P8130_final_project

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Appendix

- Data Import

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

- 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" "Moderate
##  $ 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 ...
##  $ reginol_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`, `reginol_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.

```r
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)
  )
```

```r
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
##  Moderately differentiated:2351   1            : 543   Distant :  92
##  Poorly differentiated    :1111   2            :2351   Regional:3932
##  Undifferentiated         :  19   3            :1111
##  Well differentiated      : 543   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
##  reginol_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
```

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.

```
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   reginol_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  'Moderately differentiated' 'Poorly differentiated' Undifferentiated
##   <fct>                       <int>                   <int>            <int>
## 1 Black                         141                     115                3
## 2 Other                         180                      94                0
## 3 White                        2030                     902               16
## # i 1 more variable: 'Well differentiated' <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
```
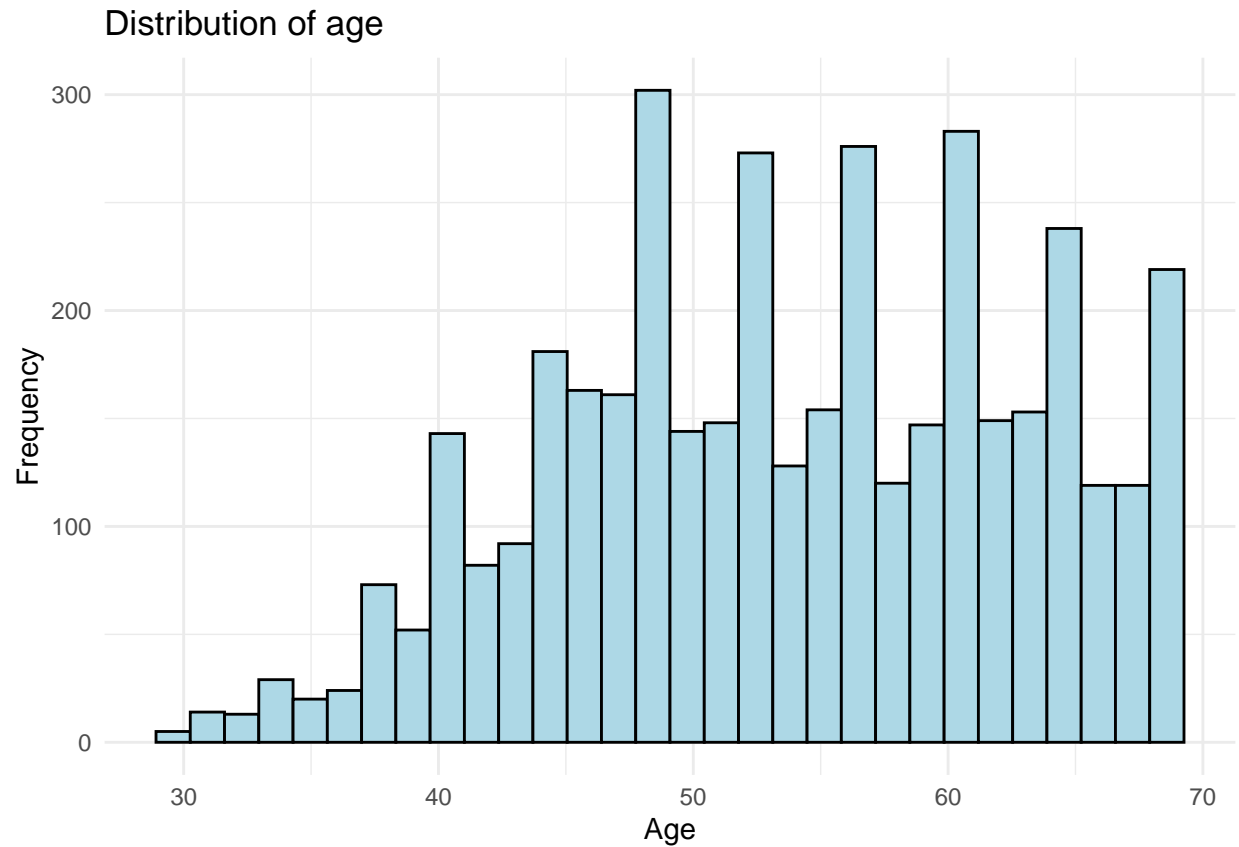
This table shows the frequency of different levels of `status` by 6th stage.

