P8130_final_project

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Appendix

- Data Import

```
survival_df = read_csv("data/Project_2_data.csv") |>
  janitor::clean_names() |>
  rename(regional_node_positive = reginol_node_positive)
```

- Data Description

```
str(survival_df)
```

```
## spc_tbl_ [4,024 x 16] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
##  $ age                   : num [1:4024] 68 50 58 58 47 51 51 40 40 69 ...
##  $ race                  : chr [1:4024] "White" "White" "White" "White" ...
##  $ marital_status        : chr [1:4024] "Married" "Married" "Divorced" "Married" ...
##  $ t_stage               : chr [1:4024] "T1" "T2" "T3" "T1" ...
##  $ n_stage               : chr [1:4024] "N1" "N2" "N3" "N1" ...
##  $ x6th_stage            : chr [1:4024] "IIA" "IIIA" "IIIC" "IIA" ...
##  $ differentiate         : chr [1:4024] "Poorly differentiated" "Moderately differentiated" "Moderat
##  $ grade                 : chr [1:4024] "3" "2" "2" "3" ...
##  $ a_stage               : chr [1:4024] "Regional" "Regional" "Regional" "Regional" ...
##  $ tumor_size            : num [1:4024] 4 35 63 18 41 20 8 30 103 32 ...
##  $ estrogen_status       : chr [1:4024] "Positive" "Positive" "Positive" "Positive" ...
##  $ progesterone_status   : chr [1:4024] "Positive" "Positive" "Positive" "Positive" ...
##  $ regional_node_examined: num [1:4024] 24 14 14 2 3 18 11 9 20 21 ...
##  $ regional_node_positive: num [1:4024] 1 5 7 1 1 2 1 1 18 12 ...
##  $ survival_months       : num [1:4024] 60 62 75 84 50 89 54 14 70 92 ...
##  $ status                : chr [1:4024] "Alive" "Alive" "Alive" "Alive" ...
##  - attr(*, "spec")=
##   .. cols(
##   ..   Age = col_double(),
##   ..   Race = col_character(),
##   ..   `Marital Status` = col_character(),
##   ..   `T Stage` = col_character(),
##   ..   `N Stage` = col_character(),
##   ..   `6th Stage` = col_character(),
##   ..   differentiate = col_character(),
##   ..   Grade = col_character(),
```

```
##   ..   `A Stage` = col_character(),
##   ..   `Tumor Size` = col_double(),
##   ..   `Estrogen Status` = col_character(),
##   ..   `Progesterone Status` = col_character(),
##   ..   `Regional Node Examined` = col_double(),
##   ..   `Reginol Node Positive` = col_double(),
##   ..   `Survival Months` = col_double(),
##   ..   Status = col_character()
##   .. )
##  - attr(*, "problems")=<externalptr>
```

Numeric variables include `age`, `tumor_size`, `regional_node_examined`, `regional_node_positive`, and `survival_months`.

These are continuous variables that can be used for our later regression analysis.

Categorical variables include `race`, `marital_status`, `t_stage`, `n_stage`, `x6th_stage`, `differentiate`, `grade`, `a_stage`, `estrogen_status`, `progesterone_status`, and `status`.

Then we will convert these variables into factors.

```
survival_df = survival_df |>
  mutate(
    race = factor(race),
    marital_status = factor(marital_status),
    t_stage = factor(t_stage),
    n_stage = factor(n_stage),
    x6th_stage = factor(x6th_stage),
    differentiate = factor(differentiate),
    grade = factor(grade),
    a_stage = factor(a_stage),
    estrogen_status = factor(estrogen_status),
    progesterone_status = factor(progesterone_status),
    status = factor(status)
  ) |>
  mutate(
    differentiate = factor(differentiate, levels = c("Well differentiated",
                                                     "Moderately differentiated",
                                                     "Poorly differentiated",
                                                     "Undifferentiated")),
    differentiate = relevel(differentiate, ref = "Well differentiated")
  )
```

```
summary(survival_df)
```

```
##       age           race        marital_status t_stage   n_stage   x6th_stage
##  Min.   :30.00   Black: 291   Divorced : 486   T1:1603   N1:2732   IIA :1305
##  1st Qu.:47.00   Other: 320   Married  :2643   T2:1786   N2: 820   IIB :1130
##  Median :54.00   White:3413   Separated:  45   T3: 533   N3: 472   IIIA:1050
##  Mean   :53.97                Single   : 615   T4: 102             IIIB:  67
##  3rd Qu.:61.00                Widowed  : 235                       IIIC: 472
##  Max.   :69.00
##                    differentiate                    grade          a_stage
##  Well differentiated      : 543   1                   : 543   Distant :  92
##  Moderately differentiated:2351   2                   :2351   Regional:3932
```

```
##  Poorly differentiated    :1111   3                    :1111
##  Undifferentiated         :  19   anaplastic; Grade IV:  19
##
##
##    tumor_size     estrogen_status progesterone_status regional_node_examined
##  Min.   :  1.00   Negative: 269   Negative: 698       Min.   : 1.00
##  1st Qu.: 16.00   Positive:3755   Positive:3326       1st Qu.: 9.00
##  Median : 25.00                                       Median :14.00
##  Mean   : 30.47                                       Mean   :14.36
##  3rd Qu.: 38.00                                       3rd Qu.:19.00
##  Max.   :140.00                                       Max.   :61.00
##  regional_node_positive survival_months   status
##  Min.   : 1.000         Min.   :  1.0   Alive:3408
##  1st Qu.: 1.000         1st Qu.: 56.0   Dead : 616
##  Median : 2.000         Median : 73.0
##  Mean   : 4.158         Mean   : 71.3
##  3rd Qu.: 5.000         3rd Qu.: 90.0
##  Max.   :46.000         Max.   :107.0
```

Descriptive table for numerical variables

```
numeric_summary = survival_df |>
  summarize(
    age_Mean = mean(age, na.rm = TRUE),
    age_SD = sd(age, na.rm = TRUE),
    age_Median = median(age, na.rm = TRUE),
    age_IQR = IQR(age, na.rm = TRUE),

    tumor_size_Mean = mean(tumor_size, na.rm = TRUE),
    tumor_size_SD = sd(tumor_size, na.rm = TRUE),
    tumor_size_Median = median(tumor_size, na.rm = TRUE),
    tumor_size_IQR = IQR(tumor_size, na.rm = TRUE),

    regional_node_examined_Mean = mean(regional_node_examined, na.rm = TRUE),
    regional_node_examined_SD = sd(regional_node_examined, na.rm = TRUE),
    regional_node_examined_Median = median(regional_node_examined, na.rm = TRUE),
    regional_node_examined_IQR = IQR(regional_node_examined, na.rm = TRUE),

    regional_node_positive_Mean = mean(regional_node_positive, na.rm = TRUE),
    regional_node_positive_SD = sd(regional_node_positive, na.rm = TRUE),
    regional_node_positive_Median = median(regional_node_positive, na.rm = TRUE),
    regional_node_positive_IQR = IQR(regional_node_positive, na.rm = TRUE),

    survival_months_Mean = mean(survival_months, na.rm = TRUE),
    survival_months_SD = sd(survival_months, na.rm = TRUE),
    survival_months_Median = median(survival_months, na.rm = TRUE),
    survival_months_IQR = IQR(survival_months, na.rm = TRUE)
  )

numeric_table = data.frame(
  Variable = c("Age", "Tumor Size", "Regional Nodes Examined", "Regional Nodes Positive", "Survival Mon
  Mean = c(numeric_summary$age_Mean, numeric_summary$tumor_size_Mean,
```

```
           numeric_summary$regional_node_examined_Mean, numeric_summary$regional_node_positive_Mean,
           numeric_summary$survival_months_Mean),
  SD = c(numeric_summary$age_SD, numeric_summary$tumor_size_SD,
         numeric_summary$regional_node_examined_SD, numeric_summary$regional_node_positive_SD,
         numeric_summary$survival_months_SD),
  Median = c(numeric_summary$age_Median, numeric_summary$tumor_size_Median,
             numeric_summary$regional_node_examined_Median, numeric_summary$regional_node_positive_Media
             numeric_summary$survival_months_Median),
  IQR = c(numeric_summary$age_IQR, numeric_summary$tumor_size_IQR,
          numeric_summary$regional_node_examined_IQR, numeric_summary$regional_node_positive_IQR,
          numeric_summary$survival_months_IQR)
)

categorical_table = survival_df |>
  summarize(
    estrogen_status_Positive = sum(estrogen_status == "Positive", na.rm = TRUE),
    estrogen_status_Negative = sum(estrogen_status == "Negative", na.rm = TRUE),
    progesterone_status_Positive = sum(progesterone_status == "Positive", na.rm = TRUE),
    progesterone_status_Negative = sum(progesterone_status == "Negative", na.rm = TRUE),
    status_Alive = sum(status == "Alive", na.rm = TRUE),
    status_Dead = sum(status == "Dead", na.rm = TRUE)
  )

categorical_long = data.frame(
  Variable = c("Estrogen Status Positive", "Estrogen Status Negative",
               "Progesterone Status Positive", "Progesterone Status Negative",
               "Status Alive", "Status Dead"),
  Count = c(categorical_table$estrogen_status_Positive, categorical_table$estrogen_status_Negative,
            categorical_table$progesterone_status_Positive, categorical_table$progesterone_status_Negati
            categorical_table$status_Alive, categorical_table$status_Dead),
  Proportion = round(c(
    categorical_table$estrogen_status_Positive / nrow(survival_df),
    categorical_table$estrogen_status_Negative / nrow(survival_df),
    categorical_table$progesterone_status_Positive / nrow(survival_df),
    categorical_table$progesterone_status_Negative / nrow(survival_df),
    categorical_table$status_Alive / nrow(survival_df),
    categorical_table$status_Dead / nrow(survival_df)
  ), 4)
)

categorical_long = categorical_long |>
  separate(Variable, into = c("Variable Name", "Level"), sep = " (?=Positive|Negative|Alive|Dead)")

final_table = list(
  Numeric_Summary = numeric_table,
  Categorical_Summary = categorical_long
)


cat("### Numeric Variables Summary\n")
```

```
## ### Numeric Variables Summary
```

```
knitr::kable(numeric_table, col.names = c("Variable Name", "Mean", "SD", "Median", "IQR"),
             caption = "Summary Statistics for Numeric Variables", format = "pipe")
```

