3035.9
## - age                  1   2998.3 3036.3
## - differentiate        3   3011.0 3045.0
## - n_stage              2   3113.8 3149.8
##
## Step:  AIC=3016.87
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age
##
##                       Df Deviance    AIC
## <none>                     2978.9 3016.9
## - marital_status       4   2987.8 3017.8
## - race                 2   2993.2 3027.2
## - sqrt_examined        1   2994.0 3030.0
## - estrogen_status      1   2995.7 3031.7
## - progesterone_status  1   2998.1 3034.1
## - age                  1   2998.4 3034.4
## - t_stage              3   3008.6 3040.6
## - differentiate        3   3011.6 3043.6
## - n_stage              2   3116.4 3150.4
```

```
bin1_backward = stepAIC(binmodel_partial_1, direction = "backward")
```

```
## Start:  AIC=3016.87
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age
##
##                       Df Deviance    AIC
## <none>                     2978.9 3016.9
## - marital_status       4   2987.8 3017.8
## - race                 2   2993.2 3027.2
## - sqrt_examined        1   2994.0 3030.0
## - estrogen_status      1   2995.7 3031.7
## - progesterone_status  1   2998.1 3034.1
## - age                  1   2998.4 3034.4
## - t_stage              3   3008.6 3040.6
## - differentiate        3   3011.6 3043.6
## - n_stage              2   3116.4 3150.4
```

```
bin2_backward = stepAIC(binmodel_partial_2, direction = "backward")
```

```
## Start:  AIC=3357.74
## status ~ a_stage + ln_tumor
##
##            Df Deviance    AIC
## <none>          3351.7 3357.7
## - a_stage   1   3370.9 3374.9
## - ln_tumor  1   3415.7 3419.7
```

```r
bin3_backward = stepAIC(binmodel_partial_3, direction = "backward")
```

```
## Start:  AIC=3031.09
## status ~ marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age +
##     a_stage + ln_tumor
##
##                       Df Deviance    AIC
## - a_stage              1   2993.1 3029.1
## - ln_tumor             1   2993.2 3029.2
## <none>                     2993.1 3031.1
## - marital_status       4   3005.1 3035.1
## - t_stage              3   3004.8 3036.8
## - sqrt_examined        1   3008.6 3044.6
## - estrogen_status      1   3010.1 3046.1
## - progesterone_status  1   3012.4 3048.4
## - age                  1   3013.0 3049.0
## - differentiate        3   3027.6 3059.6
## - n_stage              2   3123.8 3157.8
##
## Step:  AIC=3029.09
## status ~ marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age +
##     ln_tumor
##
##                       Df Deviance    AIC
## - ln_tumor             1   2993.2 3027.2
## <none>                     2993.1 3029.1
## - marital_status       4   3005.1 3033.1
## - t_stage              3   3005.8 3035.8
## - sqrt_examined        1   3008.6 3042.6
## - estrogen_status      1   3010.1 3044.1
## - progesterone_status  1   3012.4 3046.4
## - age                  1   3013.1 3047.1
## - differentiate        3   3027.6 3057.6
## - n_stage              2   3130.2 3162.2
##
## Step:  AIC=3027.25
## status ~ marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age
##
##                       Df Deviance    AIC
## <none>                     2993.2 3027.3
## - marital_status       4   3005.3 3031.3
## - sqrt_examined        1   3008.8 3040.8
## - estrogen_status      1   3010.3 3042.3
## - progesterone_status  1   3012.6 3044.6
## - age                  1   3013.1 3045.1
## - t_stage              3   3022.2 3050.2
## - differentiate        3   3028.1 3056.1
## - n_stage              2   3132.5 3162.5
```

From the backward elimination, the best model with lowest AIC of 3016.87 is: status ~ race + marital_status

+ t_stage + n_stage + differentiate + estrogen_status + progesterone_status + sqrt_examined + age.

