Logistic Regression

2023-12-06

Clean the data

```
heart_df =
  read_csv("./Project_2_data.csv") |>
  janitor::clean_names() |>
  relocate(survival_months, status) |>
  mutate(
    race = as.numeric(factor(race, levels = c("White", "Black", "Other"))),
    marital_status = as.numeric(factor(marital_status, levels = c("Married", "Divorced", "Single", "Widowed", "Separated"))),
    t_stage = as.numeric(factor(t_stage, levels = c("T1", "T2", "T3", "T4"))),
    n_stage = as.numeric(factor(n_stage, levels = c("N1", "N2", "N3"))),
    x6th_stage = as.numeric(factor(x6th_stage, levels = c("IIA", "IIIA", "IIIC", "IIB", "IIIB"))),
    differentiate = as.numeric(factor(differentiate, levels = c("Poorly differentiated", "Moderately differentiated", "Well differentiated", "Undifferentiated"))),
    grade = as.numeric(factor(grade, levels = c("3", "2", "1", "anaplastic; Grade IV"))),
    a_stage = as.numeric(factor(a_stage, levels = c("Regional", "Distant"))),
    estrogen_status = as.numeric(factor(estrogen_status, levels = c("Positive", "Negative"))),
    progesterone_status = as.numeric(factor(progesterone_status, levels = c("Positive", "Negative"))),
    status = as.numeric(factor(status, levels = c("Alive", "Dead")))
  ) |>
  rename(ms = "marital_status",
         t_s = "t_stage",
         n_s = "n_stage",
         x6_s = "x6th_stage",
         a_s = "a_stage",
         diff = "differentiate",
         est = "estrogen_status",
         pro = "progesterone_status",
         rne = "regional_node_examined",
         rnp = "reginol_node_positive"
         )
```

```
## 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.
```

```
variablesummary =
  lapply(heart_df[,3:16], table)
```

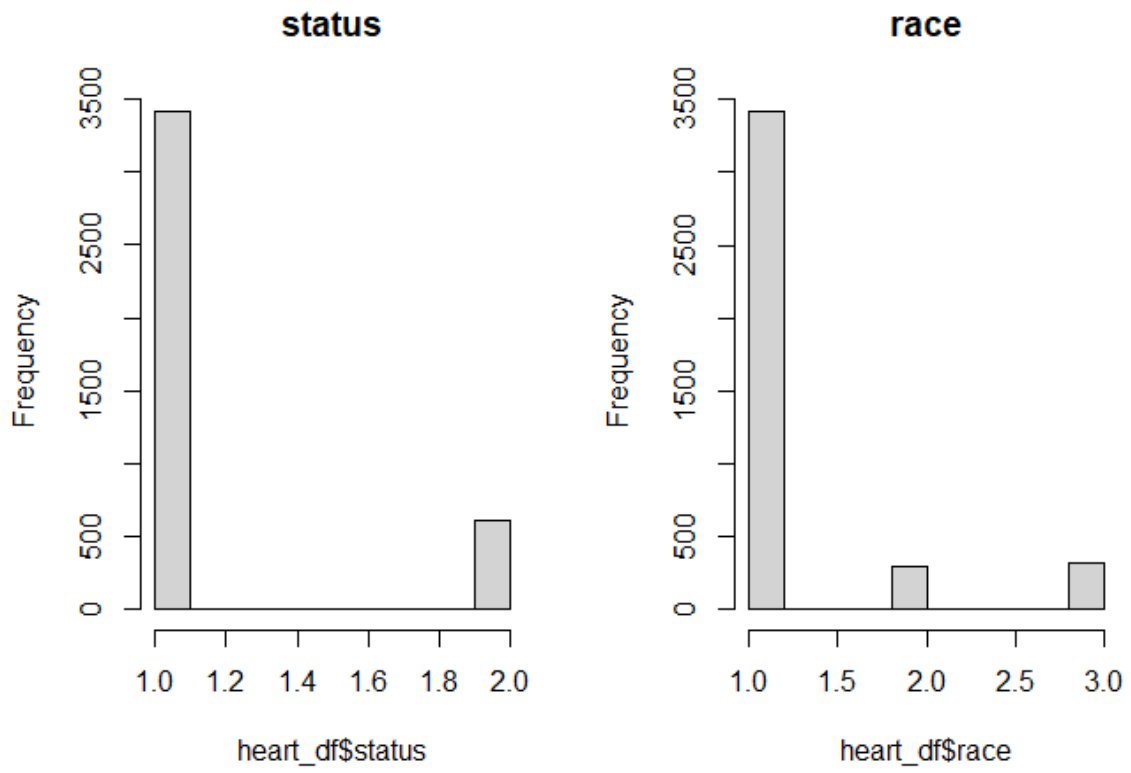
1. outcome: 1 continuous; 1 binary 2. predictors: 4 continuous; 10 categorical

Examine predictors

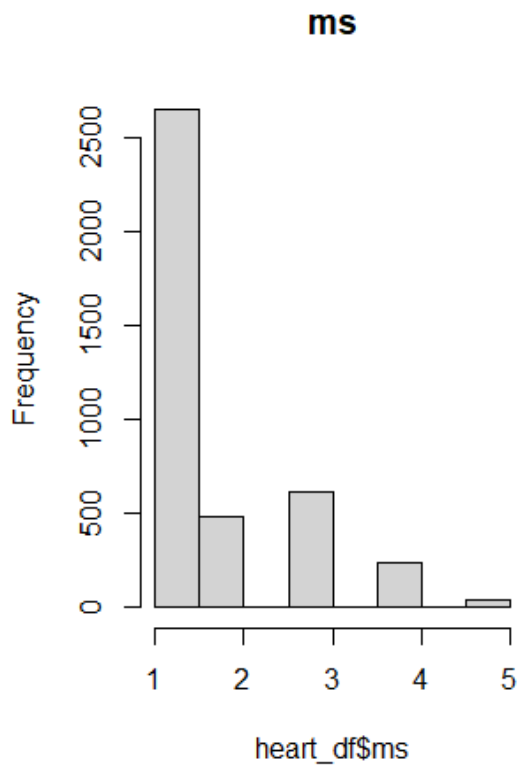
For categorical variable

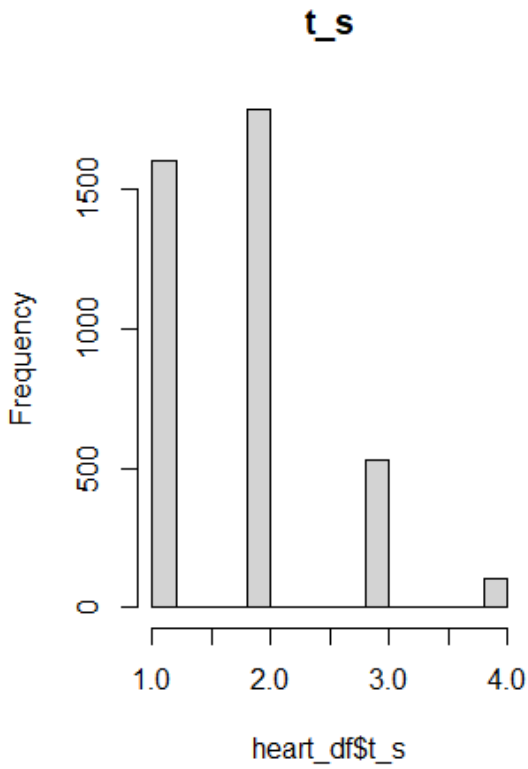
Graphic plot

```
# Histograms for each categorical variables
par(mfrow=c(1,2))
hist(heart_df$status, main='status')
hist(heart_df$race, main='race')
```

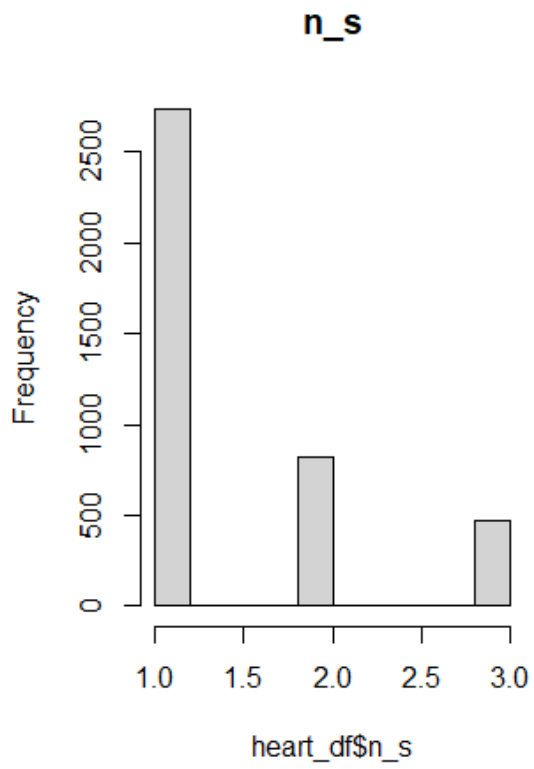


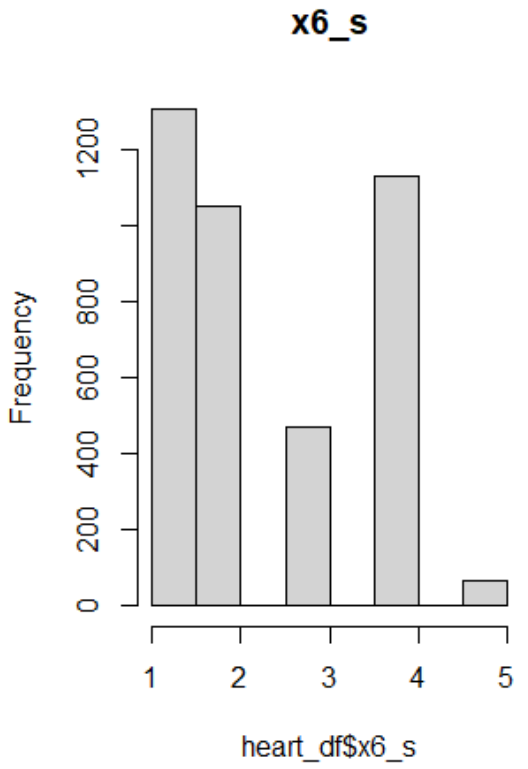
```r
hist(heart_df$ms, main='ms')
hist(heart_df$t_s, main='t_s')
```



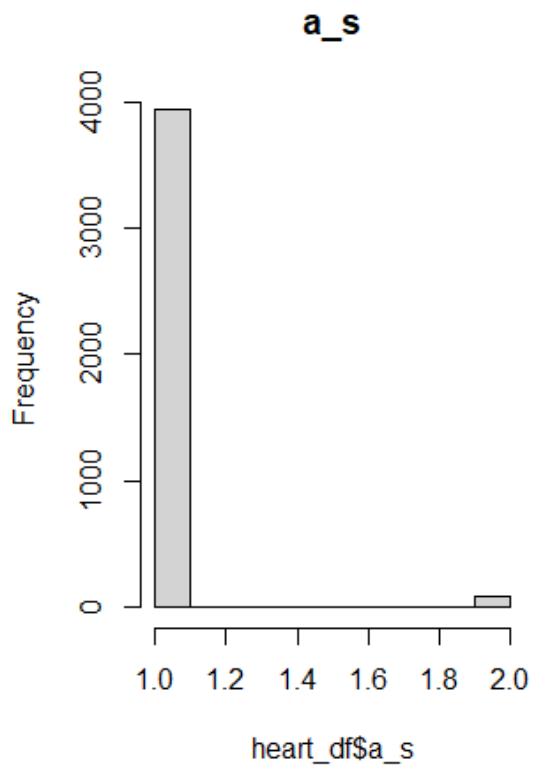


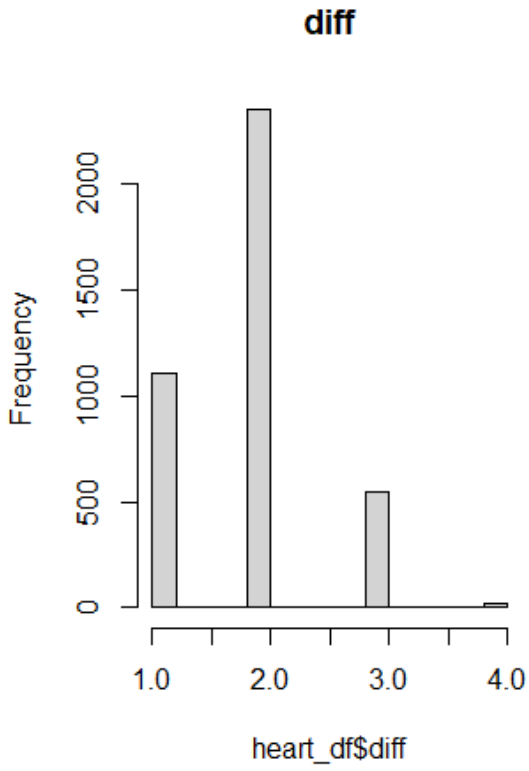

```r
hist(heart_df$n_s, main='n_s')
hist(heart_df$x6_s, main='x6_s')
```