- Data Visualization

Distributions of the numeric variables

Distribution of age

```
survival_df |>
  ggplot(aes(age)) +
  geom_histogram(fill = "light blue", color = "black") +
  theme_minimal() +
  labs(
    title = "Distribution of age",
    x = "Age",
    y = "Frequency"
  )
```

Distribution of age

The histogram shows the age distribution of patients. 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.

Distribution of tumor size

```
ggplot(survival_df, aes(x = tumor_size)) +
  geom_histogram(fill = "light blue", color = "black") +
  scale_x_continuous(breaks = seq(0, max(survival_df$tumor_size, na.rm = TRUE), by = 5)) +
  labs(
    title = "Distribution of Tumor Size",
    x = "Tumor Size (mm)",
    y = "Frequency"
  )
```

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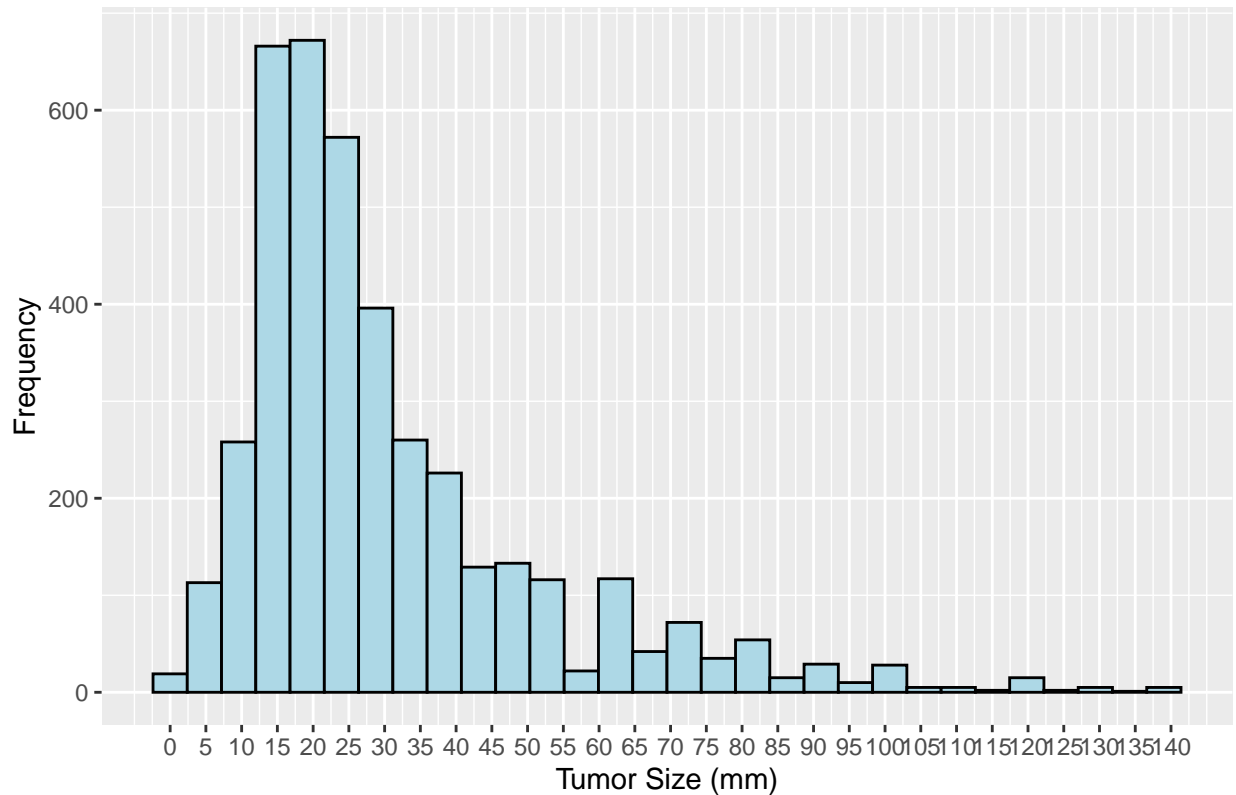
This is the distribution of all tumor sizes, and most of the tumor sizes are smaller than 50 mm. We can find that the most frequent size is around 19 mm, followed by around 14 mm. This distribution is right-skewed, so we will use the log transformation for this variable.