Table 1: Summary Statistics for Numeric Variables

Variable Name	Mean	SD	Median	IQR
Age	53.972167	8.963134	54	14
Tumor Size	30.473658	21.119696	25	22
Regional Nodes Examined	14.357107	8.099675	14	10
Regional Nodes Positive	4.158052	5.109331	2	4
Survival Months	71.297962	22.921429	73	34

```
cat("\n### Categorical Variables Summary\n")
```

```
##
## ### Categorical Variables Summary
```

```
knitr::kable(categorical_long, col.names = c("Variable Name", "Level", "Count", "Proportion"),
             caption = "Summary Statistics for Categorical Variables", format = "pipe")
```

Table 2: Summary Statistics for Categorical Variables

Variable Name	Level	Count	Proportion
Estrogen Status	Positive	3755	0.9332
Estrogen Status	Negative	269	0.0668
Progesterone Status	Positive	3326	0.8265
Progesterone Status	Negative	698	0.1735
Status	Alive	3408	0.8469
Status	Dead	616	0.1531

The majority of patients in the dataset are White, accounting for approximately 84.82% of the total population. Black patients make up 7.23%, and patients classified as "Other" constitute 7.95%. This imbalance suggests that the dataset is heavily skewed towards White patients, which could influence the generalizability of the findings to other racial groups.

The wide range of values in variables such as `tumor_size`, `regional_node_examined`, and `survival_months` indicates the need to explore relationships and their potential nonlinearities with survival, giving us a possible analytical regression model.

Since the two variables `grade` and `differentiate` represent the same variable with different names, we will not consider the variable `grade` in the further analysis.

```
colSums(is.na(survival_df))
```

```
##                   age                  race        marital_status
##                     0                     0                     0
##               t_stage               n_stage           x6th_stage
##                     0                     0                     0
##          differentiate                 grade               a_stage
```

```
##                      0                      0                      0
##             tumor_size       estrogen_status    progesterone_status
##                      0                      0                      0
## regional_node_examined regional_node_positive        survival_months
##                      0                      0                      0
##                 status
##                      0
```

We can conclude that no missing values are present in this dataset across all variables.

```
survival_df |>
  group_by(differentiate, race) |>
  summarise(count = n(), .groups = "drop") |>
  pivot_wider(
    names_from = differentiate,
    values_from = count,
    values_fill = list(count = 0)
  )
```

```
## # A tibble: 3 x 5
##   race  `Well differentiated` `Moderately differentiated` Poorly differentiate~1
##   <fct>                 <int>                       <int>                   <int>
## 1 Black                    32                         141                     115
## 2 Other                    46                         180                      94
## 3 White                   465                        2030                     902
## # i abbreviated name: 1: `Poorly differentiated`
## # i 1 more variable: Undifferentiated <int>
```

This table shows the frequency of different levels of `differentiate` by races.

```
survival_df |>
  group_by(x6th_stage, status) |>
  summarise(count = n(), .groups = "drop") |>
  pivot_wider(
    names_from = status,
    values_from = count
  )
```

```
## # A tibble: 5 x 3
##   x6th_stage Alive  Dead
##   <fct>      <int> <int>
## 1 IIA         1209    96
## 2 IIB          995   135
## 3 IIIA         866   184
## 4 IIIB          47    20
## 5 IIIC         291   181
```

This table shows the frequency of different levels of `status` by 6th stage.

- Data Visualization

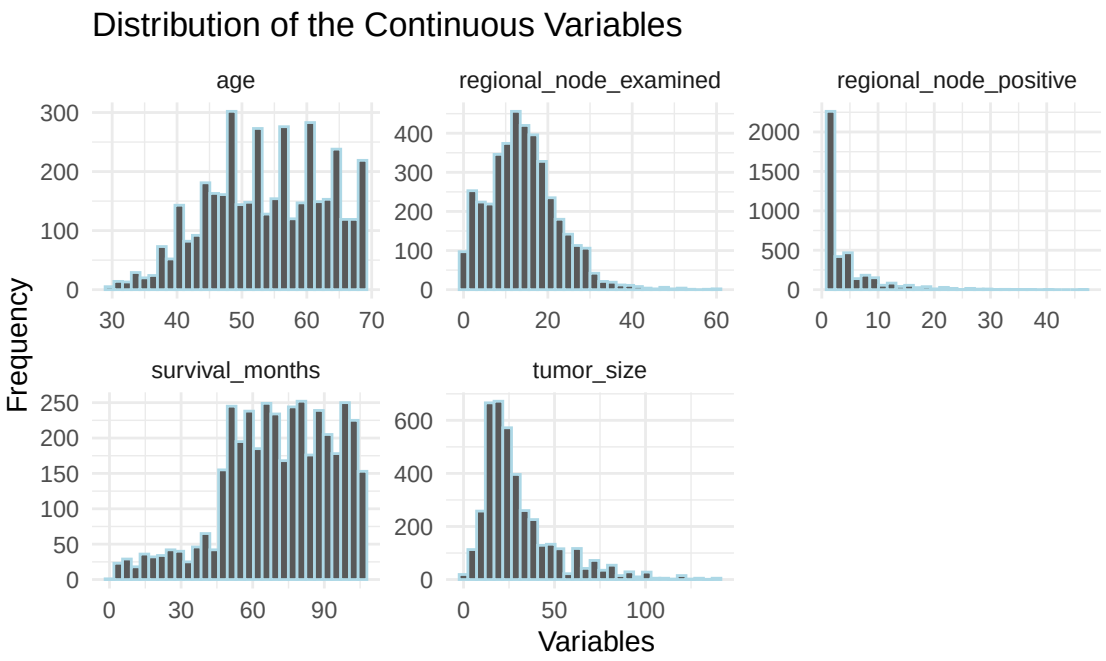


Figure 1: Distribution of the Continuous Variables

Distributions of the numeric variables

Most patients are aged between 40 and 70 years. The data is well spread across middle and older age groups, making it possible for age-related analysis. Therefore, age will likely be a significant predictor for later analysis.

Then is the distribution of different number of positive regional node for each subject. Over 2500 subjects only have 1 or 2 positive regional nodes, which is the most frequent number of positive regional nodes. It is strongly right-skewed, so we will use the log transformation for this variable.

The third plot maps the frequency of different number of examined regional nodes for each subject. The number of examined regional nodes for most subjects are smaller than 30, and the subjects with nearly 12 examined regional nodes are the most.

Then is the distribution of the survival months, most of the survival time are larger than 45 months.

The last one is the distribution of all tumor sizes, and most of the tumor sizes are smaller than 50 mm. We can find that the most frequent size is around 19 mm, followed by around 14 mm. This distribution is right-skewed, so we will use the log transformation for this variable.

Bewteen Variables

Survival Months by Status

The Alive group has a higher median survival time (approximately 75 months) with a relatively narrow interquartile range. However, there are several outliers below 15 survival months, indicating cases of unusually short survival. In contrast, the Dead group has a lower median survival time (around 45 months) with a wider interquartile range, reflecting greater variability. Overall, survival months are significantly higher for the Alive group compared to the Dead group.

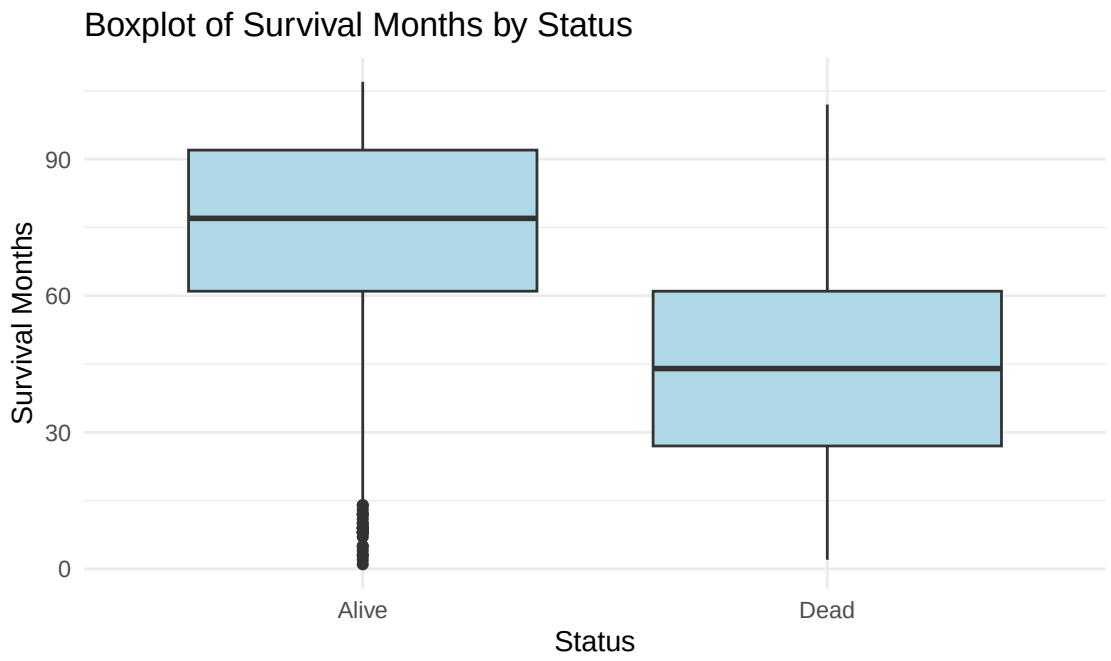


Figure 2: Survival Months by Status

Tumor Sizes by T_stage

In this plot, we explore the tumor size distribution at different T stages. From T1 to T3, as the stage changes, both the mean tumor sizes and IQR become larger. At T4 stage, the IQR of tumor sizes is much larger than others, and the mean size is smaller than the mean size at T3 stage. We notice that there are some potential outliers both ar T1 stage and T3 stage.