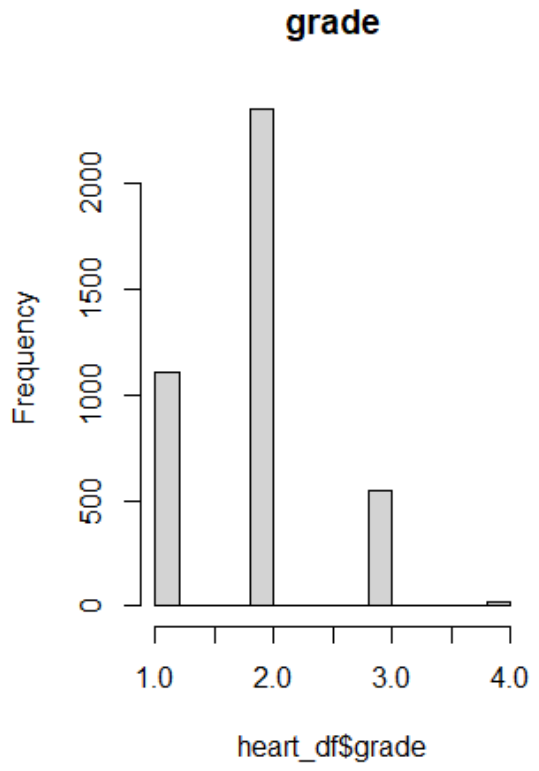


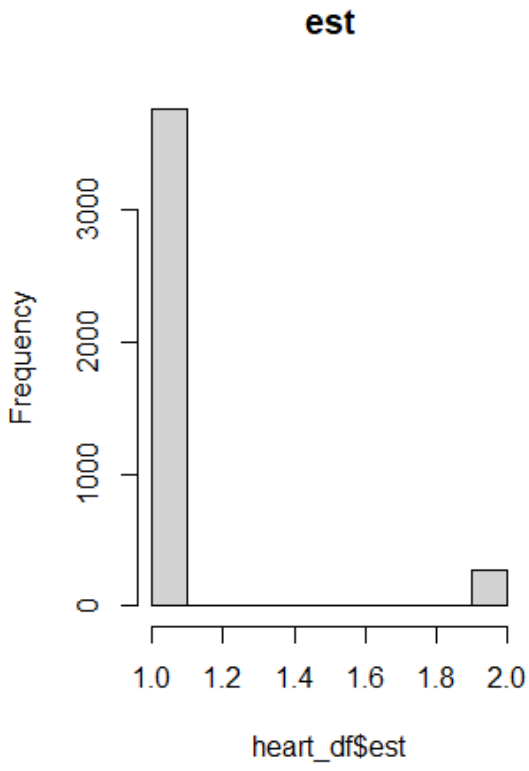
```r
hist(heart_df$a_s, main='a_s')
hist(heart_df$diff, main='diff')
```



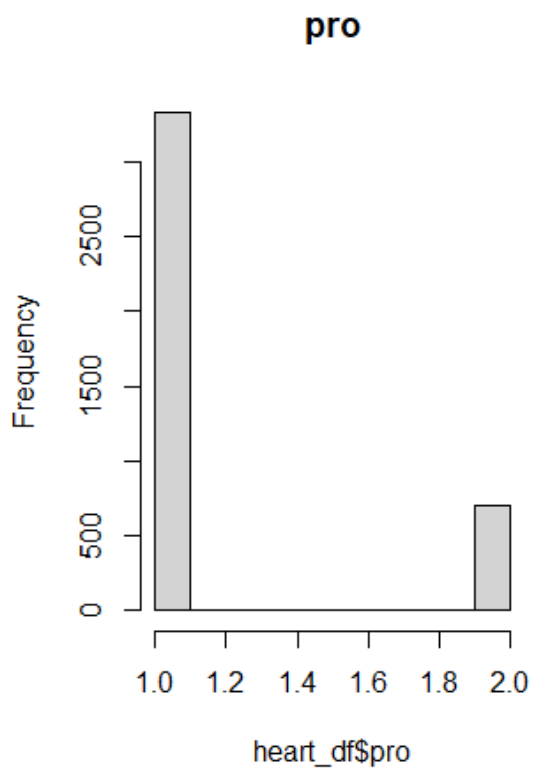



```r
hist(heart_df$grade, main='grade')
hist(heart_df$est, main='est')
```






```r
hist(heart_df$pro, main='pro')
```



most categorical variables have a extremely skewed.
And I find that some variables like `grade` has a very small level. I will focus on that in the following steps.

Char-squared test

```
heart_df_2 =
  read_csv("./Project_2_data.csv") |>
  janitor::clean_names() |>
  relocate(survival_months, status) |>
  dplyr::select("race", "marital_status", "t_stage", "n_stage", "x6th_stage", "differentiate", "grade", "a_stage", "estrogen_status", "progesterone_status") |>
  mutate_all(as.factor)
```

```
## 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.
```

```
result_table =
  data.frame(Variable1 = character(),
             Variable2 = character(),
```

```
             ChiSquare = numeric(),
             PValue = numeric(),
             stringsAsFactors = TRUE)


for (col1 in names(heart_df_2)[1:(ncol(heart_df_2) - 1)]) {
  for (col2 in names(heart_df_2)[(match(col1, names(heart_df_2)) +
1):ncol(heart_df_2)]) {

    contingency_table <- table(heart_df_2[[col1]], heart_df_2[[col2]])


    chi_sq_test_result <- chisq.test(contingency_table,
                                     correct = T)


    variable1 <- col1
    variable2 <- col2
    chi_square <- chi_sq_test_result$statistic
    p_value <- chi_sq_test_result$p.value


    result_table <- rbind(result_table, data.frame(variable1, variable2,
chi_square, p_value))
  }
}

original_row_names = rownames(result_table)
new_row_names <- as.character(1:nrow(result_table))
rownames(result_table) <- new_row_names

result_table =
  result_table |>
  arrange(desc(p_value))

knitr::kable(result_table)
```

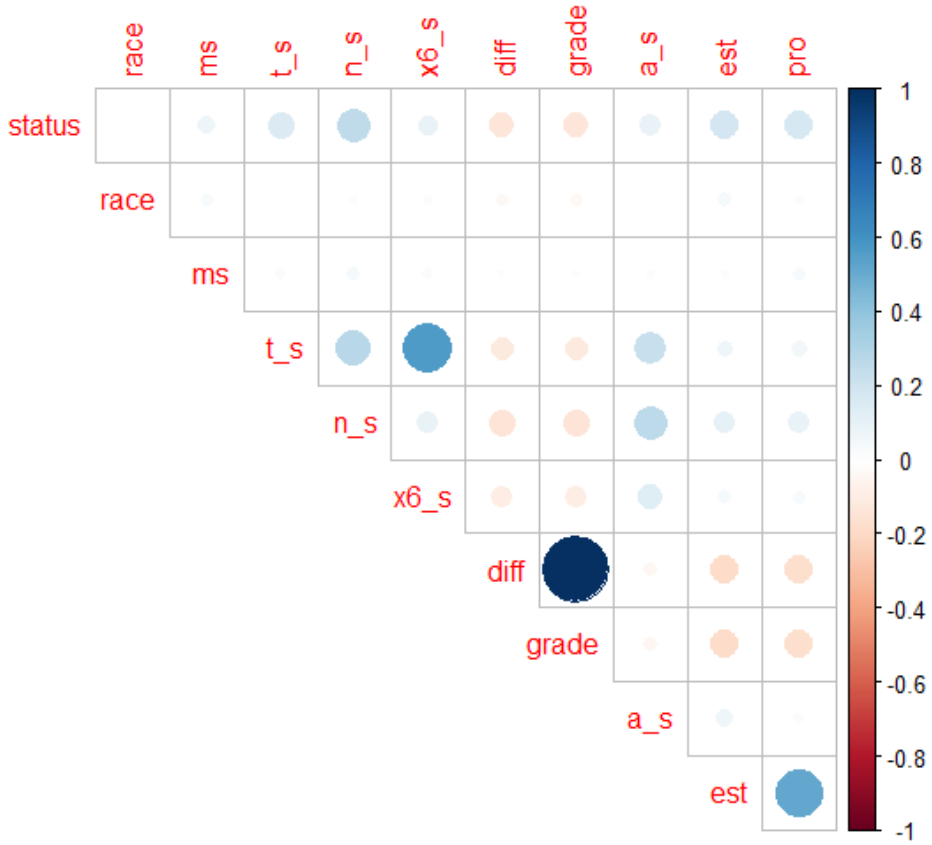
	variable1	variable2	chi_square	p_value
7	race	a_stage	3.069776e-01	0.8577104
4	race	x6th_stage	8.839562e+00	0.3560107
2	race	t_stage	8.462431e+00	0.2061430
3	race	n_stage	6.079684e+00	0.1932759
10	marital_status	t_stage	1.712041e+01	0.1451239
44	a_stage	progesterone_status	2.382806e+00	0.1226770
15	marital_status	a_stage	7.658489e+00	0.1049203
16	marital_status	estrogen_status	7.690336e+00	0.1036033
13	marital_status	differentiate	1.915564e+01	0.0848409
14	marital_status	grade	1.915564e+01	0.0848409
9	race	progesterone_status	5.043148e+00	0.0803331
12	marital_status	x6th_stage	2.810804e+01	0.0306927
17	marital_status	progesterone_status	1.104690e+01	0.0260420
37	differentiate	a_stage	1.057708e+01	0.0142471
40	grade	a_stage	1.057708e+01	0.0142471
11	marital_status	n_stage	2.235252e+01	0.0043030
24	t_stage	progesterone_status	1.380823e+01	0.0031781
8	race	estrogen_status	1.340900e+01	0.0012254
23	t_stage	estrogen_status	1.954986e+01	0.0002104
5	race	differentiate	2.790280e+01	0.0000980
6	race	grade	2.790280e+01	0.0000980
43	a_stage	estrogen_status	1.558922e+01	0.0000787
35	x6th_stage	progesterone_status	4.248544e+01	0.0000000
30	n_stage	progesterone_status	3.684600e+01	0.0000000
29	n_stage	estrogen_status	4.252308e+01	0.0000000
34	x6th_stage	estrogen_status	5.200461e+01	0.0000000
20	t_stage	differentiate	9.095689e+01	0.0000000
21	t_stage	grade	9.095689e+01	0.0000000
26	n_stage	differentiate	1.155011e+02	0.0000000
27	n_stage	grade	1.155011e+02	0.0000000

	variable1	variable2	chi_square	p_value
1	race	marital_status	1.379574e+02	0.0000000
31	x6th_stage	differentiate	1.580412e+02	0.0000000
32	x6th_stage	grade	1.580412e+02	0.0000000
39	differentiate	progesterone_status	1.478031e+02	0.0000000
42	grade	progesterone_status	1.478031e+02	0.0000000
38	differentiate	estrogen_status	2.174167e+02	0.0000000
41	grade	estrogen_status	2.174167e+02	0.0000000
18	t_stage	n_stage	3.234137e+02	0.0000000
28	n_stage	a_stage	3.555764e+02	0.0000000
22	t_stage	a_stage	5.832589e+02	0.0000000
33	x6th_stage	a_stage	7.291926e+02	0.0000000
45	estrogen_status	progesterone_status	1.054843e+03	0.0000000
19	t_stage	x6th_stage	6.784079e+03	0.0000000
25	n_stage	x6th_stage	6.686834e+03	0.0000000
36	differentiate	grade	1.207200e+04	0.0000000

There're many categorical variables correlate with others. Particularly, difference and grade should preserve one. I delete `differentiate`. What's more, delete `x6th_stage`, `est` on account of their extremely small p-values.