Distribution of examined regional node

```
ggplot(survival_df, aes(x = regional_node_examined)) +
  geom_histogram(fill = "light blue", color = "black") +
  scale_x_continuous(breaks = seq(0, max(survival_df$regional_node_examined, na.rm = TRUE), by = 5)) +
  labs(
    title = "Distribution of Examined Regional Node",
    x = "Examined Regional Node",
    y = "Frequency"
  )
```

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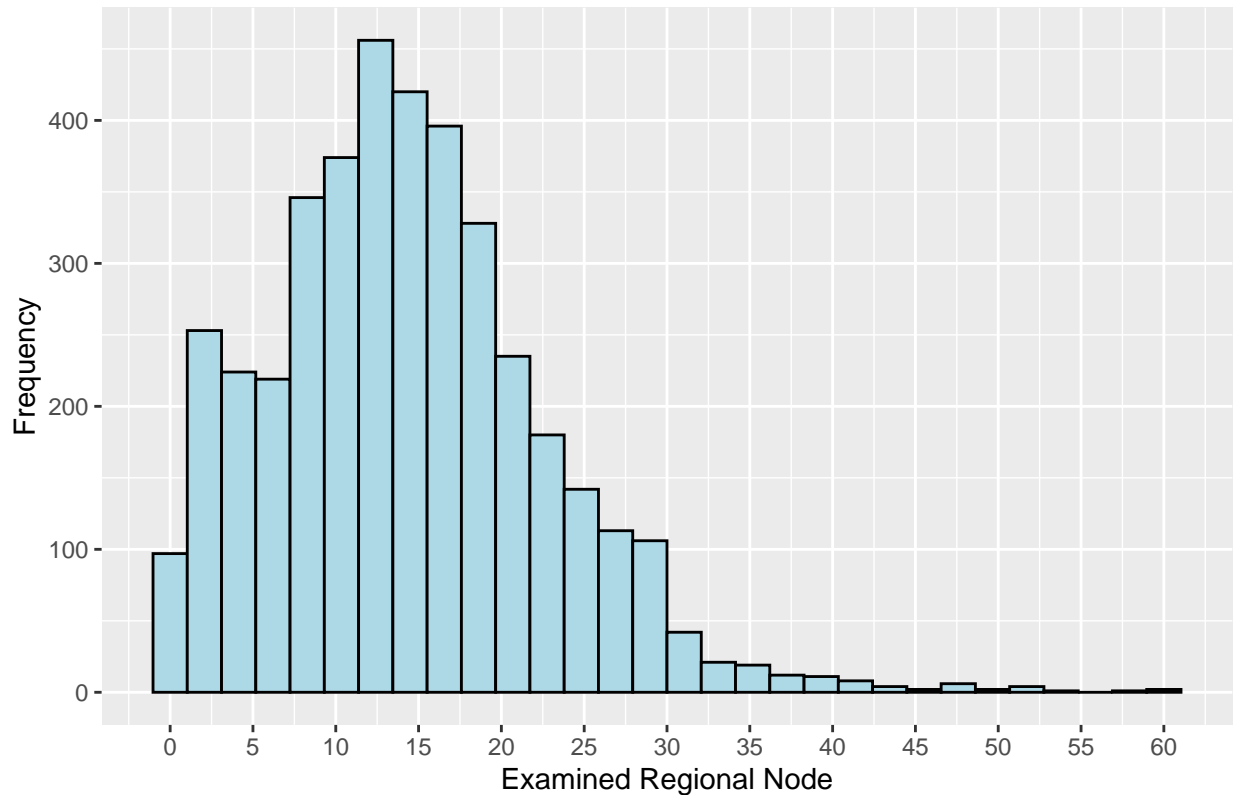
This plot maps the frequency of different number of examined regional nodes for each subject. The number of examined regional nodes for most subjects are smaller than 30, and the subjects with nearly 12 examined regional nodes are the most.