Survival Months by A_stage Based on Status

In the Regional stage, the Alive group has a higher median survival with outliers below 15 months, while the Dead group shows a lower median with no outliers. For the Distant stage, survival times are shorter overall, with the Alive group having a median of 80 months and the Dead group around 30 months, both without significant outliers. Overall, survival is longer in the Regional stage, and the Alive group shows higher survival times across both stages.

Tumor Size by Differentiate

The Undifferentiated group has larger tumor sizes compared to the other categories, while the Well, Moderately, and Poorly differentiated groups show similar distributions with many smaller tumors and numerous high-value outliers.

Relationship Between Age and Tumor Size across Status

This figure highlights the differences in tumor size distribution and trends with age between individuals who are alive and those who are deceased. While the “Alive” group shows no significant relationship between age and tumor size, the “Dead” group exhibits a pattern where larger tumors are associated with younger ages.

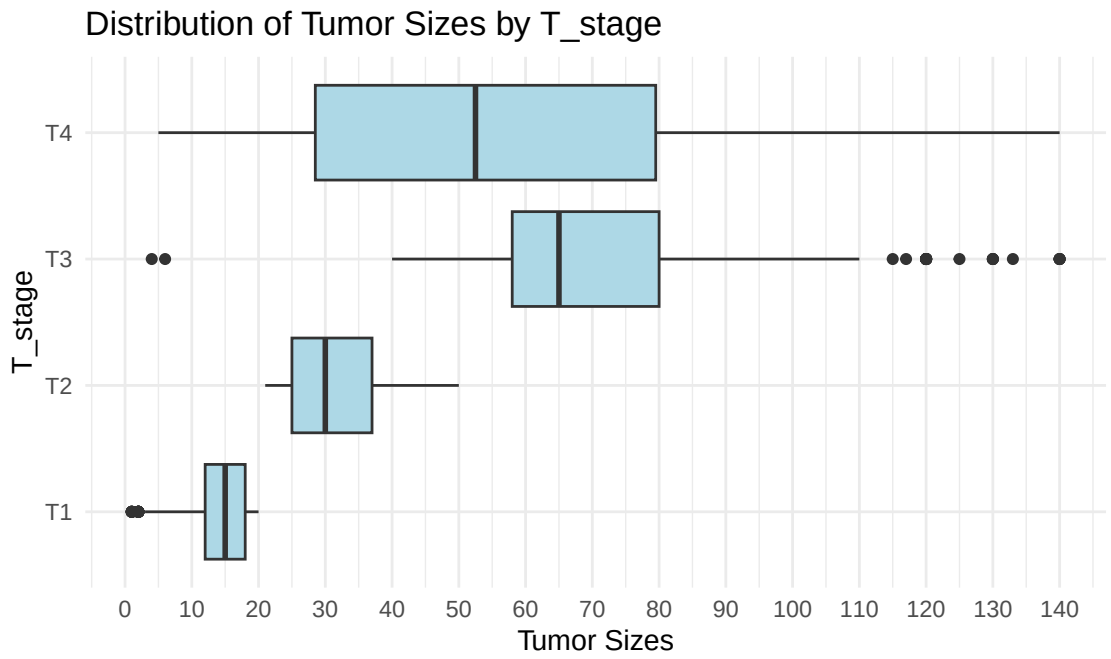


Figure 3: Tumor Sizes by T-stage

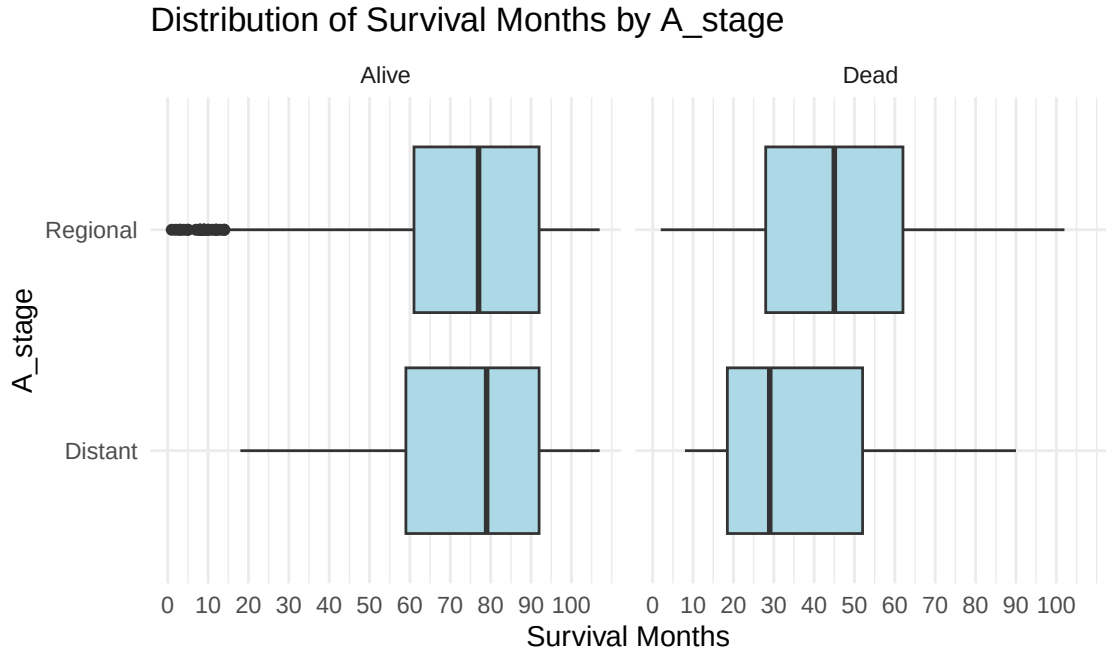


Figure 4: Survival Months by A-stage Based on Status

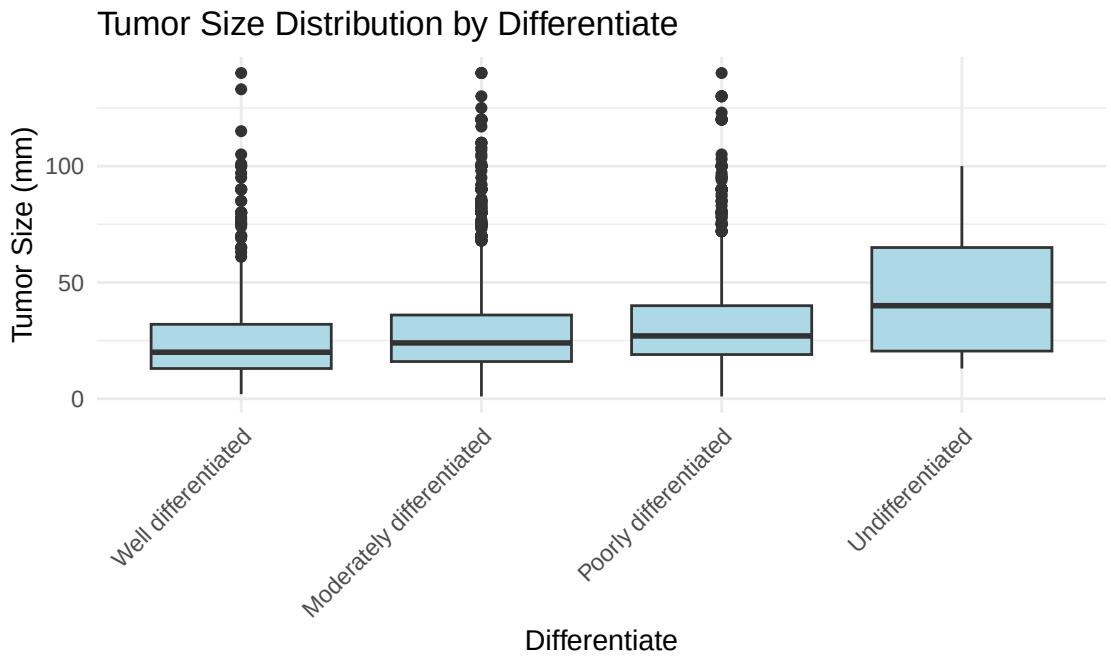


Figure 5: Tumor Size by Differentiate

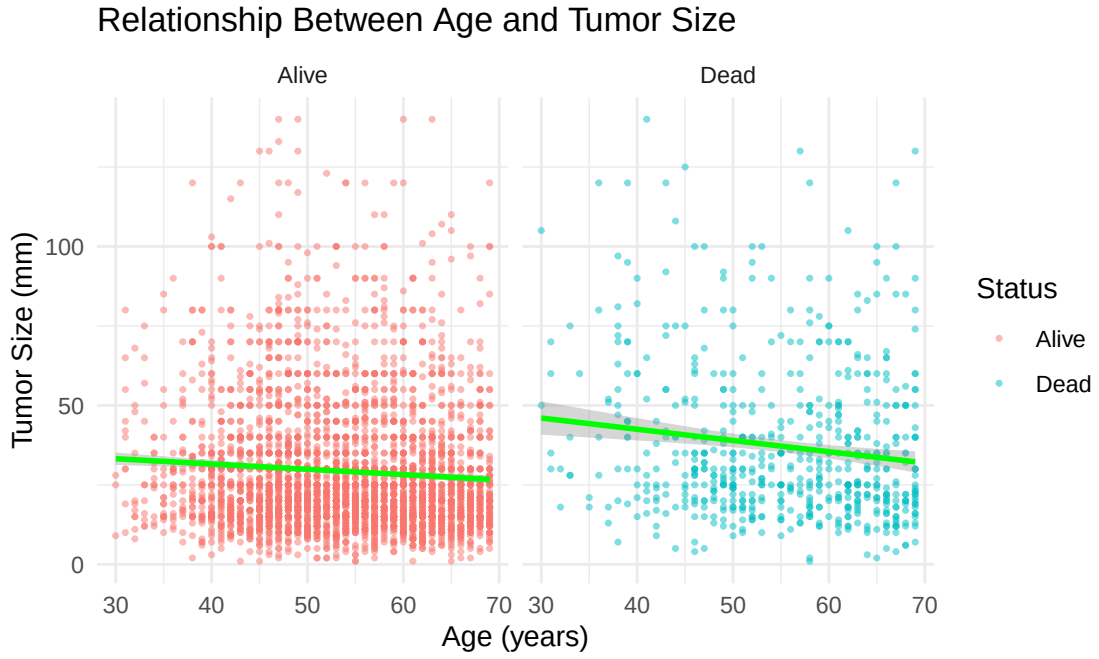


Figure 6: Relationship Between Age and Tumor Size across Status

Positive Regional Node vs Survival Months Across Differentiate

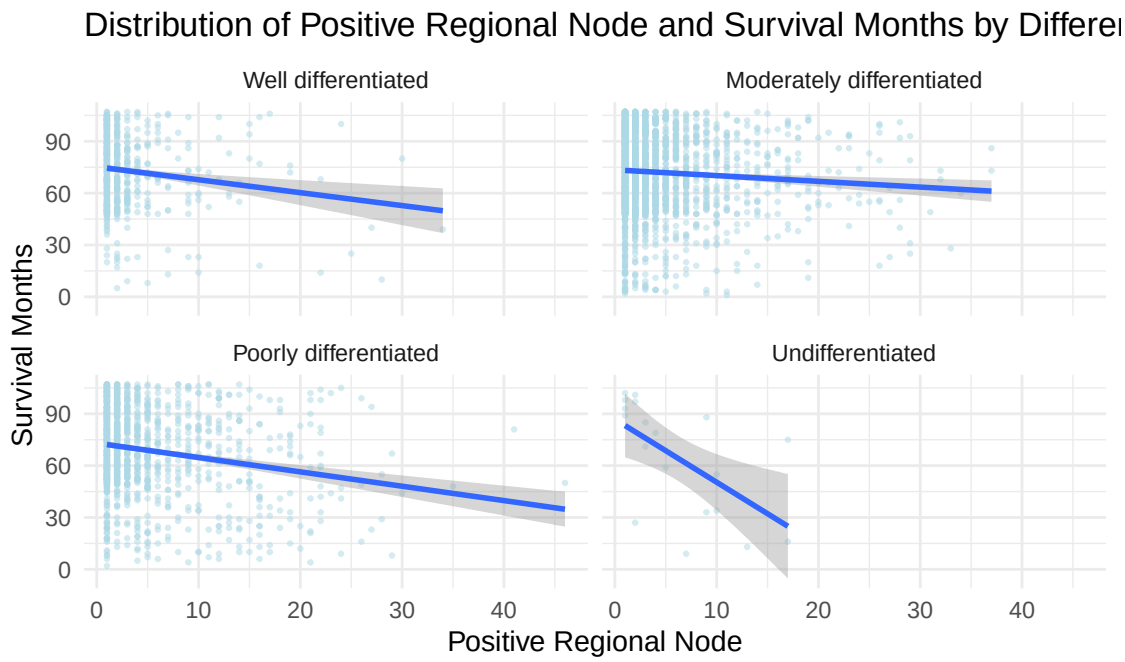


Figure 7: Positive Regional Node vs Survival Months Across Differentiate

According to the trend lines, as it changes from undifferentiated to well differentiated, the negative correlation between the number of positive regional nodes and the survival months becomes weaker. At the undifferentiated level, the correlation is strong. AS the number of positive regional nodes increases, the survival months will decrease.

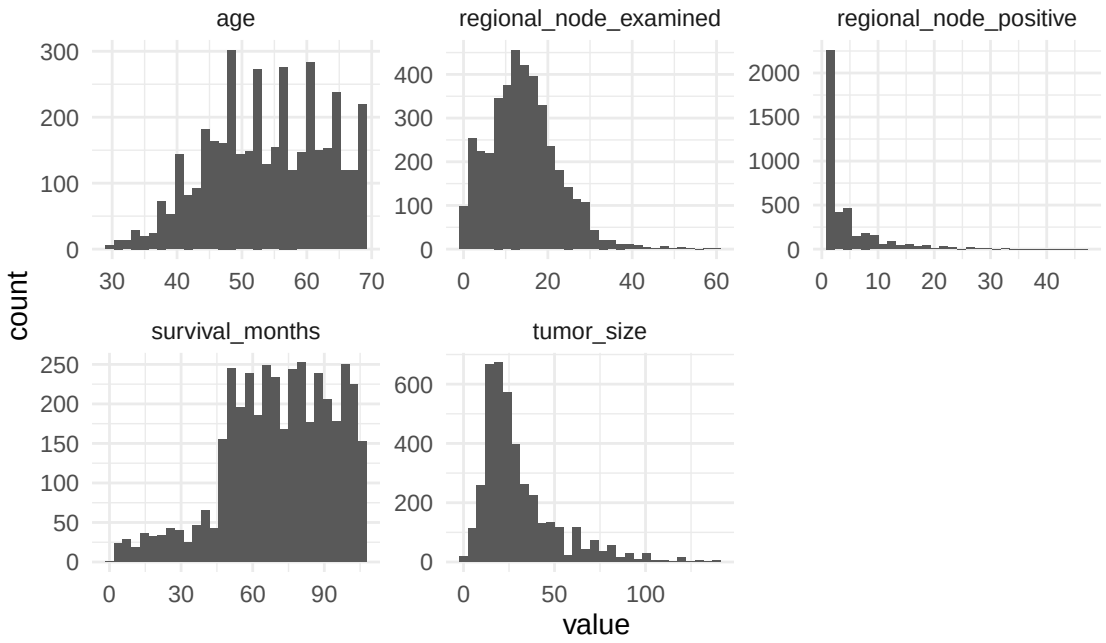
Transformations

```
survival_df = survival_df |>
  mutate(
    log_tumor_size = log(tumor_size),
    log_regional_node_positive = log(regional_node_positive)
  )
```

Since variables `tumor_size` and `regional_node_positive` are skewed to the right, we need to use the log transformation and add new variables `log_tumor_size` and `log_regional_node_positive` for further analysis.

```
survival_df |>
  pivot_longer(
    cols = c(age, tumor_size, regional_node_examined, regional_node_positive, survival_months),
    names_to = "variable",
    values_to = "value"
  ) |>
  ggplot(aes(x = value)) +
```

```
  geom_histogram() +
  facet_wrap(variable ~ .,  scales = "free")
```



Model Building

Preparation

```
survival_df =
  survival_df |>