```
binglobal_backward = stepAIC(model_global_bin, direction = "forward")
```

```
## Start:  AIC=3020.64
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     a_stage + estrogen_status + progesterone_status + ln_tumor +
##     sqrt_examined + age
```

```
bin1_backward = stepAIC(binmodel_partial_1, direction = "forward")
```

```
## Start:  AIC=3016.87
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age
```

```
bin2_backward = stepAIC(binmodel_partial_2, direction = "forward")
```

```
## Start:  AIC=3357.74
## status ~ a_stage + ln_tumor
```

```
bin3_backward = stepAIC(binmodel_partial_3, direction = "forward")
```

```
## Start:  AIC=3031.09
## status ~ marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age +
##     a_stage + ln_tumor
```

From the forward selection, the best model with lowest AIC of 3016.87 status ~ race + marital_status + t_stage + n_stage + differentiate + estrogen_status + progesterone_status + sqrt_examined + age. Backward and forward elimination selection both produce same AIC value and the models are the same.

```
binglobal_backward = stepAIC(model_global_bin, direction = "both")
```

```
## Start:  AIC=3020.64
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     a_stage + estrogen_status + progesterone_status + ln_tumor +
##     sqrt_examined + age
##
##                       Df Deviance    AIC
## - a_stage              1   2978.6 3018.6
## - ln_tumor             1   2978.9 3018.9
## <none>                     2978.6 3020.6
## - marital_status       4   2987.5 3021.5
## - t_stage              3   2990.2 3026.2
## - race                 2   2993.1 3031.1
## - sqrt_examined        1   2993.7 3033.7
## - estrogen_status      1   2995.5 3035.5
## - progesterone_status  1   2997.9 3037.9
## - age                  1   2998.3 3038.3
## - differentiate        3   3011.0 3047.0
```

```
## - n_stage              2   3107.3 3145.3
##
## Step:  AIC=3018.64
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + ln_tumor + sqrt_examined +
##     age
##
##                       Df Deviance    AIC
## - ln_tumor             1   2978.9 3016.9
## <none>                     2978.6 3018.6
## - marital_status       4   2987.5 3019.5
## + a_stage              1   2978.6 3020.6
## - t_stage              3   2991.2 3025.2
## - race                 2   2993.1 3029.1
## - sqrt_examined        1   2993.7 3031.7
## - estrogen_status      1   2995.5 3033.5
## - progesterone_status  1   2997.9 3035.9
## - age                  1   2998.3 3036.3
## - differentiate        3   3011.0 3045.0
## - n_stage              2   3113.8 3149.8
##
## Step:  AIC=3016.87
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age
##
##                       Df Deviance    AIC
## <none>                     2978.9 3016.9
## - marital_status       4   2987.8 3017.8
## + ln_tumor             1   2978.6 3018.6
## + a_stage              1   2978.9 3018.9
## - race                 2   2993.2 3027.2
## - sqrt_examined        1   2994.0 3030.0
## - estrogen_status      1   2995.7 3031.7
## - progesterone_status  1   2998.1 3034.1
## - age                  1   2998.4 3034.4
## - t_stage              3   3008.6 3040.6
## - differentiate        3   3011.6 3043.6
## - n_stage              2   3116.4 3150.4
```

```
bin1_backward = stepAIC(binmodel_partial_1, direction = "both")
```

```
## Start:  AIC=3016.87
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age
##
##                       Df Deviance    AIC
## <none>                     2978.9 3016.9
## - marital_status       4   2987.8 3017.8
## - race                 2   2993.2 3027.2
## - sqrt_examined        1   2994.0 3030.0
## - estrogen_status      1   2995.7 3031.7
## - progesterone_status  1   2998.1 3034.1
## - age                  1   2998.4 3034.4
## - t_stage              3   3008.6 3040.6
```

```
## - differentiate        3   3011.6 3043.6
## - n_stage              2   3116.4 3150.4
```

```
bin2_backward = stepAIC(binmodel_partial_2, direction = "both")
```

```
## Start:  AIC=3357.74
## status ~ a_stage + ln_tumor
##
##            Df Deviance    AIC
## <none>          3351.7 3357.7
## - a_stage   1   3370.9 3374.9
## - ln_tumor  1   3415.7 3419.7
```