Distribution of positive regional node

```
ggplot(survival_df, aes(x = reginol_node_positive)) +
  geom_histogram(fill = "light blue", color = "black") +
  scale_x_continuous(breaks = seq(0, max(survival_df$reginol_node_positive, na.rm = TRUE), by = 5)) +
  labs(
    title = "Distribution of Positive Reginol Node",
    x = "Positive Reginol Node",
    y = "Frequency"
  )
```

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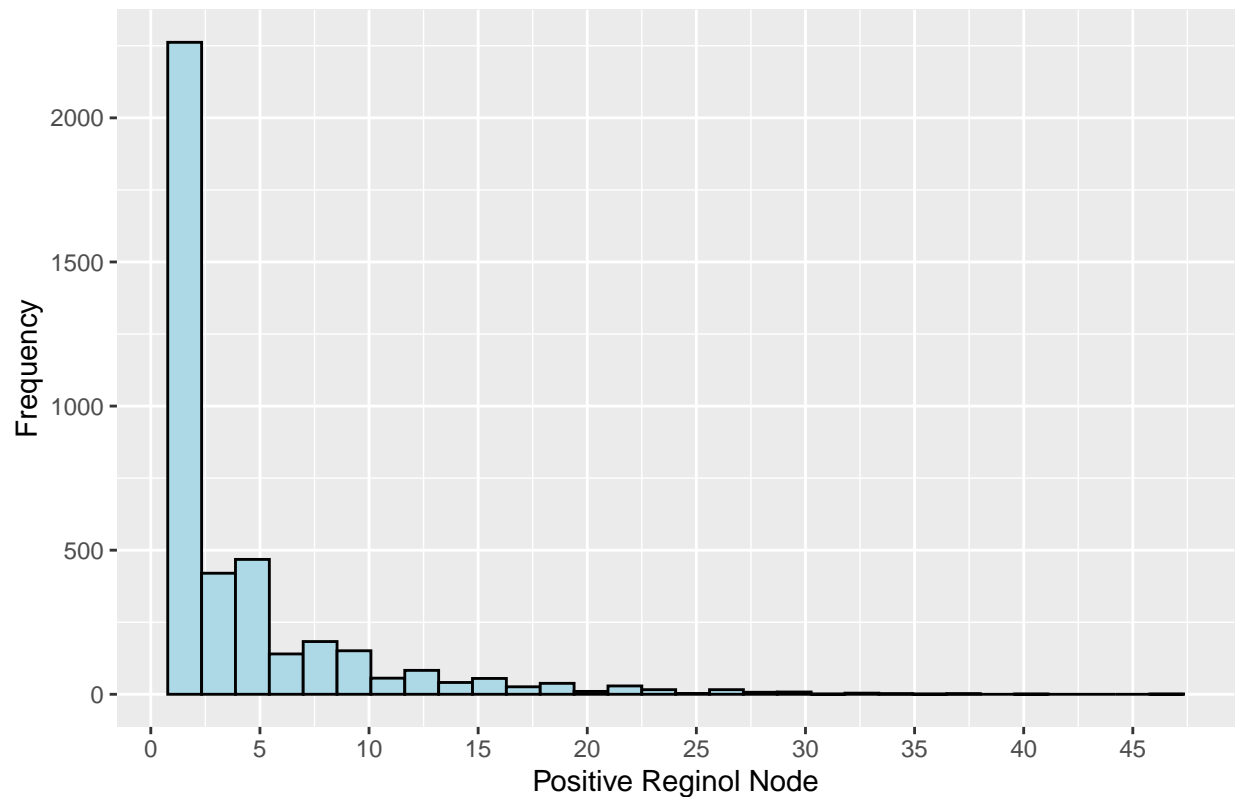
Then is the distribution of different number of positive reginol node for each subject. Over 2500 subjects only have 1 or 2 positive reginol nodes, which is the most frequent number of positive reginol nodes. It is strongly right-skewed, so we will use the log transformation for this variable.