  mutate(status = if_else(status == "Dead", 1, 0))

full_glm = glm(status ~ age + race + marital_status + t_stage + n_stage + x6th_stage +
                 differentiate + grade + a_stage + tumor_size + estrogen_status +
                 progesterone_status + regional_node_examined + regional_node_positive,
               data = survival_df, family = binomial)

alias(full_glm)$Complete %>%
  as.data.frame() %>%
  rownames_to_column("aliased_variables") %>%
  as_tibble() %>%
  pivot_longer(
    cols = -aliased_variables,
    names_to = "aliased_with",
    values_to = "value"
  ) %>%
  filter(value != 0) %>%
  select(-value)
```

```
## # A tibble: 4 x 2
##   aliased_variables         aliased_with
##   <chr>                     <chr>
## 1 x6th_stageIIIC            n_stageN3
## 2 grade2                    differentiateModerately differentiated
## 3 grade3                    differentiatePoorly differentiated
## 4 gradeanaplastic; Grade IV differentiateUndifferentiated
```

First, we use variables 1-14 to build a logistic regression. In this full model, we observe that the number of each level in the variable `grade` is the same as the variable `differentiate`, and the number of level `IIIC` in the variable `x6th_stage` is exactly the same with level `N3` in the variable `n_stage`.

By looking up the relevant information on the staging system for breast cancer, we can see that the breast cancer grade (i.e. variable `grade`) is based on how much the cancer cells look like normal cells, which is highly similar to the meaning of the variable `differentiate`. Therefore, the variable `grade` can be removed from the model.

In addition, the AJCC system (variable `x6th_stage`) is based on 7 aspects: the extent (size) of the tumor (T), the spread to nearby lymph nodes (N), the spread (metastasis) to distant sites (M), Estrogen Receptor (ER) status, Progesterone Receptor (PR) status, HER2 status and grade of the cancer (G). It can be seen that some of the evaluation criteria are already included in other variables.

However, since the AJCC system is complex and levels other than `IIIC` do not correlate with other variables, we cannot simply remove this variable from the model. We will discuss this variable further when it comes to this.

Logistic Regression Model

Automated Procedure

```
full_glm = glm(status ~ age + race + marital_status + t_stage + n_stage + x6th_stage +
                 differentiate + a_stage + tumor_size + estrogen_status +
                 progesterone_status + regional_node_examined + regional_node_positive,
               data = survival_df, family = binomial)

forward_glm = MASS::stepAIC(full_glm, direction = "forward", trace = FALSE)

forward_glm %>%
  broom::tidy() %>%
  knitr::kable(digits = 4, caption = "Results of Forward Selection Model", format = "pipe")
```