Correlation for categorical variables

```
par(mfrow = c(1, 1), mar = c(5, 4, 4, 2) + 0.1)
cor_cate = cor(heart_df[,c(2, 4:11, 13:14)])

corrplot(cor_cate, type = "upper", diag = FALSE, mar = c(0, 0, 0, 0))
```

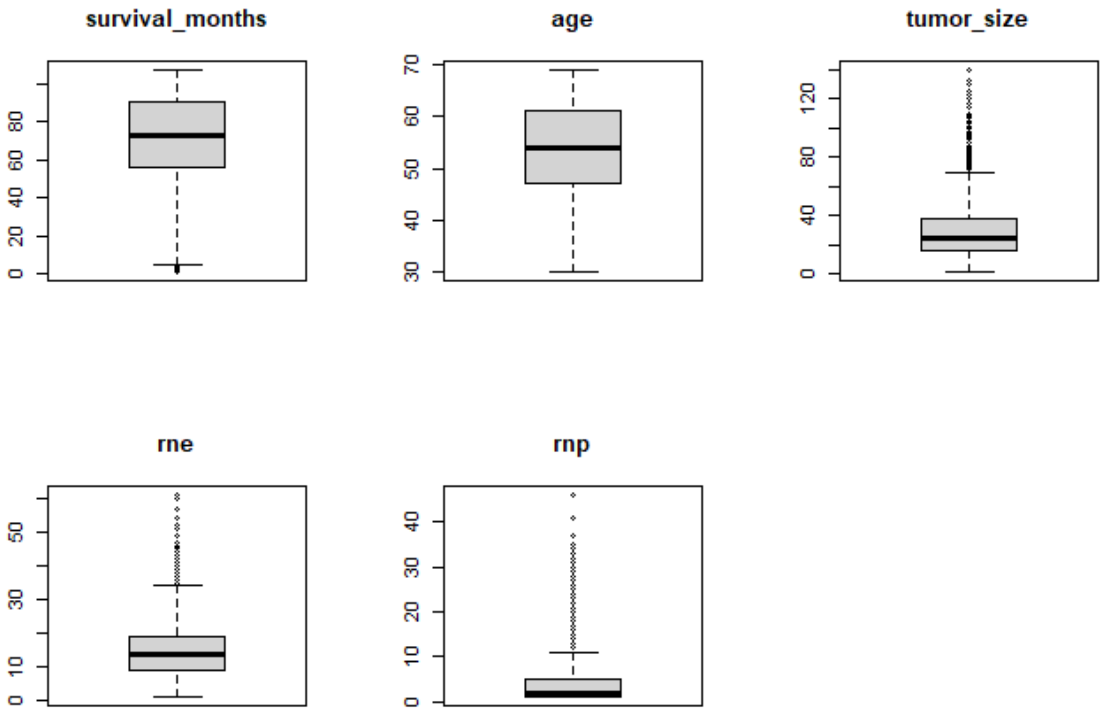


There is apparent linear correlation among variables between diff and grade; t_s and x6_s; est and pro. with the outcome we get from chi-squared test, I delete `x6th_stage`, `est` and `diff` variable for the further study.

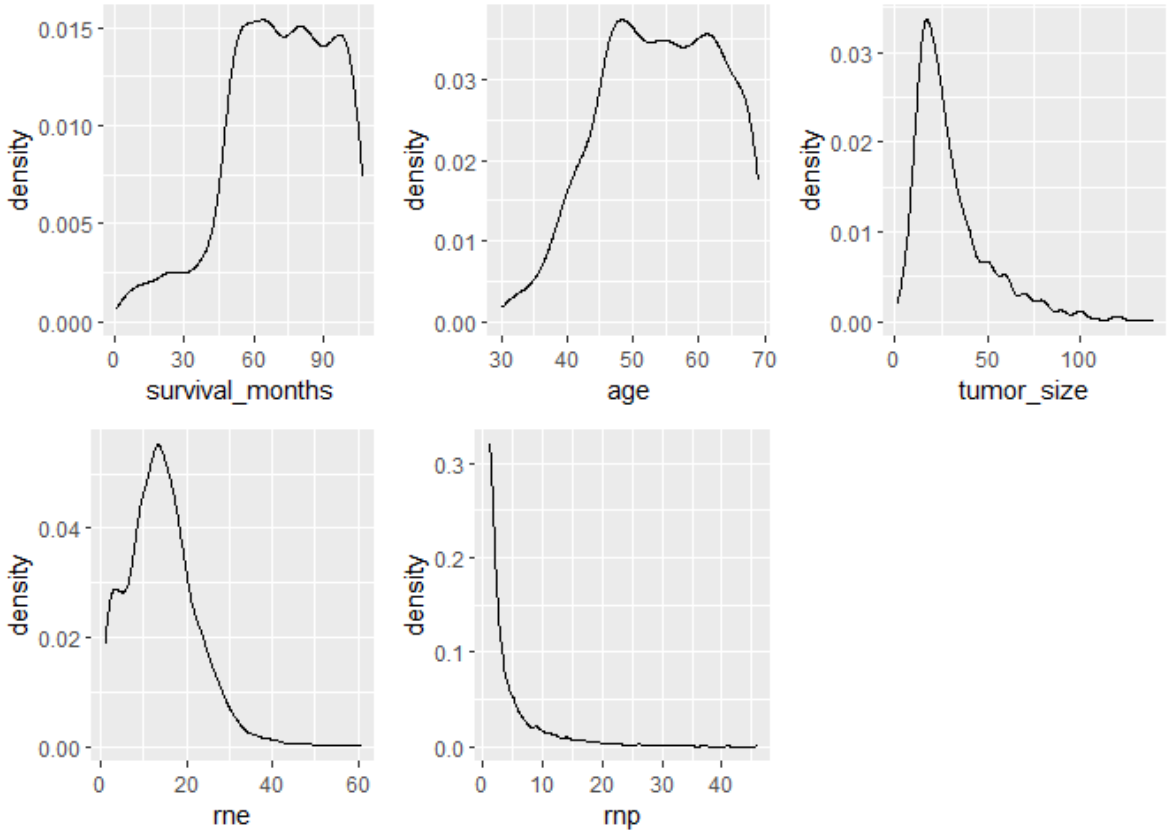
For continuous variable

Graphic plot

```
# Boxplots for each continuous variable
par(mfrow=c(2,3))
boxplot(heart_df$survival_months, main='survival_months')
boxplot(heart_df$age, main='age')
boxplot(heart_df$tumor_size, main='tumor_size')
boxplot(heart_df$rne, main='rne')
boxplot(heart_df$rnp, main='rnp')
```




```r
p1 =ggplot(heart_df, aes(x = survival_months)) + geom_density()
p2 = ggplot(heart_df, aes(x = age)) + geom_density()
p3 = ggplot(heart_df, aes(x = tumor_size)) + geom_density()
p4 = ggplot(heart_df, aes(x = rne)) + geom_density()
p5 = ggplot(heart_df, aes(x = rnp)) + geom_density()

combined_plot = plot_grid(p1, p2, p3, p4, p5,
                          ncol = 3,
                          nrow = 2)
combined_plot
```



Among all the 5 continuous variables, we can find that `age` is the only predictor which is normally distributed. The other three variables are not normally distributed. Because the logistic regression doesn't need the predictors to be normally distributed, I didn't transform these predictors.

Rank-sum test and t-test

```
result1 = t.test(age ~ status, data = heart_df)
result2 = wilcox.test(tumor_size ~ status, data = heart_df)
result3 = wilcox.test(rne ~ status, data = heart_df)
result4 = wilcox.test(rnp ~ status, data = heart_df)

broom::tidy(result1)
```

```
## # A tibble: 1 × 10
##   estimate estimate1 estimate2 statistic  p.value parameter conf.low
conf.high
##      <dbl>     <dbl>     <dbl>     <dbl>    <dbl>     <dbl>    <dbl>
<dbl>
## 1    -1.39      53.8      55.2     -3.32 0.000931      809.    -2.21
-0.570
## # ℹ 2 more variables: method <chr>, alternative <chr>
```

```
broom::tidy(result2)
```

```
## # A tibble: 1 × 4
##   statistic  p.value method
alternative
##       <dbl>    <dbl> <chr>                                                <chr>
## 1    813236 4.85e-19 Wilcoxon rank sum test with continuity correct…
two.sided
```

```
broom::tidy(result3)
```

```
## # A tibble: 1 × 4
##   statistic p.value method
alternative
##       <dbl>   <dbl> <chr>                                                <chr>
## 1   1001152  0.0673 Wilcoxon rank sum test with continuity correcti…
two.sided
```

```
broom::tidy(result4)
```

```
## # A tibble: 1 × 4
##   statistic  p.value method
alternative
##       <dbl>    <dbl> <chr>                                                <chr>
## 1   692562. 6.82e-44 Wilcoxon rank sum test with continuity correct…
two.sided
```

I use two-sample t test to check age and rank-sum test check other three variables. `rne` has a different median compared between two groups stratified by `status`. But, we can't delete this variable just on account of its rank-sum test outcome, I will focus on this variable in the further study.

Check the dataset again

```
heart_df_log =
  read_csv("./Project_2_data.csv") |>
  janitor::clean_names() |>
  relocate(survival_months, status) |>
  filter(!grade %in% c("anaplastic; Grade IV")) |>
  mutate(
    race = factor(race, levels = c("White", "Black", "Other")),
    marital_status = factor(marital_status, levels = c("Married",
"Divorced", "Single", "Widowed", "Separated")),
    t_stage = factor(t_stage, levels = c("T1", "T2", "T3", "T4")),
    n_stage = factor(n_stage, levels = c("N1", "N2", "N3")),
    grade = factor(grade, levels = c("3", "2", "1")),
    a_stage = factor(a_stage, levels = c("Regional", "Distant")),
    progesterone_status = factor(progesterone_status, levels = c("Positive",
"Negative")),
    status = factor(status, levels = c("Alive", "Dead"))) |>
```

```
  dplyr::select(-survival_months, -differentiate, -x6th_stage, -
estrogen_status)
```

```
## 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(heart_df_log)
```

```
##    status          age           race        marital_status t_stage
n_stage
##  Alive:3398   Min.   :30.00   White:3397   Married  :2632   T1:1598
N1:2722
##  Dead : 607   1st Qu.:47.00   Black: 288   Divorced : 485   T2:1781   N2:
816
##               Median :54.00   Other: 320   Single   : 610   T3: 526   N3:
467
##               Mean   :53.98                Widowed  : 234   T4: 100

##               3rd Qu.:61.00                Separated:  44

##               Max.   :69.00

##  grade        a_stage       tumor_size     progesterone_status
##  3:1111   Regional:3913   Min.   :  1.00   Positive:3311
##  2:2351   Distant :  92   1st Qu.: 16.00   Negative: 694
##  1: 543                   Median : 25.00
##                           Mean   : 30.41
##                           3rd Qu.: 38.00
##                           Max.   :140.00
##  regional_node_examined reginol_node_positive
##  Min.   : 1.00          Min.   : 1.000
##  1st Qu.: 9.00          1st Qu.: 1.000
##  Median :14.00          Median : 2.000
##  Mean   :14.36          Mean   : 4.149
##  3rd Qu.:19.00          3rd Qu.: 5.000
##  Max.   :61.00          Max.   :46.000
```

```
str(heart_df_log)
```

```
## tibble [4,005 × 12] (S3: tbl_df/tbl/data.frame)
##  $ status                : Factor w/ 2 levels "Alive","Dead": 1 1 1 1 1 1 1 2 1 1 ...
##  $ age                   : num [1:4005] 68 50 58 58 47 51 51 40 40 69 ...
##  $ race                  : Factor w/ 3 levels "White","Black",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ marital_status        : Factor w/ 5 levels "Married","Divorced",..: 1 1 2 1 1 3 1 1 2 1 ...
##  $ t_stage               : Factor w/ 4 levels "T1","T2","T3",..: 1 2 3 1 2 1 1 2 4 4 ...
##  $ n_stage               : Factor w/ 3 levels "N1","N2","N3": 1 2 3 1 1 1 1 1 3 3 ...
##  $ grade                 : Factor w/ 3 levels "3","2","1": 1 2 2 1 1 2 3 2 1 3 ...
##  $ a_stage               : Factor w/ 2 levels "Regional","Distant": 1 1 1 1 1 1 1 1 1 2 ...
##  $ tumor_size            : num [1:4005] 4 35 63 18 41 20 8 30 103 32 ...
##  $ progesterone_status   : Factor w/ 2 levels "Positive","Negative": 1 1 1 1 1 1 1 1 1 1 ...
##  $ regional_node_examined: num [1:4005] 24 14 14 2 3 18 11 9 20 21 ...
##  $ reginol_node_positive : num [1:4005] 1 5 7 1 1 2 1 1 18 12 ...
```

according to the procedure, I get the final dataset to make a logistic regression. 1,delete 4 level grade data for its anaplastic mode. 2, delete three categorical variables, namely `differentiate`, `x6th_stage`, `estrogen_status`. 3, delete the `survival_months` cause it's not the variable of our interest. 4, I'll attach more importance on the variable `regional_node_examined`, so it will be tested by Wald test to check whether it should be deleted.