```
bin3_backward = stepAIC(binmodel_partial_3, direction = "both")
```

```
## Start:  AIC=3031.09
## status ~ marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age +
##     a_stage + ln_tumor
##
##                       Df Deviance    AIC
## - a_stage              1   2993.1 3029.1
## - ln_tumor             1   2993.2 3029.2
## <none>                     2993.1 3031.1
## - marital_status       4   3005.1 3035.1
## - t_stage              3   3004.8 3036.8
## - sqrt_examined        1   3008.6 3044.6
## - estrogen_status      1   3010.1 3046.1
## - progesterone_status  1   3012.4 3048.4
## - age                  1   3013.0 3049.0
## - differentiate        3   3027.6 3059.6
## - n_stage              2   3123.8 3157.8
##
## Step:  AIC=3029.09
## status ~ marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age +
##     ln_tumor
##
##                       Df Deviance    AIC
## - ln_tumor             1   2993.2 3027.2
## <none>                     2993.1 3029.1
## + a_stage              1   2993.1 3031.1
## - marital_status       4   3005.1 3033.1
## - t_stage              3   3005.8 3035.8
## - sqrt_examined        1   3008.6 3042.6
## - estrogen_status      1   3010.1 3044.1
## - progesterone_status  1   3012.4 3046.4
## - age                  1   3013.1 3047.1
## - differentiate        3   3027.6 3057.6
## - n_stage              2   3130.2 3162.2
##
## Step:  AIC=3027.25
## status ~ marital_status + t_stage + n_stage + differentiate +
```

```
##     estrogen_status + progesterone_status + sqrt_examined + age
##
##                        Df Deviance    AIC
## <none>                      2993.2 3027.3
## + ln_tumor              1   2993.1 3029.1
## + a_stage               1   2993.2 3029.3
## - marital_status        4   3005.3 3031.3
## - sqrt_examined         1   3008.8 3040.8
## - estrogen_status       1   3010.3 3042.3
## - progesterone_status   1   3012.6 3044.6
## - age                   1   3013.1 3045.1
## - t_stage               3   3022.2 3050.2
## - differentiate         3   3028.1 3056.1
## - n_stage               2   3132.5 3162.5
```

- From the stepwise regression, we have the lowest AIC of 3016.98 which is the model of status ~ race + marital_status + t_stage + n_stage + differentiate + estrogen_status + progesterone_status + sqrt_examined + age. The model is the same compared to the one we picked from the backward elimination and forward elimination. We will go with this model for further statistical testing.

ANOVA

```
model2 <- glm(status ~ race + marital_status + t_stage + n_stage + differentiate + estrogen_status + pr
anova_result1 <- anova(model2)
print(anova_result1)
```

anova for binary Y

```
## Analysis of Deviance Table
##
## Model: gaussian, link: identity
##
## Response: status
##
## Terms added sequentially (first to last)
##
##
##                     Df Deviance Resid. Df Resid. Dev
## NULL                                 4023     521.70
## race                 2   3.6262      4021     518.08
## marital_status       4   2.9196      4017     515.16
## t_stage              3  13.1374      4014     502.02
## n_stage              2  25.1703      4012     476.85
## differentiate        3   6.8813      4009     469.97
## estrogen_status      1   8.9916      4008     460.98
## progesterone_status  1   2.9595      4007     458.02
## sqrt_examined        1   1.8003      4006     456.22
## age                  1   2.1022      4005     454.11
```