Forward Selection

Table 3: Results of Forward Selection Model

term	estimate	std.error	statistic	p.value
(Intercept)	-2.3128	0.5138	-4.5017	0.0000
age	0.0242	0.0056	4.3008	0.0000
raceOther	-0.9235	0.2486	-3.7149	0.0002
raceWhite	-0.5098	0.1618	-3.1504	0.0016
marital_statusMarried	-0.2103	0.1418	-1.4832	0.1380

term	estimate	std.error	statistic	p.value
marital_statusSeparated	0.6718	0.3875	1.7338	0.0830
marital_statusSingle	-0.0678	0.1751	-0.3871	0.6987
marital_statusWidowed	0.0235	0.2210	0.1061	0.9155
t_stageT2	0.2822	0.1954	1.4443	0.1487
t_stageT3	0.5359	0.3138	1.7079	0.0876
t_stageT4	0.9542	0.4501	2.1202	0.0340
n_stageN2	0.6208	0.2392	2.5955	0.0094
n_stageN3	0.6910	0.3007	2.2977	0.0216
x6th_stageIIB	0.2143	0.2318	0.9245	0.3552
x6th_stageIIIA	-0.0871	0.2950	-0.2954	0.7677
x6th_stageIIIB	0.0887	0.5289	0.1677	0.8668
x6th_stageIIIC	NA	NA	NA	NA
differentiateModerately differentiated	0.5368	0.1841	2.9159	0.0035
differentiatePoorly differentiated	0.9252	0.1929	4.7974	0.0000
differentiateUndifferentiated	1.8983	0.5567	3.4101	0.0006
a_stageRegional	-0.0402	0.2662	-0.1508	0.8801
tumor_size	0.0002	0.0040	0.0627	0.9500
estrogen_statusPositive	-0.7419	0.1779	-4.1703	0.0000
progesterone_statusPositive	-0.5861	0.1277	-4.5899	0.0000
regional_node_examined	-0.0359	0.0072	-4.9924	0.0000
regional_node_positive	0.0791	0.0154	5.1473	0.0000

```
backward_glm = MASS::stepAIC(full_glm, direction = "backward", trace = FALSE)

backward_glm %>%
  broom::tidy() %>%
  knitr::kable(digits = 4, caption = "Results of Backward Elimination Model", format = "pipe")
```

Backward Elimination

Table 4: Results of Backward Elimination Model

term	estimate	std.error	statistic	p.value
(Intercept)	-2.2838	0.4385	-5.2085	0.0000
age	0.0238	0.0056	4.2426	0.0000
raceOther	-0.9346	0.2485	-3.7616	0.0002
raceWhite	-0.5148	0.1617	-3.1845	0.0014
marital_statusMarried	-0.2110	0.1416	-1.4900	0.1362
marital_statusSeparated	0.6691	0.3881	1.7240	0.0847
marital_statusSingle	-0.0646	0.1748	-0.3696	0.7117
marital_statusWidowed	0.0175	0.2211	0.0791	0.9369
t_stageT2	0.4111	0.1130	3.6372	0.0003
t_stageT3	0.5516	0.1488	3.7077	0.0002
t_stageT4	1.0988	0.2445	4.4934	0.0000
n_stageN2	0.4363	0.1284	3.3987	0.0007
n_stageN3	0.5872	0.2345	2.5034	0.0123
differentiateModerately differentiated	0.5328	0.1838	2.8990	0.0037
differentiatePoorly differentiated	0.9190	0.1924	4.7772	0.0000

term	estimate	std.error	statistic	p.value
differentiateUndifferentiated	1.8649	0.5538	3.3672	0.0008
estrogen_statusPositive	-0.7480	0.1775	-4.2140	0.0000
progesterone_statusPositive	-0.5842	0.1275	-4.5811	0.0000
regional_node_examined	-0.0359	0.0072	-5.0110	0.0000
regional_node_positive	0.0797	0.0153	5.2076	0.0000

```
stepwise_glm = MASS::stepAIC(full_glm, direction = "both", trace = FALSE)

stepwise_glm %>%
  broom::tidy() %>%
  knitr::kable(digits = 4, caption = "Results of Stepwise Regression Model", format = "pipe")
```

Stepwise Regression

Table 5: Results of Stepwise Regression Model

term	estimate	std.error	statistic	p.value
(Intercept)	-2.2838	0.4385	-5.2085	0.0000
age	0.0238	0.0056	4.2426	0.0000
raceOther	-0.9346	0.2485	-3.7616	0.0002
raceWhite	-0.5148	0.1617	-3.1845	0.0014
marital_statusMarried	-0.2110	0.1416	-1.4900	0.1362
marital_statusSeparated	0.6691	0.3881	1.7240	0.0847
marital_statusSingle	-0.0646	0.1748	-0.3696	0.7117
marital_statusWidowed	0.0175	0.2211	0.0791	0.9369
t_stageT2	0.4111	0.1130	3.6372	0.0003
t_stageT3	0.5516	0.1488	3.7077	0.0002
t_stageT4	1.0988	0.2445	4.4934	0.0000
n_stageN2	0.4363	0.1284	3.3987	0.0007
n_stageN3	0.5872	0.2345	2.5034	0.0123
differentiateModerately differentiated	0.5328	0.1838	2.8990	0.0037
differentiatePoorly differentiated	0.9190	0.1924	4.7772	0.0000
differentiateUndifferentiated	1.8649	0.5538	3.3672	0.0008
estrogen_statusPositive	-0.7480	0.1775	-4.2140	0.0000
progesterone_statusPositive	-0.5842	0.1275	-4.5811	0.0000
regional_node_examined	-0.0359	0.0072	-5.0110	0.0000
regional_node_positive	0.0797	0.0153	5.2076	0.0000

The backward and stepwise procedure produced the same model.

Criterion-based Procedure

```
model_selection =
  tibble(
    type = c("full", "forward", "backward", "stepwise"),
    model = list(full_glm, forward_glm, backward_glm, stepwise_glm)
```

```
    ) %>%
  mutate(
    result = map(model, broom::glance)
    ) %>%
  unnest(result) %>%
  select(type, AIC, BIC)

model_selection %>%
  knitr::kable(digits = 4, caption = "Model Selection", format = "pipe")
```

Table 6: Model Selection

type	AIC	BIC
full	3002.000	3159.500
forward	3002.000	3159.500
backward	2993.771	3119.771
stepwise	2993.771	3119.771

```
final_glm = stepwise_glm
```

The Akaike information criterion (AIC) is an estimator of prediction error and thereby relative quality of statistical models for a given set of data, and models with lower AIC are generally preferred. Similarly, the Bayesian information criterion (BIC) is also a criterion for model selection among a finite set of models. They both resolve the overfitting problem by introducing a penalty term for the number of parameters in the model.

By comparing AIC and BIC, we can see the model given by backward elimination or stepwise regression works slightly better than the full model or forward selection model. Therefore, we will choose the former to be our "best model".

Model Diagnostics

```
vif(final_glm) %>%
  knitr::kable(digits = 4, caption = "Examination for Multicolinearity", format = "pipe")
```

Table 7: Examination for Multicolinearity

	GVIF	Df	GVIF^(1/(2*Df))
age	1.1072	1	1.0522
race	1.0629	2	1.0154
marital_status	1.1291	4	1.0153
t_stage	1.1019	3	1.0163
n_stage	3.8068	2	1.3968
differentiate	1.1171	3	1.0186
estrogen_status	1.4754	1	1.2147
progesterone_status	1.4275	1	1.1948
regional_node_examined	1.4778	1	1.2157
regional_node_positive	4.2484	1	2.0612

Variance Inflation Factor is a commonly used method for detecting multicollinearity in regression models. VIF is generally calculated for the continuous variables, and Generalized Variance Inflation Factor (GVIF) is used for evaluating the multicollinearity for categorical variables.

The adjusted GVIF (i.e. GVIFˆ(1/(2*Df))) values are corrected for the degree of freedom and provide a scale similar to VIF. The high adjusted GVIF values (GVIF $>$ 2) indicate the presence of moderate to strong multicollinearity.

The table shows that most variables do not show multicollinearity, with the exception of `regional_node_positive`. Since its adjusted GVIF is not much different from 2, we will keep this variable for now.

```
augment(final_glm) |>
  ggplot(aes(x = .fitted, y = .std.resid)) +
  geom_point() +
  geom_smooth(se = FALSE) +
  labs(x = "Fitted value", y = "Residual")
```

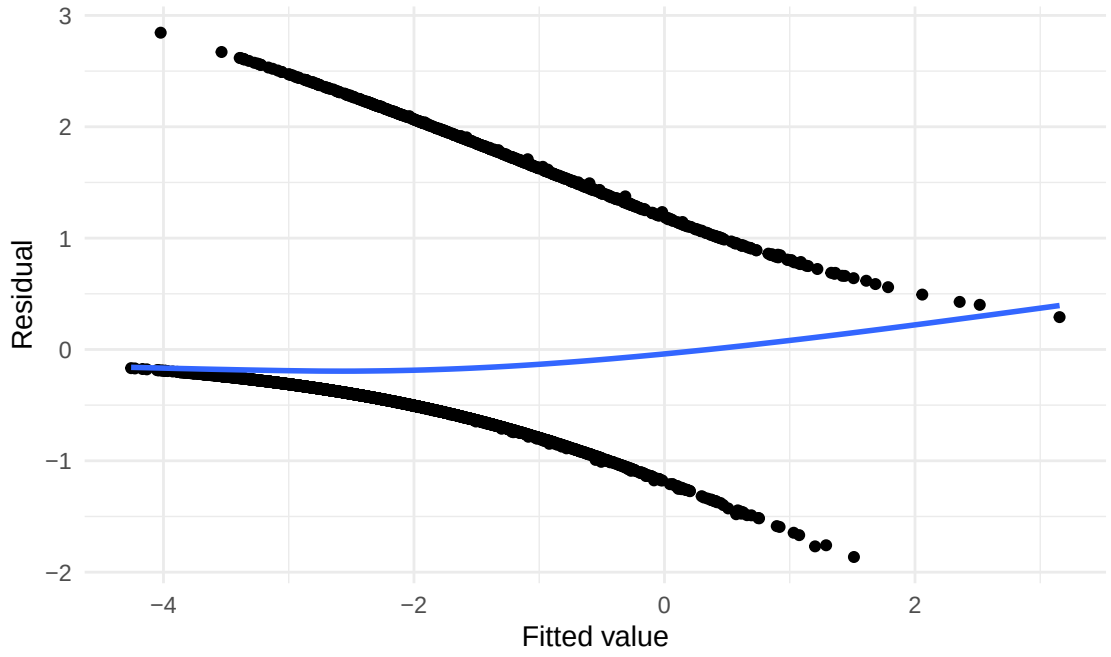


Figure 8: Residual versus Fitted Values Plot

```
augment_quantile(final_glm) |>
  ggplot(aes(x = .fitted, y = .quantile.resid)) +
  geom_point() +
  geom_smooth(se = FALSE) +
  labs(x = "Fitted value", y = "Randomized quantile residual")
```

By randomizing the quantile residuals, we resolve the problem that the RVF plot always shows a pattern in logistic regression because of the binary response variable. Since in the randomized quantile residual vs. fitted value plot, the residuals distribute randomly around the 0.5 horizontal line, the residual assumption is met and the model is a good fit.