Distribution of Cancer Grades

```
ggplot(survival_df, aes(x = grade)) +
    geom_bar(fill = "skyblue") +
    labs(title = "Frequency Distribution of Cancer Grades",
        x = "Grade",
        y = "Count") +
    theme_minimal()
```

Frequency Distribution of Cancer Grades
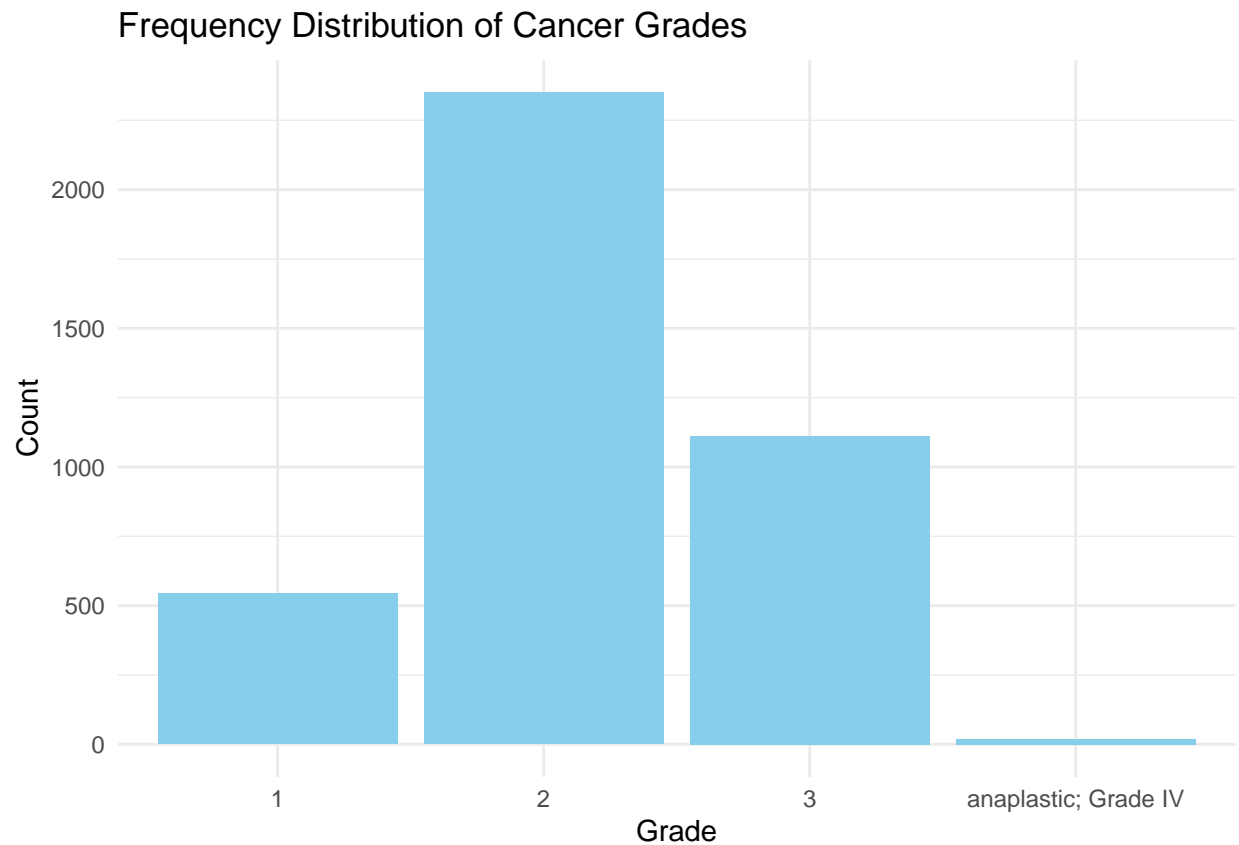
This bar chart provides an overview of how cancer cases are distributed across grades. Grade 2 represents the majority of cases, suggesting it is the most frequently observed grade, while Grade IV is exceedingly rare.