```r
summary(model2)
```

```
##
## Call:
## glm(formula = status ~ race + marital_status + t_stage + n_stage +
##     differentiate + estrogen_status + progesterone_status + sqrt_examined +
##     age, data = newbc)
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)             0.7708680  0.0439145  17.554  < 2e-16 ***
## race2                  -0.0681853  0.0209930  -3.248 0.001172 **
## race3                   0.0416639  0.0198151   2.103 0.035560 *
## marital_status2        -0.0259111  0.0167149  -1.550 0.121178
## marital_status3        -0.0175357  0.0153627  -1.141 0.253752
## marital_status4        -0.0321326  0.0235225  -1.366 0.172004
## marital_status5        -0.1345247  0.0508574  -2.645 0.008198 **
## t_stage2               -0.0396395  0.0118704  -3.339 0.000847 ***
## t_stage3               -0.0603490  0.0174234  -3.464 0.000538 ***
## t_stage4               -0.1748054  0.0350531  -4.987 6.40e-07 ***
## n_stage2               -0.0837902  0.0139153  -6.021 1.88e-09 ***
## n_stage3               -0.2421576  0.0183695 -13.183  < 2e-16 ***
## differentiate2          0.0509827  0.0127519   3.998 6.50e-05 ***
## differentiate3          0.0895198  0.0183190   4.887 1.07e-06 ***
## differentiate4         -0.1824586  0.0781803  -2.334 0.019654 *
## estrogen_status1        0.1408815  0.0252403   5.582 2.54e-08 ***
## progesterone_status1    0.0779114  0.0164916   4.724 2.39e-06 ***
## sqrt_examined           0.0191703  0.0050357   3.807 0.000143 ***
## age                    -0.0026658  0.0006191  -4.306 1.70e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.1133866)
##
##     Null deviance: 521.70  on 4023  degrees of freedom
## Residual deviance: 454.11  on 4005  degrees of freedom
## AIC: 2680.5
##
## Number of Fisher Scoring iterations: 2
```

```r
null_model <- glm(status ~ 1, family = binomial, data = newbc)

anova(null_model, model2, test = "Chisq")
```

```
## Analysis of Deviance Table
##
## Model 1: status ~ 1
## Model 2: status ~ race + marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + age
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1      4023     3444.7
## 2      4005      454.1 18   2990.6 < 2.2e-16 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