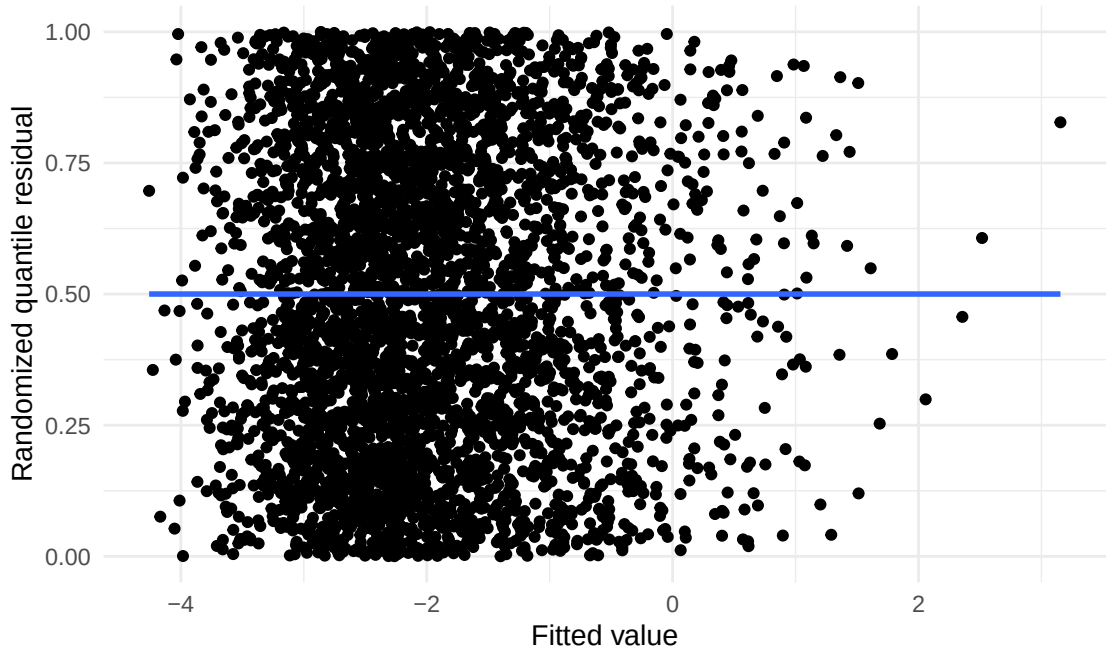


Figure 9: Random Quantile Residual versus Fitted Values Plot

```
plot(final_glm, which = 5)
```

The residual vs. leverage plot indicates that observations 3527, 1561, and 3074 may be potential outliers, but they are not necessarily influential.

Odds Ratios

```
final_glm_summary = summary(final_glm)

final_glm_df =
  as.data.frame(final_glm_summary$coefficients) |>
  janitor::clean_names() |>
  mutate(
    adjusted_odds_ratio = exp(estimate)
  ) |>
  rename(p_value = pr_z)

final_glm_df %>%
  knitr::kable(digits = 4, caption = "Final Model Results with Adjusted-Odds Ratio", format = "pipe")
```

Table 8: Final Model Results with Adjusted-Odds Ratio

	estimate	std_error	z_value	p_value	adjusted_odds_ratio
(Intercept)	-2.2838	0.4385	-5.2085	0.0000	0.1019
age	0.0238	0.0056	4.2426	0.0000	1.0241

	estimate	std_error	z_value	p_value	adjusted_odds_ratio
raceOther	-0.9346	0.2485	-3.7616	0.0002	0.3928
raceWhite	-0.5148	0.1617	-3.1845	0.0014	0.5976
marital_statusMarried	-0.2110	0.1416	-1.4900	0.1362	0.8097
marital_statusSeparated	0.6691	0.3881	1.7240	0.0847	1.9526
marital_statusSingle	-0.0646	0.1748	-0.3696	0.7117	0.9374
marital_statusWidowed	0.0175	0.2211	0.0791	0.9369	1.0176
t_stageT2	0.4111	0.1130	3.6372	0.0003	1.5085
t_stageT3	0.5516	0.1488	3.7077	0.0002	1.7360
t_stageT4	1.0988	0.2445	4.4934	0.0000	3.0005
n_stageN2	0.4363	0.1284	3.3987	0.0007	1.5470
n_stageN3	0.5872	0.2345	2.5034	0.0123	1.7989
differentiateModerately differentiated	0.5328	0.1838	2.8990	0.0037	1.7036
differentiatePoorly differentiated	0.9190	0.1924	4.7772	0.0000	2.5069
differentiateUndifferentiated	1.8649	0.5538	3.3672	0.0008	6.4551
estrogen_statusPositive	-0.7480	0.1775	-4.2140	0.0000	0.4733
progesterone_statusPositive	-0.5842	0.1275	-4.5811	0.0000	0.5576
regional_node_examined	-0.0359	0.0072	-5.0110	0.0000	0.9647
regional_node_positive	0.0797	0.0153	5.2076	0.0000	1.0829

Cross Validation

```
log_loss = function(actual, predicted) {

  -mean(actual * log(predicted) + (1 - actual) * log(1 - predicted))

}

glm_fit = function(data) {

  fit = glm(formula = status ~ age + race + marital_status + t_stage + n_stage +
        differentiate + estrogen_status + progesterone_status +
        regional_node_examined + regional_node_positive,
        family = binomial, data = data)

  return(fit)

}

cv_df =
  crossv_kfold(survival_df, k = 10) |>
  mutate(
    train = map(train, as_tibble),
    test = map(test, as_tibble)
  )

cv_res_df =
  cv_df |>
  mutate(
    final_model = map(train, \(x) glm_fit(data = x)),
    predicted_probs = map2(final_model, test, \(fit, data)
```

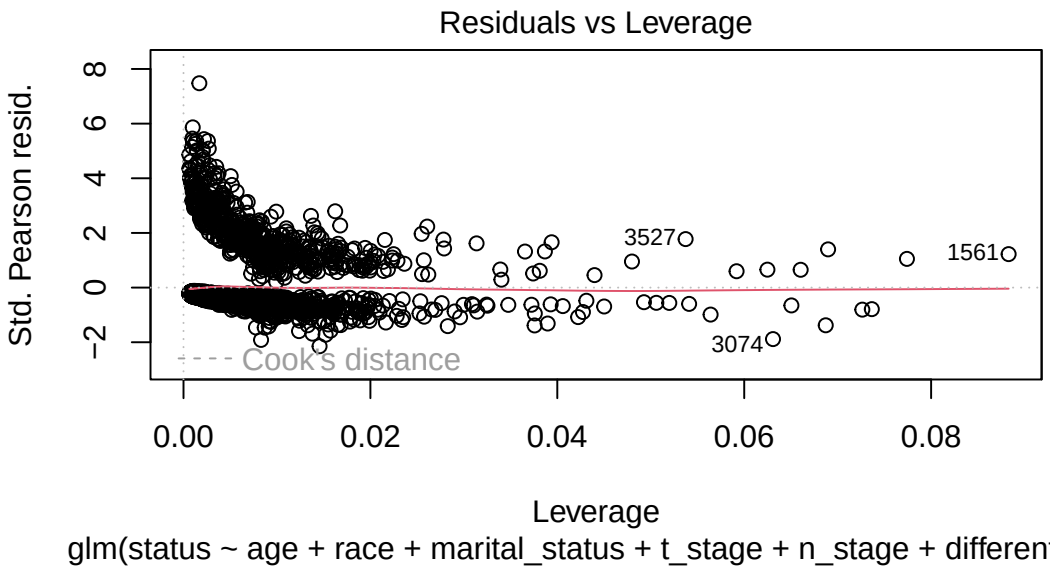


Figure 10: Residual versus Leverage Plot

```
                              predict(fit, newdata = data, type = "response")),
    actual_outcomes = map(test, pull, status),
    log_loss = map2_dbl(actual_outcomes, predicted_probs, \(x, y) log_loss(x, y)),
    AUC = map2_dbl(actual_outcomes, predicted_probs, \(x, y) {
      roc_obj = roc(x, y)
      auc(roc_obj)
    })
  )

cv_res_df %>%
  select(log_loss, AUC) %>%
  knitr::kable(digits = 4, caption = "Results of 10-Fold Cross Validation", format = "pipe")
```

Table 9: Results of 10-Fold Cross Validation

log_loss	AUC
0.3681	0.6999
0.3639	0.7463
0.4069	0.7498
0.3773	0.7552
0.3575	0.7792
0.3780	0.7317
0.3679	0.6604
0.3636	0.7951
0.3681	0.7644
0.3718	0.7405

After applying 10-fold cross-validation, we evaluate the goodness of fit by log loss and AUC. The mean of

log loss is 0.3723182, and the mean of AUC is 0.7422428.

Evaluation Across Races

- Evaluate the performance of your model(s). Is your model achieving similar performance between the majority race group "White" and the minority "Black" (or "Black" + "Other")? If not, could you try to improve the fairness (i.e., reducing the gap of prediction performance between the majority and minority) of your model(s)?

```
race_combine_df =
  survival_df %>%
  mutate(
    race = fct_collapse(
      race,
      "Black or other" = c("Black", "Other")
    )
  )

eval_produce = function(model, df) {

  results =
    df %>%
    mutate(predicted_probs = predict(model, newdata = ., type = "response")) %>%
    group_by(race) %>%
    summarize(
      log_loss = log_loss(status, predicted_probs),
      AUC = {
        roc_obj = roc(status, predicted_probs)
        auc_value = auc(roc_obj)  # Extract the numeric value of AUC
        as.numeric(auc_value)
        }
      ) %>%
    ungroup() %>%
    select(race, log_loss, AUC)

  return(results)

}

stra_cv_df =
  race_combine_df %>%
  vfold_cv(v = 10, strata = race) %>%
  mutate(
    train = map(splits, training),
    test = map(splits, testing)
  )

stra_res_df =
  stra_cv_df %>%
  mutate(
    final_model = map(train, \(x) glm_fit(data = x)),
    results = map2(final_model, test, \(x, y) eval_produce(x, y))
  )
```

```r
stra_res_df %>%
  select(results) %>%
  unnest(cols = c(results)) %>%
  group_by(race) %>%
  summarise(
    avg_log_loss = mean(log_loss),
    avg_AUC = mean(AUC)
  ) %>%
  knitr::kable(digits = 4, caption = "Race Comparison Before Adding Interaction Terms", format = "pipe")
```

Table 10: Race Comparison Before Adding Interaction Terms

race	avg_log_loss	avg_AUC
Black or other	0.4231	0.6997
White	0.3651	0.7502

Low log loss and high AUC indicate better test performance.