Examine interaction

```
glm_result_1 = glm(data = heart_df_log,
                   status ~ a_stage * reginol_node_positive,
                   binomial(link = 'logit'))
broom::tidy(glm_result_1)
```

```
## # A tibble: 4 × 5
##   term                                estimate std.error statistic
p.value
##   <chr>                                  <dbl>     <dbl>     <dbl>
<dbl>
## 1 (Intercept)                           -2.28    0.0629     -36.3  6.51e-
288
## 2 a_stageDistant                         1.81    0.397        4.55 5.25e-
6
## 3 reginol_node_positive                  0.107   0.00774     13.8  1.48e-
43
## 4 a_stageDistant:reginol_node_positive  -0.108   0.0286      -3.79 1.50e-
4
```

```
glm_result_2 = glm(data = heart_df_log,
                   status ~ regional_node_examined * reginol_node_positive,
                   binomial(link = 'logit'))
broom::tidy(glm_result_2)
```

```
## # A tibble: 4 × 5
##   term                                    estimate std.error statistic
p.value
##   <chr>                                      <dbl>     <dbl>     <dbl>
<dbl>
## 1 (Intercept)                             -2.13     0.120       -17.8
1.52e-70
## 2 regional_node_examined                  -0.0218   0.00790      -2.76
5.74e- 3
## 3 reginol_node_positive                    0.199    0.0196       10.2
3.03e-24
## 4 regional_node_examined:reginol_node_pos… -0.00300  0.000744     -4.02
5.71e- 5
```

I check all the 2 variable group to find whether there exists a correlation effect, and find `a_stage` and `reginol_node_positive`'s interaction p-value is 1.50e-4. `regional_node_examined` and `reginol_node_positive`'s interaction p-value is 5.71e-5. Their interaction events play vital roles in our model. Therefore, I will put these two interaction event in my following models.

Model variable select

1. Stepwise

build model

```
model =
  glm(status ~ . + a_stage * reginol_node_positive + regional_node_examined *
reginol_node_positive,
      data = heart_df_log,
      family = binomial(link = 'logit'))

summary(model)
```

```
##
## Call:
## glm(formula = status ~ . + a_stage * reginol_node_positive +
##     regional_node_examined * reginol_node_positive, family =
binomial(link = "logit"),
##     data = heart_df_log)
##
## Coefficients:
##                                             Estimate Std. Error z
value
## (Intercept)                                -3.3157333  0.3565548
-9.299
```

```
## age                                              0.0214016  0.0055957
3.825
## raceBlack                                        0.5285528  0.1617692
3.267
## raceOther                                       -0.4105070  0.2015324
-2.037
## marital_statusDivorced                           0.1979062  0.1413430
1.400
## marital_statusSingle                             0.1233095  0.1354483
0.910
## marital_statusWidowed                            0.2141907  0.1925412
1.112
## marital_statusSeparated                          0.8660280  0.3712285
2.333
## t_stageT2                                        0.3805790  0.1313527
2.897
## t_stageT3                                        0.5016913  0.2663068
1.884
## t_stageT4                                        0.9958936  0.3197436
3.115
## n_stageN2                                        0.3312383  0.1474584
2.246
## n_stageN3                                        0.3904381  0.2757280
1.416
## grade2                                          -0.4487602  0.1030829
-4.353
## grade1                                          -0.9931654  0.1916765
-5.181
## a_stageDistant                                   0.7656274  0.4833319
1.584
## tumor_size                                       0.0003454  0.0039406
0.088
## progesterone_statusNegative                      0.8338434  0.1082163
7.705
## regional_node_examined                          -0.0316316  0.0084370
-3.749
## reginol_node_positive                            0.1125016  0.0324023
3.472
## a_stageDistant:reginol_node_positive            -0.0542828  0.0319926
-1.697
## regional_node_examined:reginol_node_positive -0.0007918  0.0008745
-0.905
##                                                 Pr(>|z|)
## (Intercept)                                      < 2e-16 ***
## age                                             0.000131 ***
## raceBlack                                       0.001086 **
## raceOther                                       0.041657 *
## marital_statusDivorced                          0.161458
## marital_statusSingle                            0.362622
## marital_statusWidowed                           0.265949
## marital_statusSeparated                         0.019655 *
## t_stageT2                                       0.003763 **
## t_stageT3                                       0.059581 .
## t_stageT4                                       0.001842 **
## n_stageN2                                       0.024684 *
## n_stageN3                                       0.156768
## grade2                                          1.34e-05 ***
## grade1                                          2.20e-07 ***
```

```
## a_stageDistant                                    0.113180
## tumor_size                                        0.930156
## progesterone_statusNegative                       1.30e-14 ***
## regional_node_examined                            0.000177 ***
## reginol_node_positive                             0.000517 ***
## a_stageDistant:reginol_node_positive              0.089748 .
## regional_node_examined:reginol_node_positive 0.365255
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3407.5  on 4004  degrees of freedom
## Residual deviance: 2946.1  on 3983  degrees of freedom
## AIC: 2990.1
##
## Number of Fisher Scoring iterations: 5
```

```
model_step = step(model, direction = "both")
```

```
## Start:  AIC=2990.1
## status ~ age + race + marital_status + t_stage + n_stage + grade +
##     a_stage + tumor_size + progesterone_status + regional_node_examined +
##     reginol_node_positive + a_stage * reginol_node_positive +
##     regional_node_examined * reginol_node_positive
##
##                                              Df Deviance    AIC
## - tumor_size                                  1   2946.1 2988.1
## - regional_node_examined:reginol_node_positive  1   2946.9 2988.9
## - marital_status                              4   2953.5 2989.5
## <none>                                            2946.1 2990.1
## - a_stage:reginol_node_positive               1   2949.0 2991.0
## - n_stage                                     2   2951.1 2991.1
## - t_stage                                     3   2958.9 2996.9
## - race                                        2   2961.9 3001.9
## - age                                         1   2960.9 3002.9
## - grade                                       2   2981.9 3021.9
## - progesterone_status                         1   3002.6 3044.6
##
## Step:  AIC=2988.11
## status ~ age + race + marital_status + t_stage + n_stage + grade +
##     a_stage + progesterone_status + regional_node_examined +
##     reginol_node_positive + a_stage:reginol_node_positive +
regional_node_examined:reginol_node_positive
##
##                                              Df Deviance    AIC
## - regional_node_examined:reginol_node_positive  1   2946.9 2986.9
## - marital_status                              4   2953.5 2987.5
## <none>                                            2946.1 2988.1
## - a_stage:reginol_node_positive               1   2949.0 2989.0
## - n_stage                                     2   2951.2 2989.2
## + tumor_size                                  1   2946.1 2990.1
## - race                                        2   2962.0 3000.0
## - age                                         1   2960.9 3000.9
## - t_stage                                     3   2969.1 3005.1
## - grade                                       2   2982.0 3020.0
```

```
## - progesterone_status                              1   3002.7 3042.7
##
## Step:  AIC=2986.93
## status ~ age + race + marital_status + t_stage + n_stage + grade +
##     a_stage + progesterone_status + regional_node_examined +
##     reginol_node_positive + a_stage:reginol_node_positive
##
##                                                Df Deviance    AIC
## - marital_status                                4   2954.4 2986.4
## <none>                                              2946.9 2986.9
## - a_stage:reginol_node_positive                 1   2949.6 2987.6
## + regional_node_examined:reginol_node_positive  1   2946.1 2988.1
## + tumor_size                                    1   2946.9 2988.9
## - n_stage                                       2   2956.3 2992.3
## - race                                          2   2962.8 2998.8
## - age                                           1   2961.7 2999.7
## - t_stage                                       3   2971.3 3005.3
## - regional_node_examined                        1   2973.0 3011.0
## - grade                                         2   2982.9 3018.9
## - progesterone_status                           1   3003.4 3041.4
##
## Step:  AIC=2986.4
## status ~ age + race + t_stage + n_stage + grade + a_stage +
progesterone_status +
##     regional_node_examined + reginol_node_positive +
a_stage:reginol_node_positive
##
##                                                Df Deviance    AIC
## <none>                                              2954.4 2986.4
## + marital_status                                4   2946.9 2986.9
## - a_stage:reginol_node_positive                 1   2956.9 2986.9
## + regional_node_examined:reginol_node_positive  1   2953.5 2987.5
## + tumor_size                                    1   2954.4 2988.4
## - n_stage                                       2   2963.6 2991.6
## - age                                           1   2970.9 3000.9
## - race                                          2   2973.2 3001.2
## - t_stage                                       3   2979.5 3005.5
## - regional_node_examined                        1   2981.0 3011.0
## - grade                                         2   2989.9 3017.9
## - progesterone_status                           1   3012.5 3042.5
```

```
summary(model_step)
```

```
##
## Call:
## glm(formula = status ~ age + race + t_stage + n_stage + grade +
##     a_stage + progesterone_status + regional_node_examined +
##     reginol_node_positive + a_stage:reginol_node_positive, family =
binomial(link = "logit"),
##     data = heart_df_log)
##
## Coefficients:
##                                      Estimate Std. Error z value
Pr(>|z|)
## (Intercept)                         -3.207333   0.332597  -9.643  < 2e-
16 ***
```

```
## age                                    0.021862   0.005419   4.034 5.48e-
05 ***
## raceBlack                              0.580034   0.158385   3.662
0.000250 ***
## raceOther                             -0.418754   0.201019  -2.083
0.037237 *
## t_stageT2                              0.406565   0.112837   3.603
0.000314 ***
## t_stageT3                              0.532044   0.148621   3.580
0.000344 ***
## t_stageT4                              1.042480   0.268893   3.877
0.000106 ***
## n_stageN2                              0.389858   0.129955   3.000
0.002700 **
## n_stageN3                              0.505349   0.241470   2.093
0.036367 *
## grade2                                -0.449129   0.102872  -4.366 1.27e-
05 ***
## grade1                                -0.980279   0.190720  -5.140 2.75e-
07 ***
## a_stageDistant                         0.726733   0.479490   1.516
0.129611
## progesterone_statusNegative            0.844014   0.107933   7.820 5.29e-
15 ***
## regional_node_examined                -0.036050   0.007232  -4.985 6.20e-
07 ***
## reginol_node_positive                  0.088394   0.015965   5.537 3.08e-
08 ***
## a_stageDistant:reginol_node_positive -0.050505   0.031625  -1.597
0.110274
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3407.5  on 4004  degrees of freedom
## Residual deviance: 2954.4  on 3989  degrees of freedom
## AIC: 2986.4
##
## Number of Fisher Scoring iterations: 5
```

```
waldtest(model_step, "regional_node_examined")
```

```
## Wald test
##
## Model 1: status ~ age + race + t_stage + n_stage + grade + a_stage +
progesterone_status +
##     regional_node_examined + reginol_node_positive +
a_stage:reginol_node_positive
## Model 2: status ~ age + race + t_stage + n_stage + grade + a_stage +
progesterone_status +
##     reginol_node_positive + a_stage:reginol_node_positive
##   Res.Df Df      F    Pr(>F)
## 1   3989
## 2   3990 -1 24.848 6.467e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

1.stepwise: delete the variable `tumor_size`, `regional_node_examined:reginol_node_positive`, `marital_status` 2. Wald test shows a p-value 6.467e-07, which demonstrates that we should preserve the variable `regional_node_examined` though it has a different median between two groups stratified by status.

Attention here please! In this process, the stepwise help me delete the interaction event `regional_node_examined:reginol_node_positive` but preserve the interaction `a_stage:reginol_node_positive` which means the latter one has a larger influence upon the whole model.

the model

```
formula1 =
  as.formula(
  status ~ age + race + t_stage + n_stage + grade + a_stage +
progesterone_status + regional_node_examined + reginol_node_positive +
a_stage:reginol_node_positive)

model = glm(formula1,
            data = heart_df_log,
            family = binomial(link = 'logit'))

summary(model)
```

```
##
## Call:
## glm(formula = formula1, family = binomial(link = "logit"), data =
heart_df_log)
##
## Coefficients:
##                                     Estimate Std. Error z value
Pr(>|z|)
## (Intercept)                        -3.207333   0.332597  -9.643  < 2e-
16 ***
## age                                 0.021862   0.005419   4.034 5.48e-
05 ***
## raceBlack                           0.580034   0.158385   3.662
0.000250 ***
```

```
## raceOther                              -0.418754   0.201019  -2.083
0.037237 *
## t_stageT2                               0.406565   0.112837   3.603
0.000314 ***
## t_stageT3                               0.532044   0.148621   3.580
0.000344 ***
## t_stageT4                               1.042480   0.268893   3.877
0.000106 ***
## n_stageN2                               0.389858   0.129955   3.000
0.002700 **
## n_stageN3                               0.505349   0.241470   2.093
0.036367 *
## grade2                                 -0.449129   0.102872  -4.366 1.27e-
05 ***
## grade1                                 -0.980279   0.190720  -5.140 2.75e-
07 ***
## a_stageDistant                          0.726733   0.479490   1.516
0.129611
## progesterone_statusNegative             0.844014   0.107933   7.820 5.29e-
15 ***
## regional_node_examined                 -0.036050   0.007232  -4.985 6.20e-
07 ***
## reginol_node_positive                   0.088394   0.015965   5.537 3.08e-
08 ***
## a_stageDistant:reginol_node_positive -0.050505   0.031625  -1.597
0.110274
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3407.5  on 4004  degrees of freedom
## Residual deviance: 2954.4  on 3989  degrees of freedom
## AIC: 2986.4
##
## Number of Fisher Scoring iterations: 5
```