Criterion procedures

```r
# For the binary outcome, we will use the AIC criterion as well
aic_selected_bin_model <- stepAIC(glmfit, direction = "both")
```

```
## Start:  AIC=2997.39
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     a_stage + estrogen_status + progesterone_status + ln_tumor +
##     sqrt_examined + reginol_node_positive + age
##
##                          Df Deviance    AIC
## - a_stage                 1   2953.4 2995.4
## - ln_tumor                1   2953.6 2995.6
## - marital_status          4   2961.2 2997.2
## <none>                        2953.4 2997.4
## - t_stage                 3   2964.7 3002.7
## - n_stage                 2   2967.3 3007.3
## - race                    2   2969.2 3009.2
## - estrogen_status         1   2970.5 3012.5
## - age                     1   2971.4 3013.4
## - progesterone_status     1   2973.6 3015.6
## - reginol_node_positive   1   2978.6 3020.6
## - sqrt_examined           1   2980.4 3022.4
## - differentiate           3   2986.8 3024.8
##
## Step:  AIC=2995.41
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + ln_tumor + sqrt_examined +
##     reginol_node_positive + age
##
##                          Df Deviance    AIC
## - ln_tumor                1   2953.6 2993.6
## - marital_status          4   2961.2 2995.2
## <none>                        2953.4 2995.4
## + a_stage                 1   2953.4 2997.4
## - t_stage                 3   2966.0 3002.0
## - n_stage                 2   2967.5 3005.5
## - race                    2   2969.2 3007.2
## - estrogen_status         1   2970.6 3010.6
## - age                     1   2971.4 3011.4
## - progesterone_status     1   2973.6 3013.6
## - reginol_node_positive   1   2978.6 3018.6
## - sqrt_examined           1   2980.4 3020.4
## - differentiate           3   2986.8 3022.8
```

```
##
## Step:  AIC=2993.57
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + reginol_node_positive +
##     age
##
##                          Df Deviance    AIC
## - marital_status          4   2961.5 2993.5
## <none>                        2953.6 2993.6
## + ln_tumor                1   2953.4 2995.4
## + a_stage                 1   2953.6 2995.6
## - n_stage                 2   2967.9 3003.9
## - race                    2   2969.3 3005.3
## - estrogen_status         1   2970.7 3008.7
## - age                     1   2971.4 3009.4
## - progesterone_status     1   2973.8 3011.8
## - reginol_node_positive   1   2978.9 3016.9
## - t_stage                 3   2983.2 3017.2
## - sqrt_examined           1   2980.6 3018.6
## - differentiate           3   2987.3 3021.3
##
## Step:  AIC=2993.48
## status ~ race + t_stage + n_stage + differentiate + estrogen_status +
##     progesterone_status + sqrt_examined + reginol_node_positive +
##     age
##
##                          Df Deviance    AIC
## <none>                        2961.5 2993.5
## + marital_status          4   2953.6 2993.6
## + ln_tumor                1   2961.2 2995.2
## + a_stage                 1   2961.4 2995.4
## - n_stage                 2   2975.7 3003.7
## - race                    2   2980.3 3008.3
## - estrogen_status         1   2978.4 3008.4
## - age                     1   2981.4 3011.4
## - progesterone_status     1   2982.6 3012.6
## - reginol_node_positive   1   2987.8 3017.8
## - t_stage                 3   2992.1 3018.1
## - sqrt_examined           1   2989.1 3019.1
## - differentiate           3   2995.1 3021.1
```

```
summary(aic_selected_bin_model)
```

```
##
## Call:
## glm(formula = status ~ race + t_stage + n_stage + differentiate +
##     estrogen_status + progesterone_status + sqrt_examined + reginol_node_positive +
##     age, family = binomial, data = newbc)
##
## Coefficients:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)              1.623139   0.371232   4.372 1.23e-05 ***
## race2                   -0.574227   0.158413  -3.625 0.000289 ***
## race3                    0.430601   0.201848   2.133 0.032901 *
```

```
## t_stage2              -0.429230   0.112954  -3.800 0.000145 ***
## t_stage3              -0.561433   0.148563  -3.779 0.000157 ***
## t_stage4              -1.122611   0.242936  -4.621 3.82e-06 ***
## n_stage2              -0.474258   0.128697  -3.685 0.000229 ***
## n_stage3              -0.644148   0.234160  -2.751 0.005943 **
## differentiate2         0.389412   0.104623   3.722 0.000198 ***
## differentiate3         0.908192   0.191600   4.740 2.14e-06 ***
## differentiate4        -0.954165   0.525800  -1.815 0.069571 .
## estrogen_status1       0.731594   0.176812   4.138 3.51e-05 ***
## progesterone_status1   0.600531   0.127305   4.717 2.39e-06 ***
## sqrt_examined          0.259110   0.049645   5.219 1.80e-07 ***
## reginol_node_positive -0.076301   0.014939  -5.107 3.27e-07 ***
## age                   -0.024052   0.005443  -4.419 9.90e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2961.5  on 4008  degrees of freedom
## AIC: 2993.5
##
## Number of Fisher Scoring iterations: 5
```