To reduce the gap of prediction performance between the majority and minority, we focused on whether there were interactions between the variables. We extracted each variable from the best model and examined how it differed in survival months of survival by race. Most variables did not show significant differences by race, suggesting that there may not be an interaction between these variables and race. However, the variable marital status showed a different pattern.

```r
race_combine_df %>%
  ggplot(aes(x = marital_status, y = survival_months, fill = race)) +
  geom_boxplot()  +
  geom_smooth(method = "lm") +
  scale_fill_brewer(palette = "RdBu") +
  labs(
    title = "Survival Months Distribution by Marital Status in Race Groups",
    x = "Marital Status",
    y = "Survival Months",
    fill = "Race"
  )
```

From the figure we can see that the distribution of survival months is different between races with different marital status. This indicates the potential interaction between race and marital status, and the interaction term can be added in the model to improve the fairness of the model.

```r
glm_inter_fit = function(data) {

  fit = glm(formula = status ~ age + race + marital_status + t_stage + n_stage +
        differentiate + estrogen_status + progesterone_status +
        regional_node_examined + regional_node_positive + marital_status * race,
        family = binomial, data = data)

  return(fit)

}
```

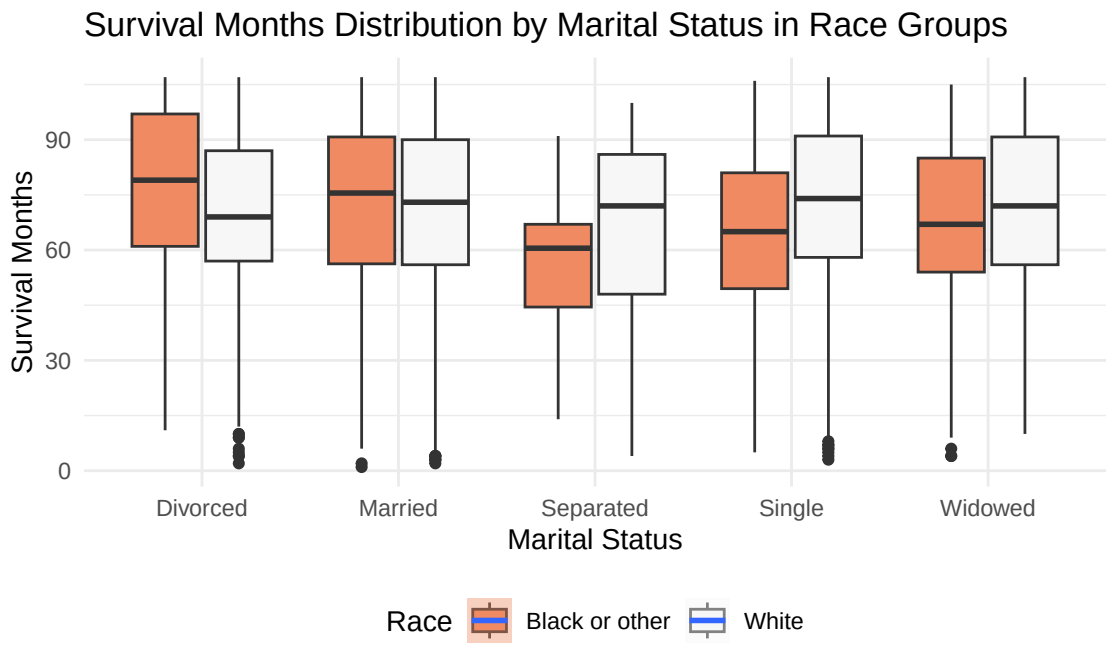


Figure 11: Survival Months Distribution by Marital Status in Race Groups

```
inter_res_df =
  stra_cv_df %>%
  mutate(
    final_model = map(train, \(x) glm_inter_fit(data = x)),
    results = map2(final_model, test, \(x, y) eval_produce(x, y))
  )

inter_res_df %>%
  select(results) %>%
  unnest(cols = c(results)) %>%
  group_by(race) %>%
  summarise(
    avg_log_loss = mean(log_loss),
    avg_AUC = mean(AUC)
  ) %>%
  knitr::kable(digits = 4, caption = "Race Comparison After Adding Interaction Terms", format = "pipe")
```

Table 11: Race Comparison After Adding Interaction Terms

race	avg_log_loss	avg_AUC
Black or other	0.4169	0.7251
White	0.3647	0.7501

By adding interaction term `marital_status * race`, we can observe a decrease in log loss and an increase in AUC, which means an improve in the fairness between group "White" and the minority "Black" + "Other".

Survival Analysis

```
surv_obj = Surv(time = survival_df$survival_months, event = survival_df$status)
```

Kaplan Meier Curve

The Kaplan Meier curve graphically represent the survival rate. Time is plotted on the x-axis and the survival rate is plotted on the y-axis.

```
km_fit = survfit(surv_obj ~ 1, data = survival_df)

ggsurvfit(km_fit, type = "survival", linewidth = 1) +
  labs(x = "Months",
       y = "Overall survival",
       title = "Kaplan-Meier Survival Curve") +
  add_confidence_interval() +
  scale_ggsurvfit()
```

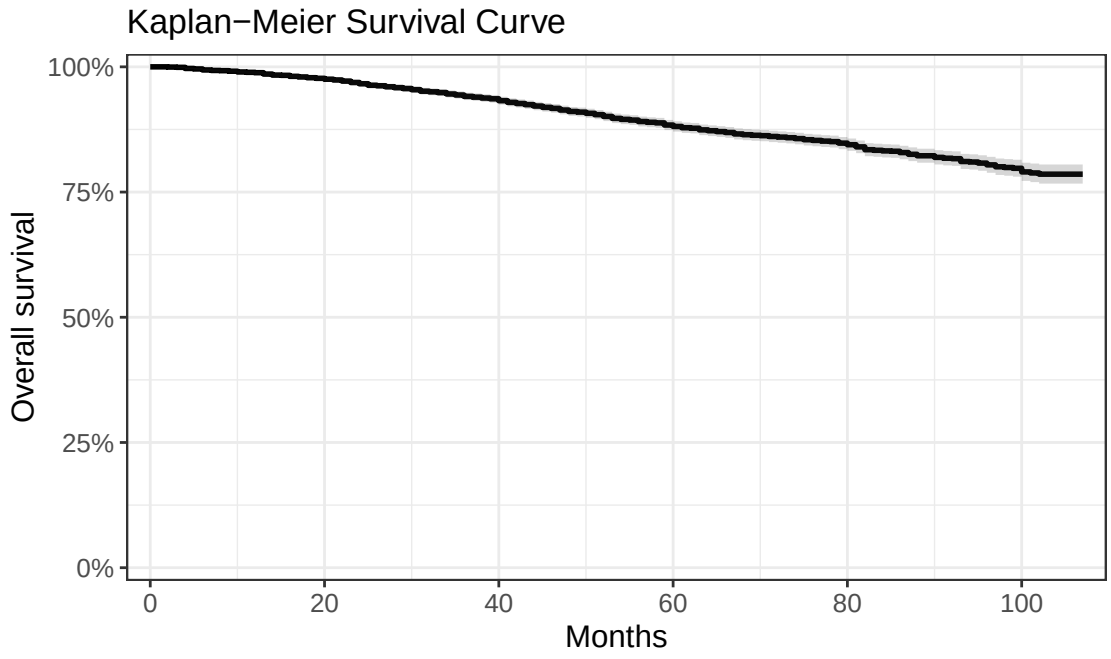


Figure 12: Kaplan-Meier Survival Curve

Log Rank Test

The log rank test lets us test whether there is a difference in survival times between groups of patients. For example, we want to find out whether there is a significant difference in survival between patients whose cells have different degrees of differentiation.

```r
log_rank_fit = survfit(surv_obj ~ differentiate, data = survival_df)


log_rank_plot =
  ggsurvplot(log_rank_fit, data = survival_df,
             size = 1, palette = "RdBu",
             censor.shape = '|', censor.size = 2,
             conf.int = TRUE, pval = TRUE,
             ggtheme = theme_bw(),
             legend = "bottom",
             legend.title = "Legend",
             legend.labs = c("Well differentiated", "Moderately differentiated",
                             "Poorly differentiated", "Undifferentiated"))

log_rank_plot$plot +
  ggtitle("Survival Time Across Differentiated Stages") +
  guides(color = guide_legend(nrow = 2))
```