```
check_collinearity(model)
```

```
## # Check for Multicollinearity
##
## Low Correlation
##
##                              Term  VIF   VIF 95% CI Increased SE Tolerance
##                               age 1.03 [1.01, 1.09]         1.01      0.97
##                              race 1.02 [1.00, 1.10]         1.01      0.98
##                           t_stage 1.36 [1.31, 1.41]         1.16      0.74
##                           n_stage 4.10 [3.88, 4.33]         2.02      0.24
##                             grade 1.08 [1.05, 1.12]         1.04      0.93
##                           a_stage 4.27 [4.04, 4.51]         2.07      0.23
##               progesterone_status 1.04 [1.02, 1.09]         1.02      0.96
##            regional_node_examined 1.48 [1.43, 1.55]         1.22      0.67
##             reginol_node_positive 4.68 [4.43, 4.94]         2.16      0.21
##  a_stage:reginol_node_positive 3.90 [3.70, 4.12]         1.98      0.26
##  Tolerance 95% CI
##      [0.92, 0.99]
```

```
##      [0.91, 1.00]
##      [0.71, 0.76]
##      [0.23, 0.26]
##      [0.89, 0.95]
##      [0.22, 0.25]
##      [0.92, 0.98]
##      [0.65, 0.70]
##      [0.20, 0.23]
##      [0.24, 0.27]
```

We find our first model and check its collinearity, the model's performance is good.

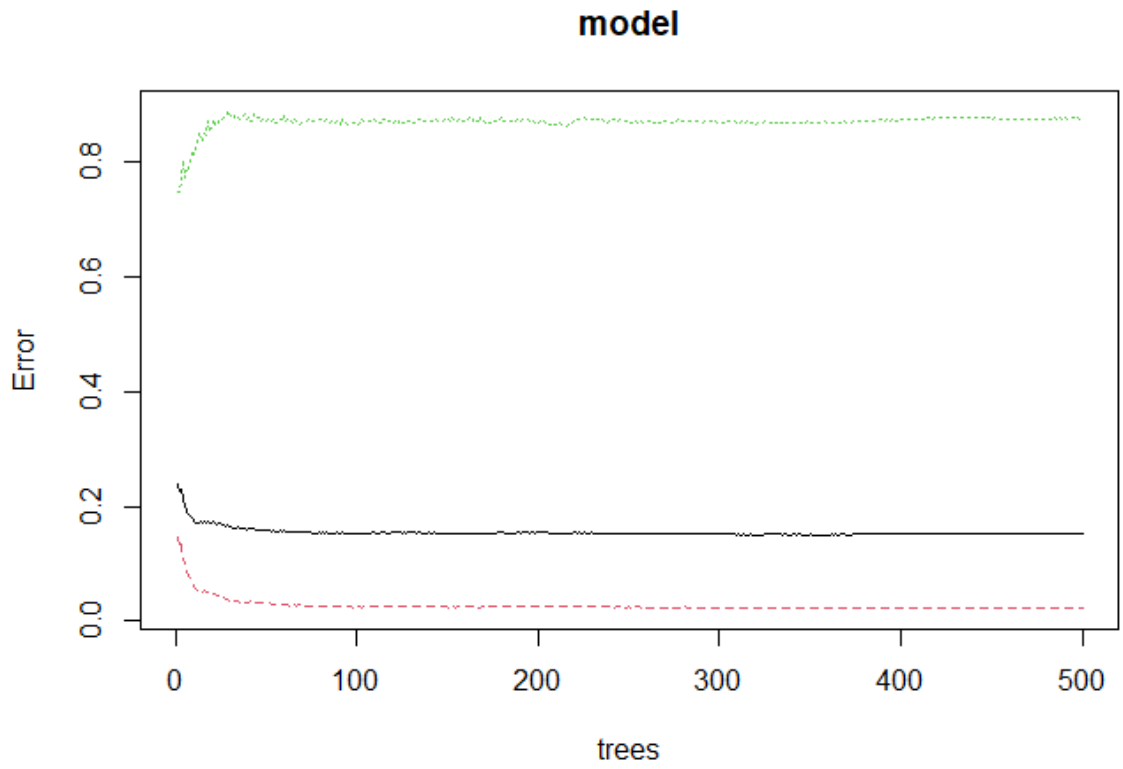
2. Random forest

build model

```
set.seed(123)
model =
  randomForest(status ~ . + a_stage * reginol_node_positive + regional_node_examined * reginol_node_positive,
               data = heart_df_log)

summary(model)
```

```
##                 Length Class  Mode
## call               3   -none- call
## type               1   -none- character
## predicted       4005   factor numeric
## err.rate        1500   -none- numeric
## confusion          6   -none- numeric
## votes           8010   matrix numeric
## oob.times       4005   -none- numeric
## classes            2   -none- character
## importance        11   -none- numeric
## importanceSD       0   -none- NULL
## localImportance    0   -none- NULL
## proximity          0   -none- NULL
## ntree              1   -none- numeric
## mtry               1   -none- numeric
## forest            14   -none- list
## y               4005   factor numeric
## test               0   -none- NULL
## inbag              0   -none- NULL
## terms              3   terms  call
```

```
plot(model)
```




```
forest_min = which.min(model$err.rate[,1])
```

the forest_min which is the best parameter in the regression is 320

```
model_forest =
  randomForest(status ~ . + a_stage * reginol_node_positive + regional_node_examined * reginol_node_positive,
               data = heart_df_log,
               ntree = forest_min,
               mtry = 4)

knitr::kable(model_forest$confusion)
```

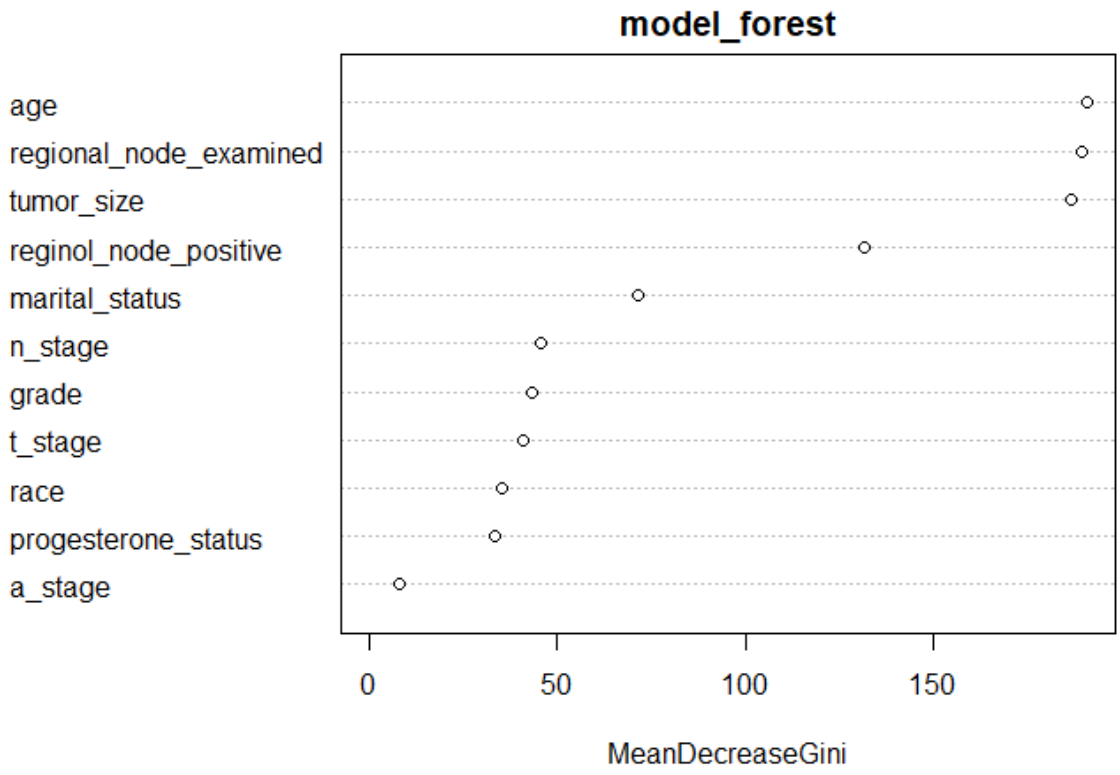
	Alive	Dead	class.error
Alive	3303	95	0.0279576
Dead	531	76	0.8747941

in the simulation process, we get a outcome: the model prediction ability towards alive is good ,but when it comes to the dead, the class.error reaches nearly 0.87 which is a large number.

```
importance(model_forest)
```

```
##                          MeanDecreaseGini
## age                             190.67222
## race                             35.25882
## marital_status                   71.36831
## t_stage                          40.70758
## n_stage                          45.74057
## grade                            43.35355
## a_stage                           8.17414
## tumor_size                      186.30685
## progesterone_status              33.25173
## regional_node_examined          189.38867
## reginol_node_positive           131.57251
```

```
par(mfrow = c(1, 1), mar = c(4, 4, 2, 1), oma = c(0, 0, 2, 0))
varImpPlot(model_forest)
```




```
par(mfrow = c(1, 1), mar = c(5, 4, 4, 2) + 0.1, oma = c(0, 0, 0, 0))
```

according to the picture, I find the first 5 most important variables have a mean decrease gini over 50, which is significantly larger than other variables, so I use these variables to build my final model.

the model

```r
formula2 =
  as.formula(
  status ~ age + regional_node_examined + tumor_size + reginol_node_positive
+ marital_status)

model = glm(formula2,
            data = heart_df_log,
            family = binomial(link = 'logit'))

summary(model)
```

```
##
## Call:
## glm(formula = formula2, family = binomial(link = "logit"), data =
heart_df_log)
##
## Coefficients:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)             -3.248738   0.325798  -9.972  < 2e-16 ***
## age                      0.018089   0.005398   3.351 0.000805 ***
## regional_node_examined  -0.034997   0.006990  -5.007 5.52e-07 ***
## tumor_size               0.010230   0.001977   5.175 2.28e-07 ***
## reginol_node_positive    0.117507   0.008906  13.194  < 2e-16 ***
## marital_statusDivorced   0.275010   0.136973   2.008 0.044668 *
## marital_statusSingle     0.258083   0.129079   1.999 0.045563 *
## marital_statusWidowed    0.318806   0.184381   1.729 0.083799 .
## marital_statusSeparated  0.971231   0.353981   2.744 0.006074 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3407.5  on 4004  degrees of freedom
## Residual deviance: 3124.2  on 3996  degrees of freedom
## AIC: 3142.2
##
## Number of Fisher Scoring iterations: 5
```

```r
check_collinearity(model)
```

```
## # Check for Multicollinearity
##
## Low Correlation
##
##                    Term  VIF   VIF 95% CI Increased SE Tolerance
##                     age 1.08 [1.05, 1.12]         1.04      0.93
##  regional_node_examined 1.47 [1.41, 1.53]         1.21      0.68
##              tumor_size 1.05 [1.03, 1.10]         1.03      0.95
##   reginol_node_positive 1.51 [1.45, 1.57]         1.23      0.66
##          marital_status 1.07 [1.04, 1.12]         1.03      0.94
##  Tolerance 95% CI
##      [0.89, 0.95]
##      [0.65, 0.71]
##      [0.91, 0.97]
##      [0.64, 0.69]
```

```
##      [0.90, 0.96]
```

We find our second model and check its collinearity, the model's performance is good.

3. LASSO

build model

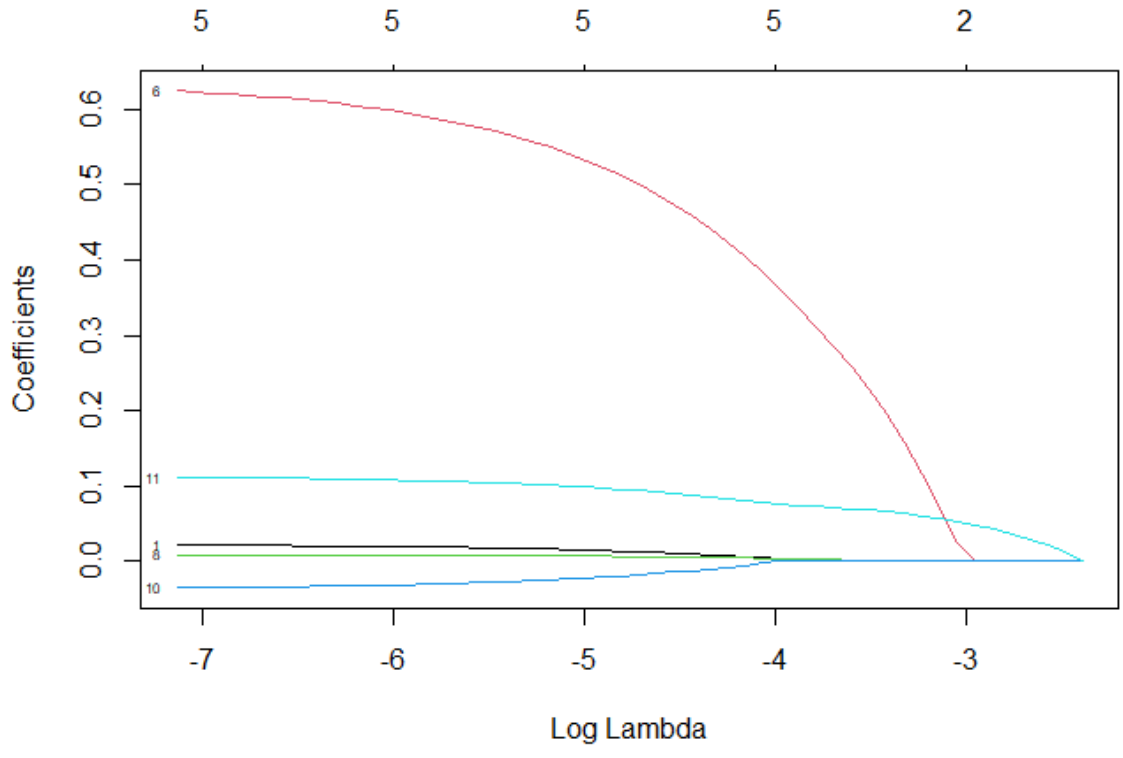
```
x = as.matrix(heart_df_log[,2:12])
y = as.matrix(heart_df_log[,1])