```
# And the BIC criterion
bic_selected_bin_model <- stepAIC(glmfit, direction = "both", family = binomial, k = log(nrow(newbc)))
```

```
## Start:  AIC=3135.99
## status ~ race + marital_status + t_stage + n_stage + differentiate +
##     a_stage + estrogen_status + progesterone_status + ln_tumor +
##     sqrt_examined + reginol_node_positive + age
##
##                         Df Deviance    AIC
## - marital_status         4   2961.2 3110.6
## - t_stage                3   2964.7 3122.4
## - a_stage                1   2953.4 3127.7
## - ln_tumor               1   2953.6 3127.8
## - n_stage                2   2967.3 3133.3
## - race                   2   2969.2 3135.2
## <none>                       2953.4 3136.0
## - differentiate          3   2986.8 3144.5
## - estrogen_status        1   2970.5 3144.8
## - age                    1   2971.4 3145.7
## - progesterone_status    1   2973.6 3147.9
## - reginol_node_positive  1   2978.6 3152.9
## - sqrt_examined          1   2980.4 3154.7
##
## Step:  AIC=3110.59
## status ~ race + t_stage + n_stage + differentiate + a_stage +
##     estrogen_status + progesterone_status + ln_tumor + sqrt_examined +
##     reginol_node_positive + age
##
##                         Df Deviance    AIC
## - t_stage                3   2972.7 3097.2
```

```
## - a_stage                1   2961.2 3102.3
## - ln_tumor               1   2961.4 3102.5
## - n_stage                2   2974.9 3107.7
## <none>                       2961.2 3110.6
## - race                   2   2980.1 3112.9
## - differentiate          3   2994.5 3119.0
## - estrogen_status        1   2978.0 3119.1
## - age                    1   2981.3 3122.4
## - progesterone_status    1   2982.3 3123.4
## - reginol_node_positive  1   2987.5 3128.6
## - sqrt_examined          1   2988.7 3129.8
## + marital_status         4   2953.4 3136.0
##
## Step:  AIC=3097.15
## status ~ race + n_stage + differentiate + a_stage + estrogen_status +
##     progesterone_status + ln_tumor + sqrt_examined + reginol_node_positive +
##     age
##
##                          Df Deviance    AIC
## - a_stage                 1   2974.2 3090.4
## - n_stage                 2   2987.1 3095.0
## <none>                        2972.7 3097.2
## - race                    2   2991.8 3099.7
## - estrogen_status         1   2989.9 3106.1
## - ln_tumor                1   2989.9 3106.1
## - differentiate           3   3007.4 3107.0
## - progesterone_status     1   2993.3 3109.5
## - age                     1   2993.4 3109.7
## + t_stage                 3   2961.2 3110.6
## - reginol_node_positive   1   2999.2 3115.4
## - sqrt_examined           1   2999.9 3116.1
## + marital_status          4   2964.7 3122.4
##
## Step:  AIC=3090.36
## status ~ race + n_stage + differentiate + estrogen_status + progesterone_status +
##     ln_tumor + sqrt_examined + reginol_node_positive + age
##
##                          Df Deviance    AIC
## - n_stage                 2   2989.3 3088.9
## <none>                        2974.2 3090.4
## - race                    2   2993.3 3092.9
## + a_stage                 1   2972.7 3097.2
## - estrogen_status         1   2991.9 3099.8
## - differentiate           3   3008.5 3099.8
## - ln_tumor                1   2992.1 3100.0
## + t_stage                 3   2961.2 3102.3
## - progesterone_status     1   2994.5 3102.4
## - age                     1   2994.7 3102.6
## - reginol_node_positive   1   3000.4 3108.3
## - sqrt_examined           1   3001.7 3109.6
## + marital_status          4   2966.0 3115.4
##
## Step:  AIC=3088.9
## status ~ race + differentiate + estrogen_status + progesterone_status +
```

```
##     ln_tumor + sqrt_examined + reginol_node_positive + age
##
##                         Df Deviance    AIC
## <none>                       2989.3 3088.9
## + n_stage                2   2974.2 3090.4
## - race                   2   3009.5 3092.5
## + a_stage                1   2987.1 3095.0
## - estrogen_status        1   3008.0 3099.3
## + t_stage                3   2975.1 3099.6
## - age                    1   3009.9 3101.2
## - progesterone_status    1   3010.3 3101.6
## - differentiate          3   3027.0 3101.7
## - ln_tumor               1   3013.8 3105.1
## - sqrt_examined          1   3015.5 3106.8
## + marital_status         4   2981.4 3114.2
## - reginol_node_positive  1   3146.2 3237.5
```

```
summary(bic_selected_bin_model)
```