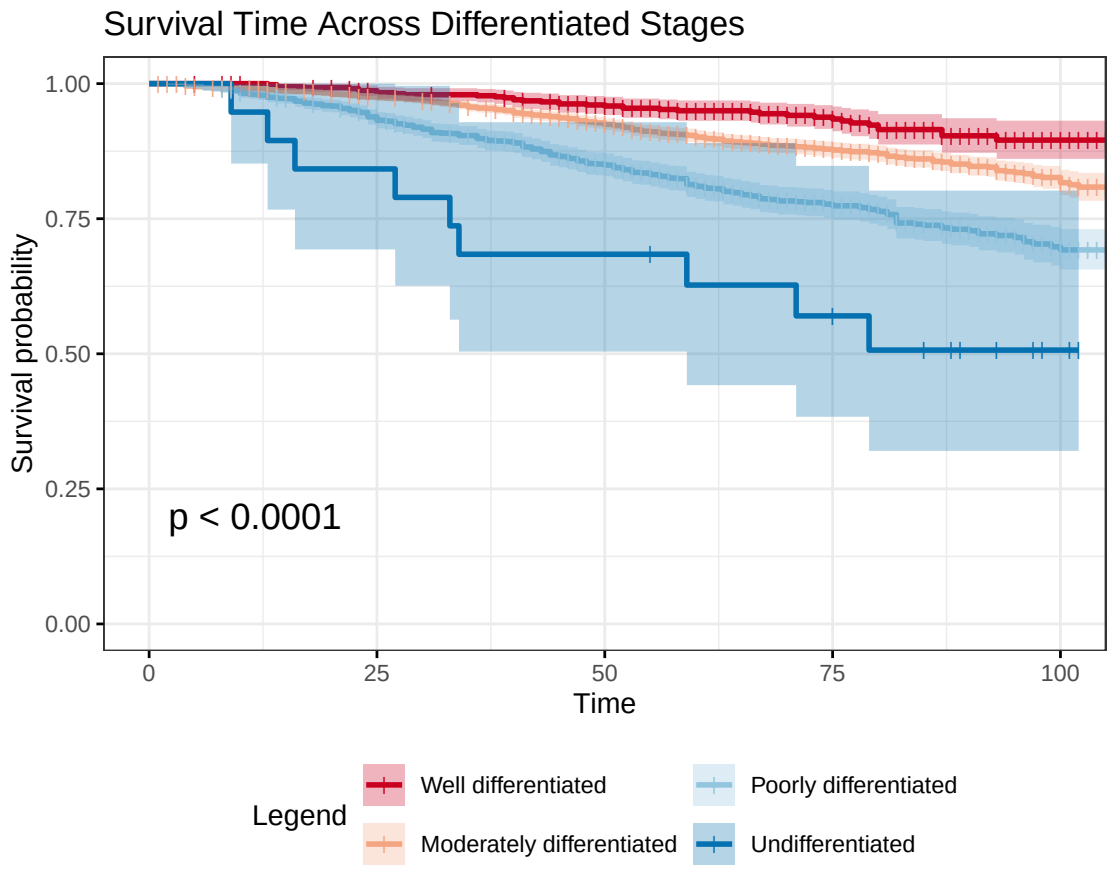


Figure 13: Survival Time Across Differentiated Stages

Cox Model

The limitation of KM curves and log-rank tests is that we can only test one variable at a time. To further discuss the risk factors to survival time, we will compute the cox proportional hazard model to adjusts for multiple risk factors simultaneously.

```
cox_model = coxph(surv_obj ~
                    age + race + marital_status + t_stage + n_stage + x6th_stage +
                      differentiate + a_stage + tumor_size + estrogen_status +
                      progesterone_status + regional_node_examined + regional_node_positive,
                  data = as.data.frame(survival_df))
```

The cox proportional hazard model has a assumption: the survival curves for two different strata of a risk factor must have hazard functions that are proportional over time. This assumption is satisfied when the change in hazard from one category to the next does not depend on time. That is, a person in one stratum has the same instantaneous relative risk compared to a person in a different stratum, irrespective of how much time has passed.

We will test this assumption based on the scaled Schoenfeld residuals. Here is an interpretation of the results: When p-val < 0.05, there is evidence against the proportional hazards assumption, meaning that the HR is not constant over time. Similarly, the larger the chi-square value, the greater the violation of the assumption.

```
cox.zph(cox_model) %>%
  .$table %>%
  as.data.frame() %>%
  knitr::kable(digits = 4, caption = "Results of Cox Proportional Hazard Model", format = "pipe")
```

Table 12: Results of Cox Proportional Hazard Model

	chisq	df	p
age	0.1328	1	0.7156
race	0.9335	2	0.6270
marital_status	2.6670	4	0.6150
t_stage	0.2144	3	0.9752
n_stage	1.7178	2	0.4236
x6th_stage	3.8545	3	0.2776
differentiate	1.8899	3	0.5956
a_stage	5.2218	1	0.0223
tumor_size	0.9310	1	0.3346
estrogen_status	28.9294	1	0.0000
progesterone_status	32.1281	1	0.0000
regional_node_examined	0.0187	1	0.8912
regional_node_positive	0.0324	1	0.8571
GLOBAL	57.2155	24	0.0002

We can see from the table that variable `a_stage`, `estrogen_status`, `progesterone_status` are not constant over time, which means it's not proper to contain these covariates in cox regression. To reduce bias of the model, we can remove these variables and take a closer look at the result.

```
cox_new_model = coxph(surv_obj ~ age + race + marital_status + t_stage + n_stage + x6th_stage +
                        differentiate + tumor_size + regional_node_examined + regional_node_positive,
                      data = as.data.frame(survival_df))

ggforest(cox_new_model,
         fontsize = 0.6)
```

The hazard ratio is similar to relative risk, but differs in that the HR is the instantaneous risk rather than the cumulative risk over the entire study.

The x-axis of this forest plot represents hazard ratios. Hazard ratio = 1 means no significant difference compared to the reference, and a HR higher than 1 means it increases the hazard ratio of the event, death, and a HR lower than 1 decreases it. The smaller the p-value is the stronger the weight of evidence that the two groups are different.

We can conclude from the plot that for the variable race, blacks have the highest risk of death, followed by whites, while the lowest mortality rate is for other ethnic groups. In the variable marital status, the risk of death is significantly higher for separated people, but this may be due to information bias caused by fewer observations. The confidence intervals for the other categories of marital status all contain the null hypothesis, meaning that there is no significant difference.

The risk of death is highest for patients with N stage N3, followed by N2, and finally N1. Differently, although T stage also shows a similar trend, the confidence intervals of each stage level contain the null hypothesis, meaning that there is no significant difference between levels. For the 6th stage, IIIB has the highest risk of death, followed by IIB, and then IIA, but there is no significant difference. For stage IIIC, since it contains the same information as N3 of N stage, no comparison is made in this variable.

In the variable differentiated, the risk of death is significantly highest for undifferentiated, and then decreases in the order of poorly differentiated, moderately differentiated, and well differentiated.

For the variables tumor size, regional node examined, and regional node postive, we did not observe significant differences in the risk of death.

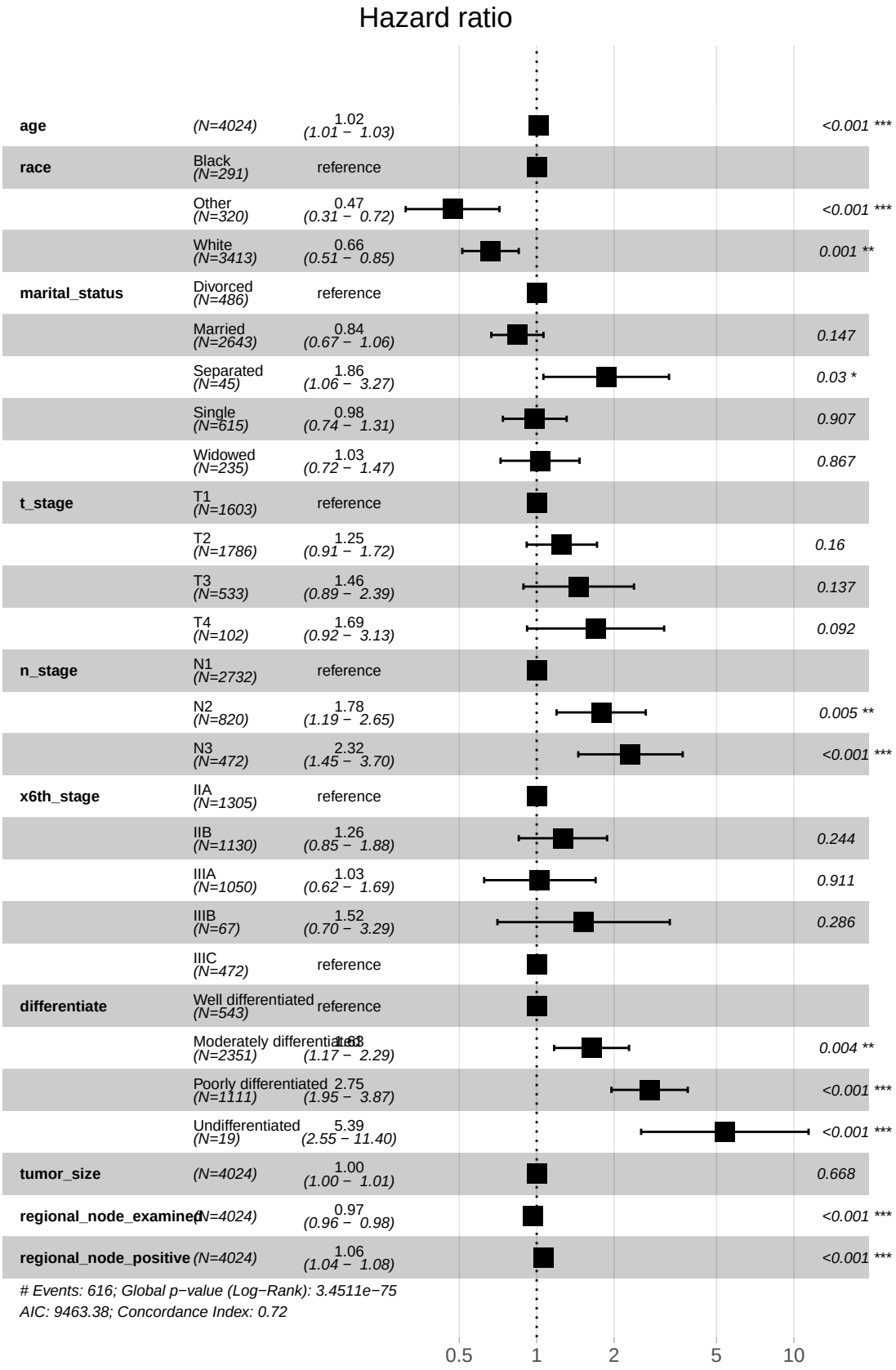


Figure 14: Forest Plot of Hazard Ratios