model_lasso =
  glmnet(x, y, alpha = 1, family = "binomial")

model_lasso
```

```
##
## Call:  glmnet(x = x, y = y, family = "binomial", alpha = 1)
##
##    Df %Dev   Lambda
## 1   0 0.00 0.091580
## 2   1 1.23 0.083440
## 3   1 2.16 0.076030
## 4   1 2.88 0.069270
## 5   1 3.45 0.063120
## 6   1 3.91 0.057510
## 7   1 4.27 0.052400
## 8   2 4.72 0.047750
## 9   2 5.26 0.043510
## 10  2 5.70 0.039640
## 11  2 6.07 0.036120
## 12  3 6.40 0.032910
## 13  3 6.75 0.029990
## 14  3 7.04 0.027320
## 15  3 7.28 0.024900
## 16  3 7.48 0.022680
## 17  4 7.71 0.020670
## 18  4 7.94 0.018830
## 19  5 8.24 0.017160
## 20  5 8.52 0.015640
## 21  5 8.75 0.014250
## 22  5 8.95 0.012980
## 23  5 9.11 0.011830
## 24  5 9.25 0.010780
## 25  5 9.36 0.009819
## 26  5 9.46 0.008947
## 27  5 9.54 0.008152
## 28  5 9.61 0.007428
## 29  5 9.67 0.006768
## 30  5 9.71 0.006167
## 31  5 9.75 0.005619
## 32  5 9.79 0.005120
## 33  5 9.81 0.004665
## 34  5 9.84 0.004251
## 35  5 9.86 0.003873
```

```
## 36   5 9.87 0.003529
## 37   5 9.89 0.003215
## 38   5 9.90 0.002930
## 39   5 9.91 0.002669
## 40   5 9.92 0.002432
## 41   5 9.92 0.002216
## 42   5 9.93 0.002019
## 43   5 9.93 0.001840
## 44   5 9.94 0.001676
## 45   5 9.94 0.001528
## 46   5 9.94 0.001392
## 47   5 9.94 0.001268
## 48   5 9.95 0.001156
## 49   5 9.95 0.001053
## 50   5 9.95 0.000959
## 51   5 9.95 0.000874
## 52   5 9.95 0.000796
```

lambda = 0.000796 only 5 predictors were preserved

```
plot(model_lasso, xvar = "lambda", label = TRUE)
```



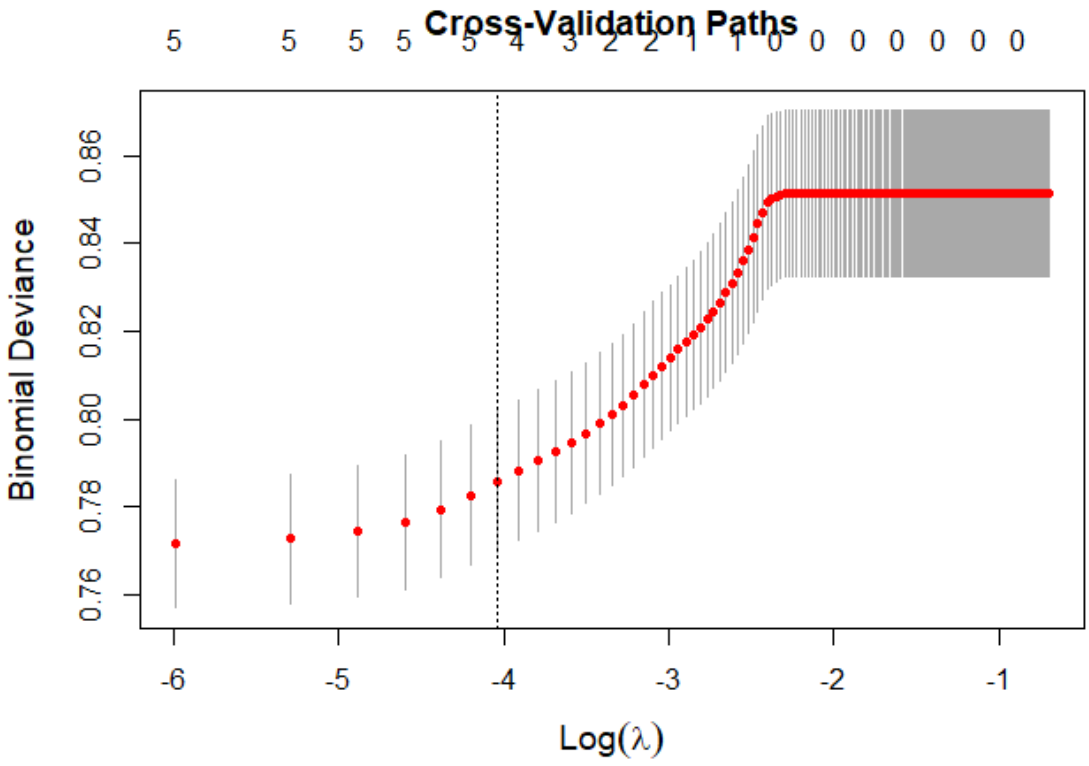

```
lasso.coef = coef(model_lasso, s = 0.000796)
lasso.coef
```

```
## 12 x 1 sparse Matrix of class "dgCMatrix"
##                                 s1
## (Intercept)           -4.65972880
## age                    0.02173778
## race                   .
```

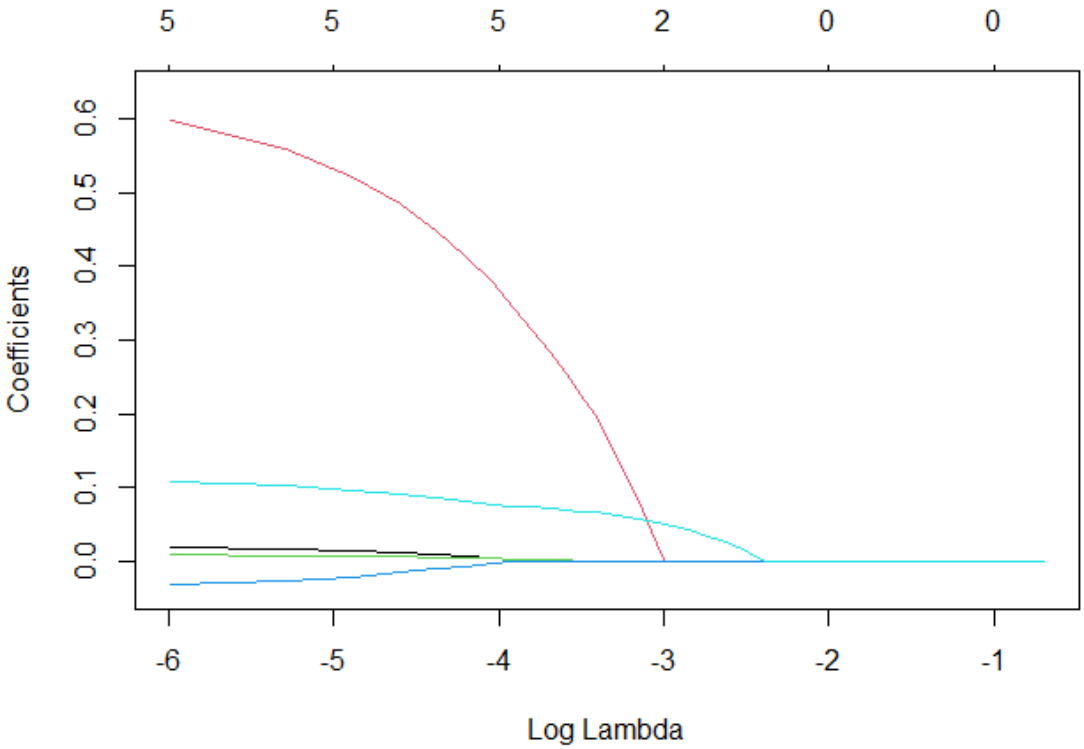
```
## marital_status           .
## t_stage                  .
## n_stage                  .
## grade                    0.62443173
## a_stage                  .
## tumor_size               0.00894751
## progesterone_status      .
## regional_node_examined -0.03496491
## reginol_node_positive    0.11203866
```

we can get the coeffieients under this situation.
(lambda = 0.000796). Now, we want to find the best lamda.

```
set.seed(123)
lambdas = seq(0, 0.5, length.out = 200)
cv.lasso =
  cv.glmnet(x,
            y,
            alpha = 1,
            lambda = lambdas,
            nfolds = 5,
            family = "binomial")

par(mfrow = c(1, 1), mar = c(5, 5, 4, 2) + 0.1)
plot(cv.lasso,
     main = "Cross-Validation Paths",
     cex.lab = 1.2, cex.main = 1.2)
```




```
plot(cv.lasso$glmnet.fit,
     xvar = "lambda",
     label = T)
```




```
lasso_1se =
  cv.lasso$lambda.1se
lasso_1se
```

```
## [1] 0.01758794
```

```
lasso.coef =
  coef(cv.lasso$glmnet.fit,
       s = lasso_1se,
       exact = F)
lasso.coef
```

```
## 12 x 1 sparse Matrix of class "dgCMatrix"
##                                      s1
## (Intercept)            -3.288096024
## age                     0.004409007
## race                    .
## marital_status          .
## t_stage                 .
## n_stage                 .
## grade                   0.377930648
## a_stage                 .
## tumor_size              0.004255330
## progesterone_status     .
## regional_node_examined -0.001651846
## reginol_node_positive   0.077769351
```

according to the outcome, the lasso process help me select these variables: `age`, `grade`, `tumor_size`, `regional_node_examined`, `reginol_node_positive`.

the model

```
formula3 =
  as.formula(
  status ~ age + grade + tumor_size + regional_node_examined +
reginol_node_positive)

model = glm(formula3,
            data = heart_df_log,
            family = binomial(link = 'logit'))

summary(model)
```

```
##
## Call:
## glm(formula = formula3, family = binomial(link = "logit"), data =
heart_df_log)
##
## Coefficients:
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)            -2.816484   0.319834  -8.806  < 2e-16 ***
## age                     0.022642   0.005281   4.288 1.81e-05 ***
## grade2                 -0.646807   0.098600  -6.560 5.38e-11 ***
## grade1                 -1.257807   0.186371  -6.749 1.49e-11 ***
## tumor_size              0.009180   0.002015   4.556 5.22e-06 ***
## regional_node_examined -0.036780   0.007073  -5.200 1.99e-07 ***
## reginol_node_positive   0.113925   0.008944  12.737  < 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: 3407.5  on 4004  degrees of freedom
## Residual deviance: 3068.3  on 3998  degrees of freedom
## AIC: 3082.3
##
## Number of Fisher Scoring iterations: 5
```

```
check_collinearity(model)
```

```
## # Check for Multicollinearity
##
## Low Correlation
##
##                    Term  VIF   VIF 95% CI Increased SE Tolerance
##                     age 1.02 [1.00, 1.10]         1.01      0.98
##                   grade 1.02 [1.00, 1.10]         1.01      0.98
##              tumor_size 1.05 [1.03, 1.10]         1.03      0.95
##  regional_node_examined 1.47 [1.42, 1.54]         1.21      0.68
##   reginol_node_positive 1.51 [1.45, 1.58]         1.23      0.66
##  Tolerance 95% CI
##      [0.91, 1.00]
##      [0.91, 1.00]
##      [0.91, 0.97]
##      [0.65, 0.71]
```

```
##       [0.63, 0.69]
```

We find our third model and check its collinearity, the model's performance is good.

Diagnosis