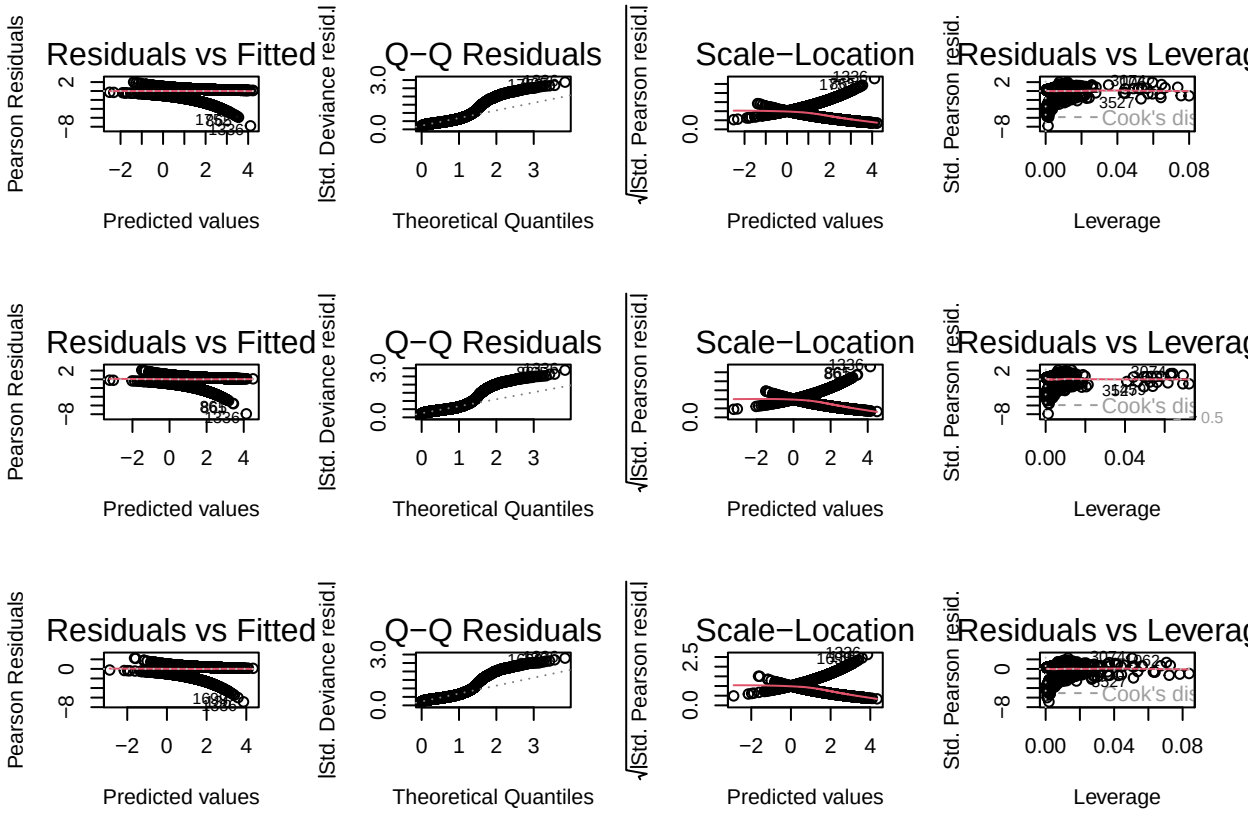
```
##
## Call:
## glm(formula = status ~ race + differentiate + estrogen_status +
##     progesterone_status + ln_tumor + sqrt_examined + reginol_node_positive +
##     age, family = binomial, data = newbc)
##
## Coefficients:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)              2.451459   0.448634   5.464 4.65e-08 ***
## race2                   -0.595023   0.157272  -3.783 0.000155 ***
## race3                    0.440768   0.201932   2.183 0.029054 *
## differentiate2           0.417805   0.103868   4.022 5.76e-05 ***
## differentiate3           0.957010   0.190932   5.012 5.38e-07 ***
## differentiate4          -0.916981   0.506763  -1.809 0.070375 .
## estrogen_status1         0.763842   0.175498   4.352 1.35e-05 ***
## progesterone_status1     0.596058   0.126629   4.707 2.51e-06 ***
## ln_tumor                -0.366801   0.075028  -4.889 1.01e-06 ***
## sqrt_examined            0.248487   0.048812   5.091 3.57e-07 ***
## reginol_node_positive -0.109570   0.008846 -12.386  < 2e-16 ***
## age                     -0.024373   0.005417  -4.500 6.80e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3444.7  on 4023  degrees of freedom
## Residual deviance: 2989.3  on 4012  degrees of freedom
## AIC: 3013.3
##
## Number of Fisher Scoring iterations: 5
```

In the binary model, the final model according to the AIC selection is status ~ race + t_stage + n_stage + differentiate + estrogen_status + progesterone_status + sqrt_examined + reginol_node_positive + age.

The BIC had the selection of model status ~ race + differentiate + estrogen_status + progesterone_status + ln_tumor + sqrt_examined + reginol_node_positive + age.

Plots to check the model assumptions:

```
par(mfrow = c(3,4))
plot(aic_selected_bin_model)
plot(bic_selected_bin_model)
plot(binmodel_partial_1)
```



VIF

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