```
fit1 = lrm(formula1, data = heart_df_log, x = T, y = T)
fit2 = lrm(formula2, data = heart_df_log, x = T, y = T)
fit3 = lrm(formula3, data = heart_df_log, x = T, y = T)
```

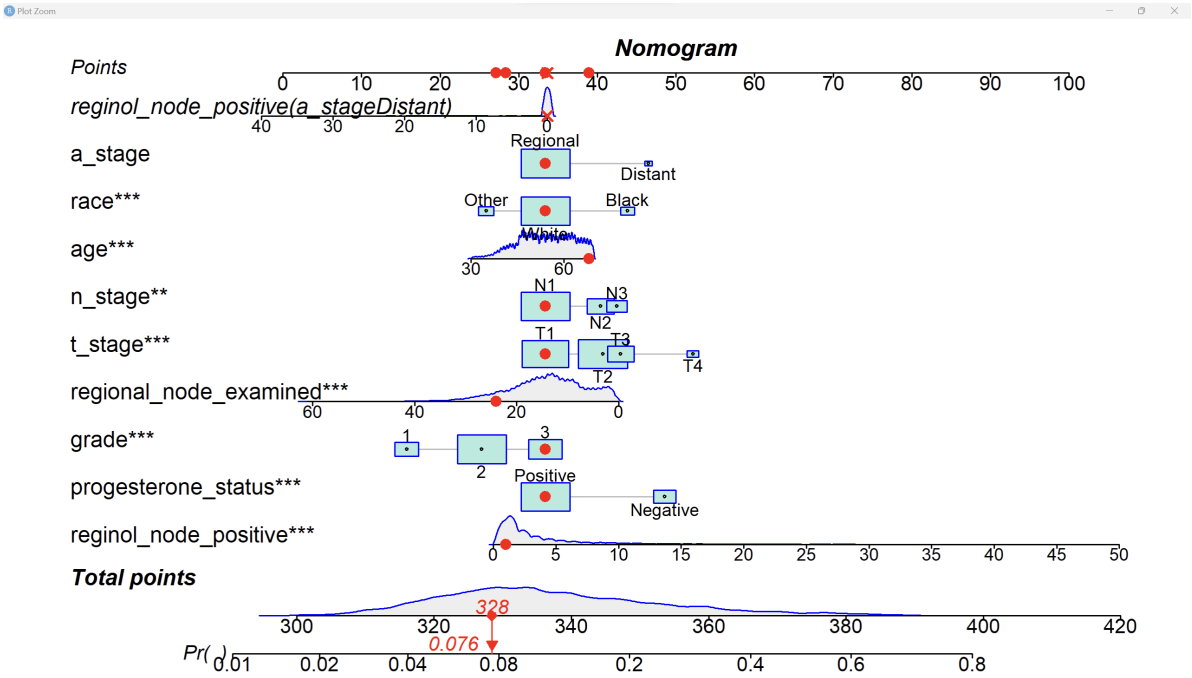
Nomogram

```
dd = datadist(heart_df_log)
options(datadist = "dd")

nomogram_plot = function(input, number){
  nomo_plot =
    regplot(input,
            observation = heart_df_log[number,],
            center = TRUE,
            title = "Nomogram",
            points = TRUE,
            odds = FALSE,
            showP = TRUE,
            rank= "sd",
            clickable = FALSE)
}
```

```
nomogram_plot(fit1, 1)
```

```
## Regression  input lrm formula:

## status `~` age + race + t_stage + n_stage + grade + a_stage +
progesterone_status + regional_node_examined + reginol_node_positive +
a_stage:reginol_node_positive
```

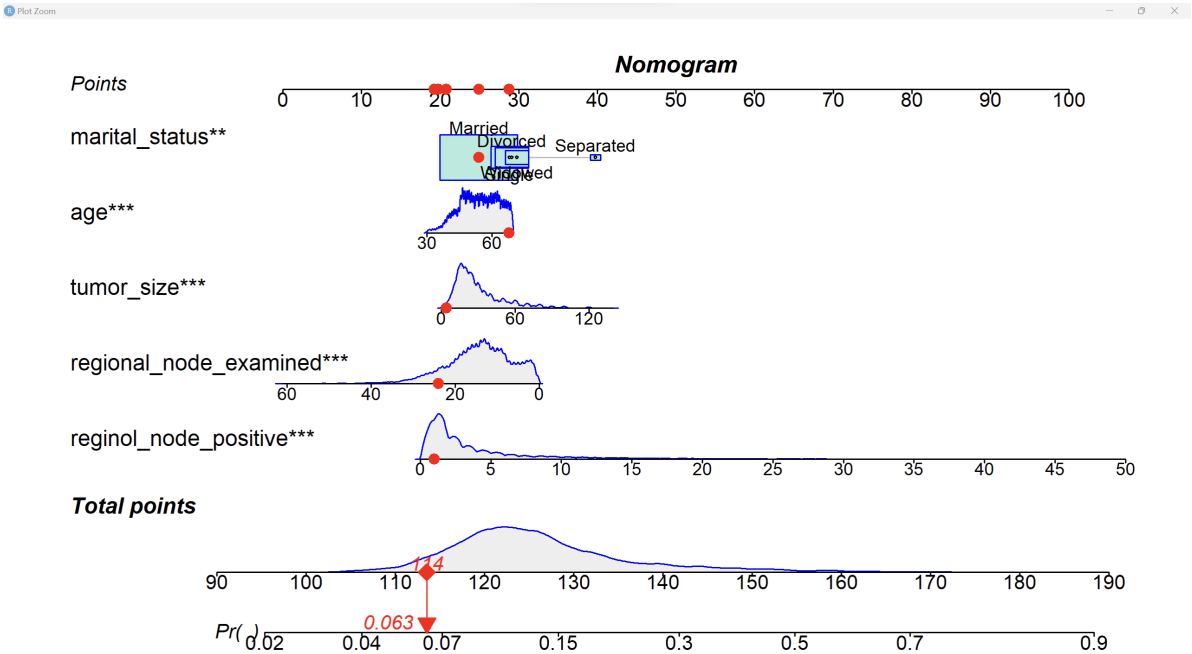
```
knitr::include_graphics("nomogram_plot_1.png")
```




```
nomogram_plot(fit2, 1)
```

```
## Regression  input lrm formula:

## status `~` age + regional_node_examined + tumor_size +
reginol_node_positive + marital_status
```

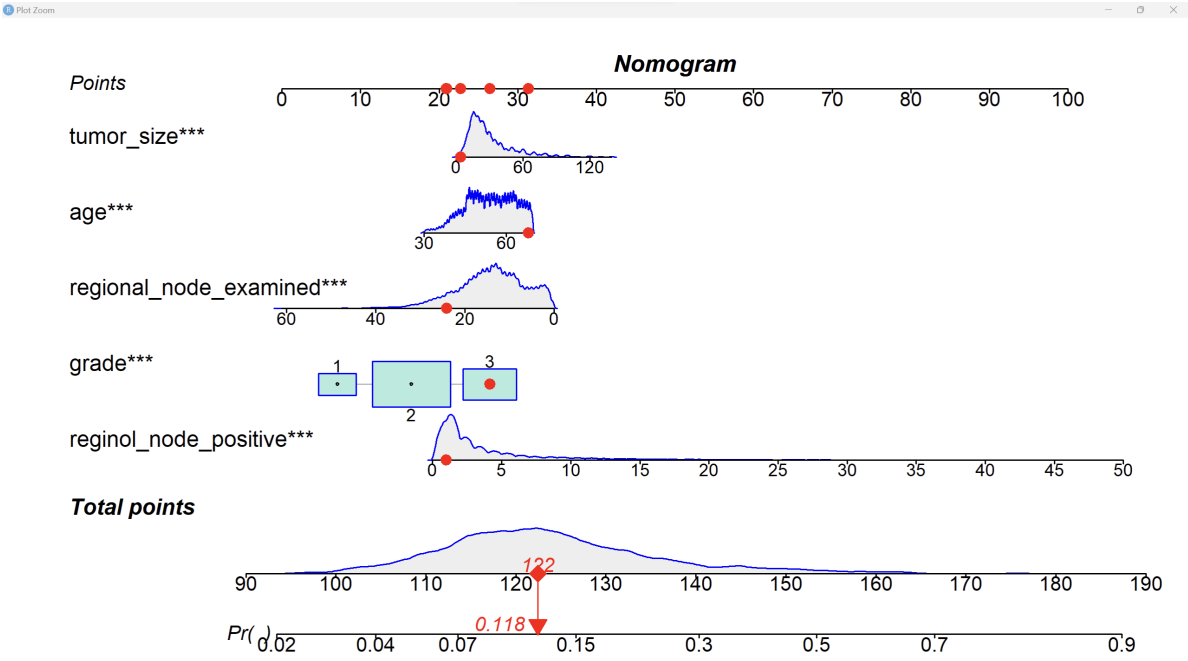
```
knitr::include_graphics("nomogram_plot_2.png")
```




```
nomogram_plot(fit3, 1)
```

```
## Regression  input lrm formula:

## status `~` age + grade + tumor_size + regional_node_examined +
reginol_node_positive
```

```
knitr::include_graphics("nomogram_plot_3.png")
```



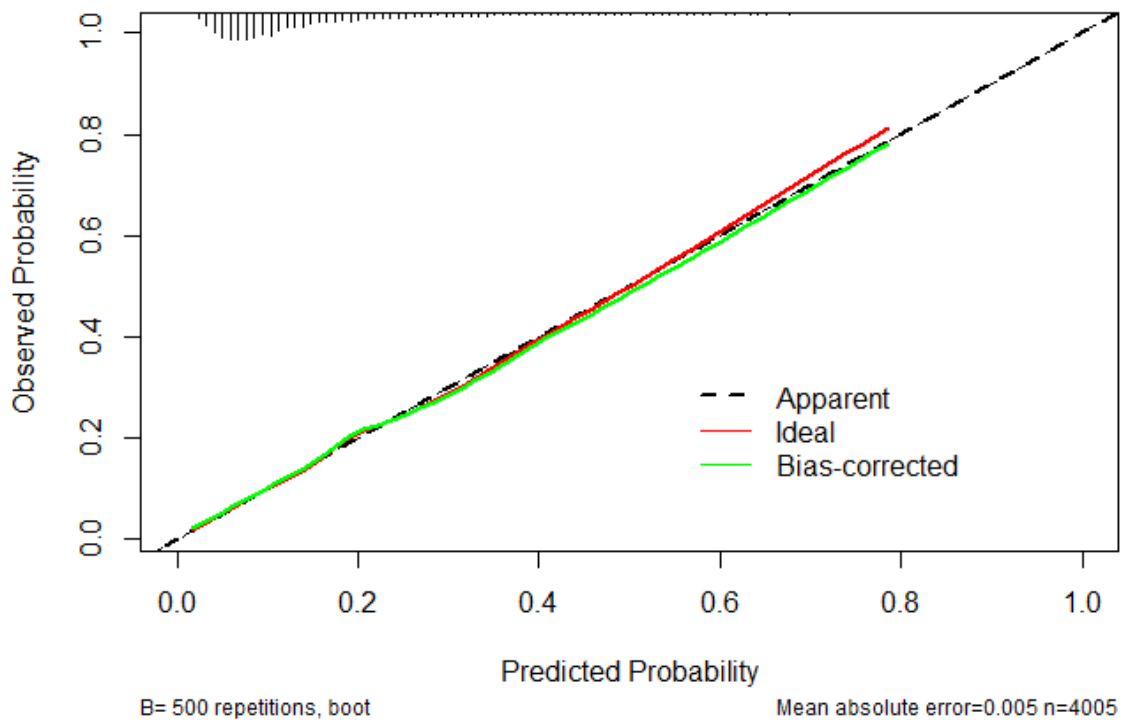
According to the monogram graph, we can compare three model by random choosing am observation from our dataset. In my code, I choose the first observation. We find that the probability to dead calculated in three models are 7.6%, 6.3% and 11.8%, the truth is that this persion is alive, so the model 2 has the best simulation effect.

Calibration curve

```
cali_plot = function(input){
  cal = calibrate(input, method = "boot", B = 500)

  plot(cal,
       xlim = c(0,1),
       xlab = "Predicted Probability",
       ylab = "Observed Probability",
       legend = FALSE,
       subtitles = TRUE)
  abline(0,1,col = "black",
         lty = 2,
         lwd = 2)
  lines(cal[,c("predy", "calibrated.orig")],
        type = "l",
        lwd = 2,
        col = "red",
        pch = 16)
  lines(cal[,c("predy", "calibrated.corrected")],
        type = "l",
```

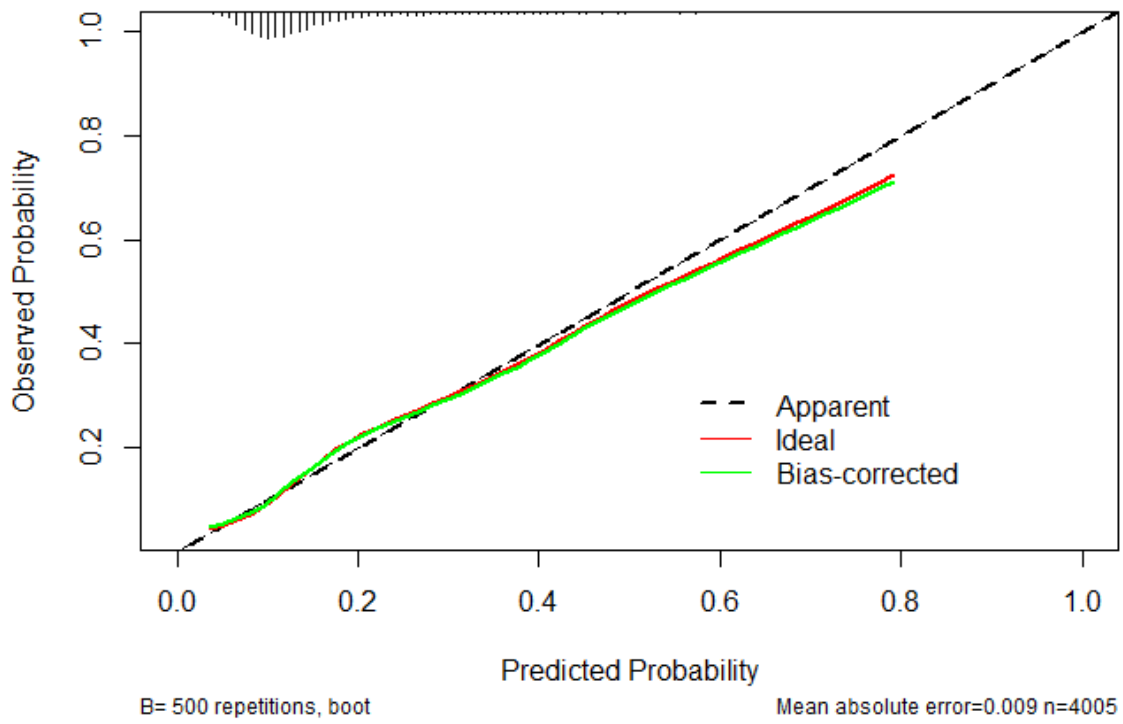
```
        lwd = 2,
        col = "green",
        pch = 16)
  legend(0.55, 0.35,
         c("Apparent", "Ideal", "Bias-corrected"),
         lty = c(2, 1, 1),
         lwd = c(2, 1, 1),
         col = c("black", "red", "green"),
         bty = "n")
}
```

```
cali_plot(fit1)
```



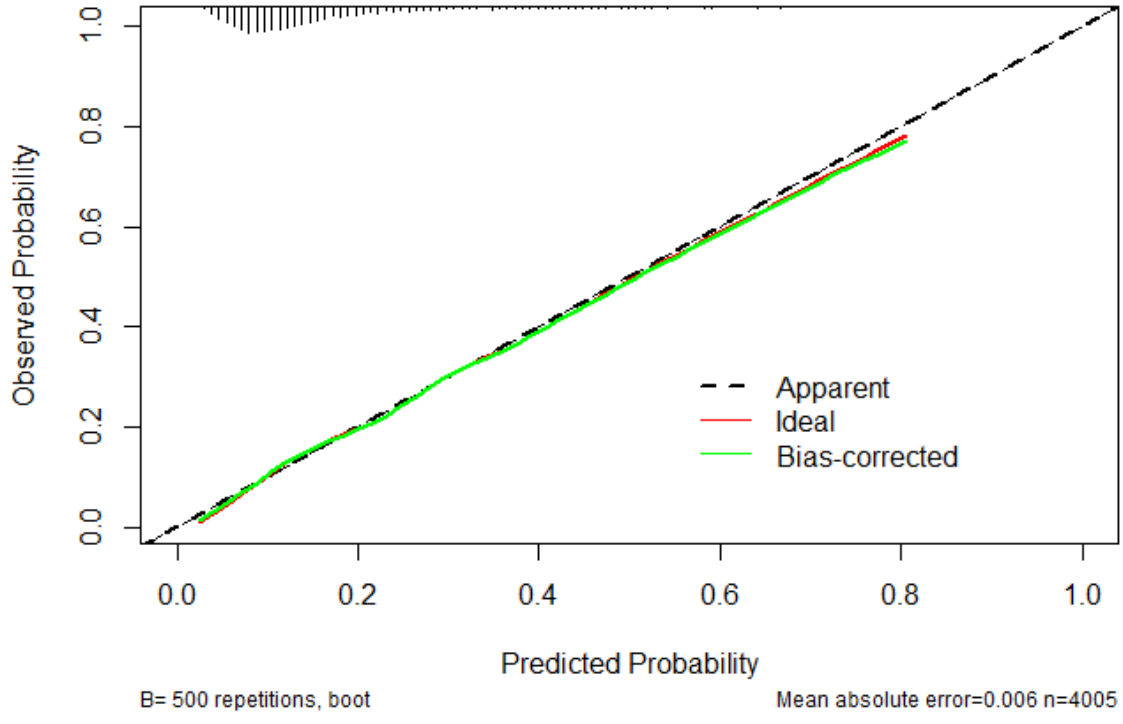

```
##
## n=4005   Mean absolute error=0.005   Mean squared error=4e-05
## 0.9 Quantile of absolute error=0.012
```

```
cali_plot(fit2)
```




```
##
## n=4005   Mean absolute error=0.009   Mean squared error=0.00014
## 0.9 Quantile of absolute error=0.019
```

```
cali_plot(fit3)
```



```
##
## n=4005   Mean absolute error=0.006   Mean squared error=5e-05
## 0.9 Quantile of absolute error=0.01
```

According to the calibration, all of three models have a good performance. Their calibration curves closely follow the diagonal line (45-degree line).

Hosmer and Lemeshow Goodness-of-Fit Test

```
fit1 = glm(formula1,
           data = heart_df_log,
           family = binomial(link = logit))
fit2 = glm(formula2,
           data = heart_df_log,
           family = binomial(link = logit))
fit3 = glm(formula3,
           data = heart_df_log,
           family = binomial(link = logit))

hl1 = hoslem.test(fit1$y, fitted(fit1), g = 10)
hl2 = hoslem.test(fit2$y, fitted(fit2), g = 10)
hl3 = hoslem.test(fit3$y, fitted(fit3), g = 10)

hl1$p.value
```

```
## [1] 0.6940802
```

```
hl2$p.value
```

```
## [1] 0.2399465
```

```
hl3$p.value
```

```
## [1] 0.7272005
```

according to the outcome, we can find that all of three model's p-value are bigger than 5% which means they all have a good simulation performance. However, the model3 is the best and the model2 is the worst.

Validation

```
cro_validation = function(input, num){
  train =
  trainControl(method = "cv", number = num)

model_caret =
  train(input,
        data = heart_df_log,
        trControl = train,
```

```
        method = "glm",
        na.action = na.pass)

model_caret$finalModel
print(model_caret)
}
```

```
set.seed(123)
result1 = cro_validation(formula1, 5)
```

```
## Generalized Linear Model
##
## 4005 samples
##    9 predictor
##    2 classes: 'Alive', 'Dead'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 3204, 3205, 3203, 3205, 3203
## Resampling results:
##
##   Accuracy   Kappa
##   0.8566796  0.1874696
```

```
result2 = cro_validation(formula2, 5)
```

```
## Generalized Linear Model
##
## 4005 samples
##    5 predictor
##    2 classes: 'Alive', 'Dead'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 3203, 3204, 3205, 3204, 3204
## Resampling results:
##
##   Accuracy   Kappa
##   0.8524347  0.1152586
```

```
result3 = cro_validation(formula3, 5)
```

```
## Generalized Linear Model
##
## 4005 samples
##    5 predictor
##    2 classes: 'Alive', 'Dead'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 3205, 3203, 3205, 3203, 3204
## Resampling results:
##
##   Accuracy   Kappa
##   0.8521874  0.1191757
```

```
result_tb =
  tibble(model = c("model1", "model2", "model3"),
         cro_val_accuracy = c(result1[1,1], result2[1,1], result3[1,1]),
         cro_val_kappa = c(result1[1,2], result2[1,2], result3[1,2]))

knitr::kable(result_tb)
```

model	cro_val_accuracy	cro_val_kappa
model1	0.8566796	0.1874696
model2	0.8524347	0.1152586
model3	0.8521874	0.1191757

To test the probability to predict a new observation, I use the method cross-validation with 5 folds. We can find no matter from a accuracy perspective or a kappa perspective, the model 1 is the best among these three models.

Conclusion

```
result_tb =
  result_tb |>
  mutate(
    nomo_plot = c("7.6%", "6.3%", "11.8%"),
    hl_pvalue = c(hl1$p.value, hl2$p.value, hl3$p.value)
  )

knitr::kable(result_tb)
```

model	cro_val_accuracy	cro_val_kappa	nomo_plot	hl_pvalue
model1	0.8566796	0.1874696	7.6%	0.6940802
model2	0.8524347	0.1152586	6.3%	0.2399465
model3	0.8521874	0.1191757	11.8%	0.7272005

According to the outcome form, I will choose the model1 as my final model. Though it has a worse performance in monogram plot procedure, It performs perfectly in other procedures.

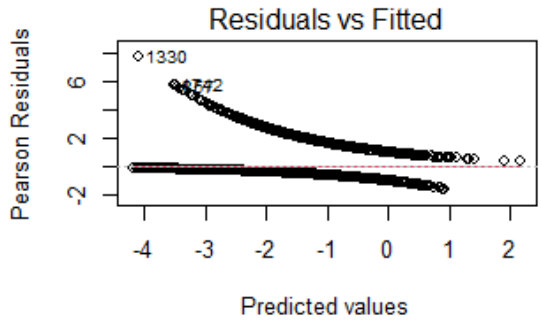
Interpretation

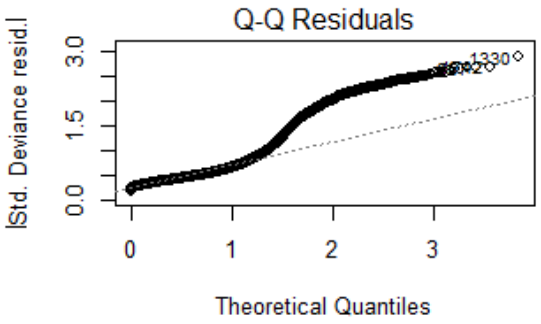
```
coef_model = coef(fit1)
```

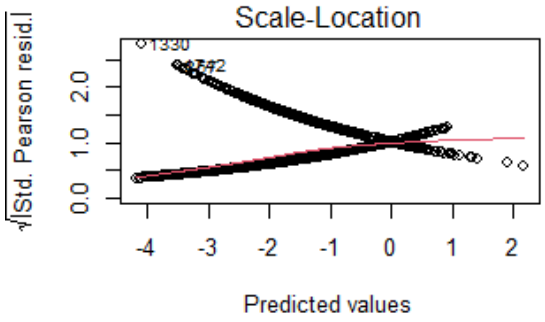

1, continuous: controlling other conditions unchanged, increasing by one year in age is associated with a 0.02186205-fold increase in the risk of death. 2, categorical variable: All other conditions being constant, the probability of death for Black individuals is 0.58 times higher than that for White individuals. 3, interaction: if two observations are each in a distant a_stage and a regional a_stage, then one unit increase in regional node positive will make a distant one 0.6762288 more times probability to die.

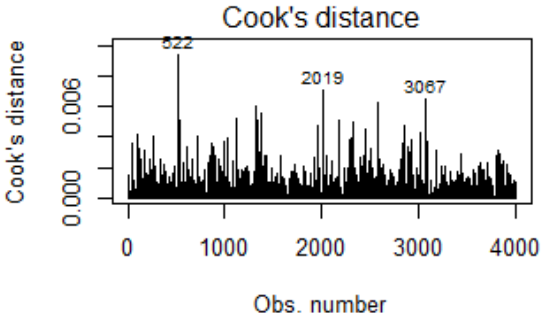
Check model's effect with data stratified by race

```
par(mfrow = c(2, 2), mar = c(5, 4, 4, 2) + 0.1)
# residual vs fitted plot
plot(fit1, which = 1)

# QQ plot
plot(fit1, which = 2)

plot(fit1, which = 3)
plot(fit1, which = 4)
```










```
heart_df_white =
  heart_df_log |>
  filter(race == "White")

heart_df_other =
  heart_df_log |>
  filter(!race == "White")
```

```
cal_predict_value = function(input, data){

  predicted_values =
    predict(input,
            newdata = data,
            type = "response")

    predicted_classes =
      ifelse(predicted_values > 0.5, "Dead", "Alive")


    accuracy =
      sum(predicted_classes == data$status) / length(data$status)

    return(accuracy)
}
```

```
cal_predict_value(fit1, heart_df_white)
```

```
## [1] 0.8622314
```

```
cal_predict_value(fit1, heart_df_other)
```

```
## [1] 0.8355263
```

According to the outcome here, we can find that the model's prediction accuracy is 0.836 to the white people and 0.836 to the other race people. There has a difference between two groups, but the degree is small which is just 3% and we can tolerate it. I f we want to make a more accurate modification towards this shortcoming, we can just separate our original dataset and get two different model in different race condition.