Bewteen Variables
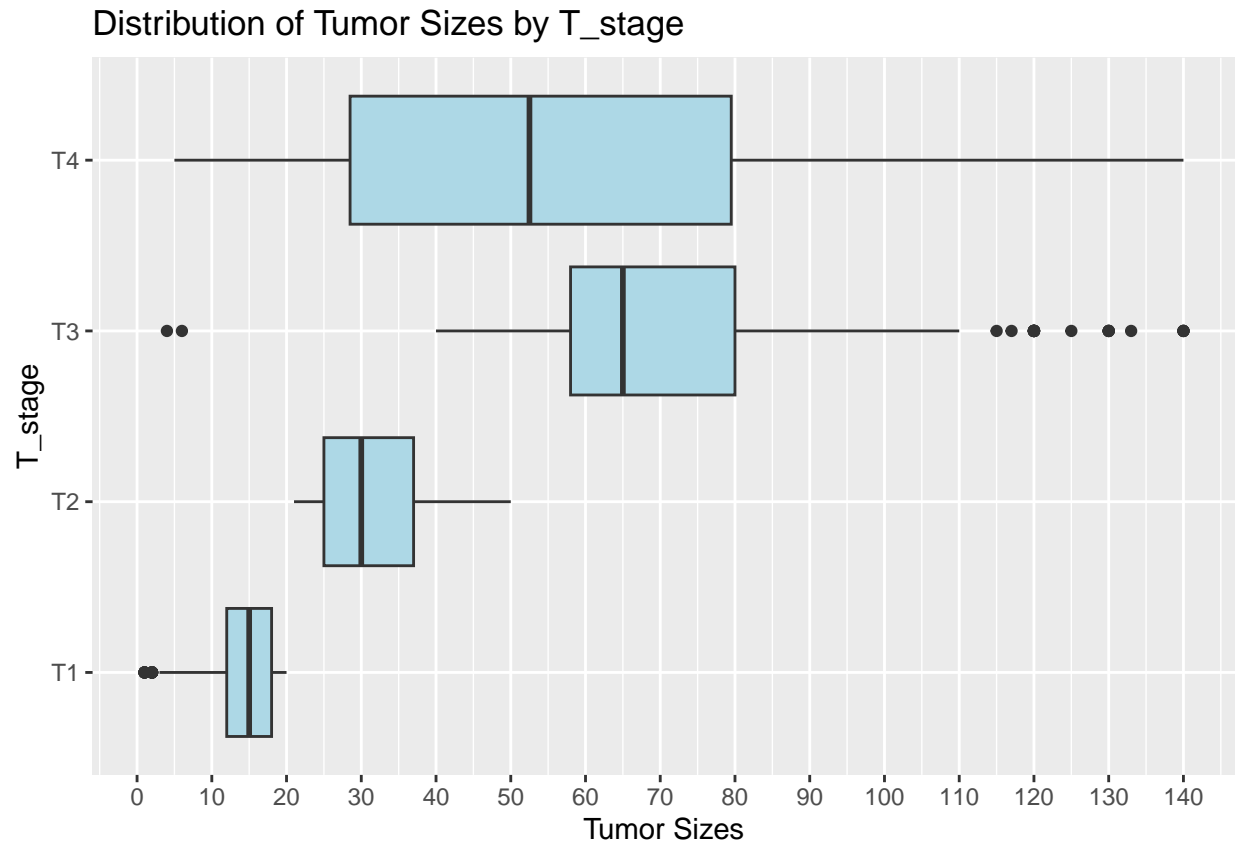
Distribution of survival months by status

```
ggplot(survival_df, aes(x = survival_months, fill = status)) +
  geom_histogram(binwidth = 5, position = "dodge") +
  labs(title = "Distribution of Survival Months", x = "Survival Months", y = "Frequency") +
  theme_minimal()
```

Distribution of Survival Months
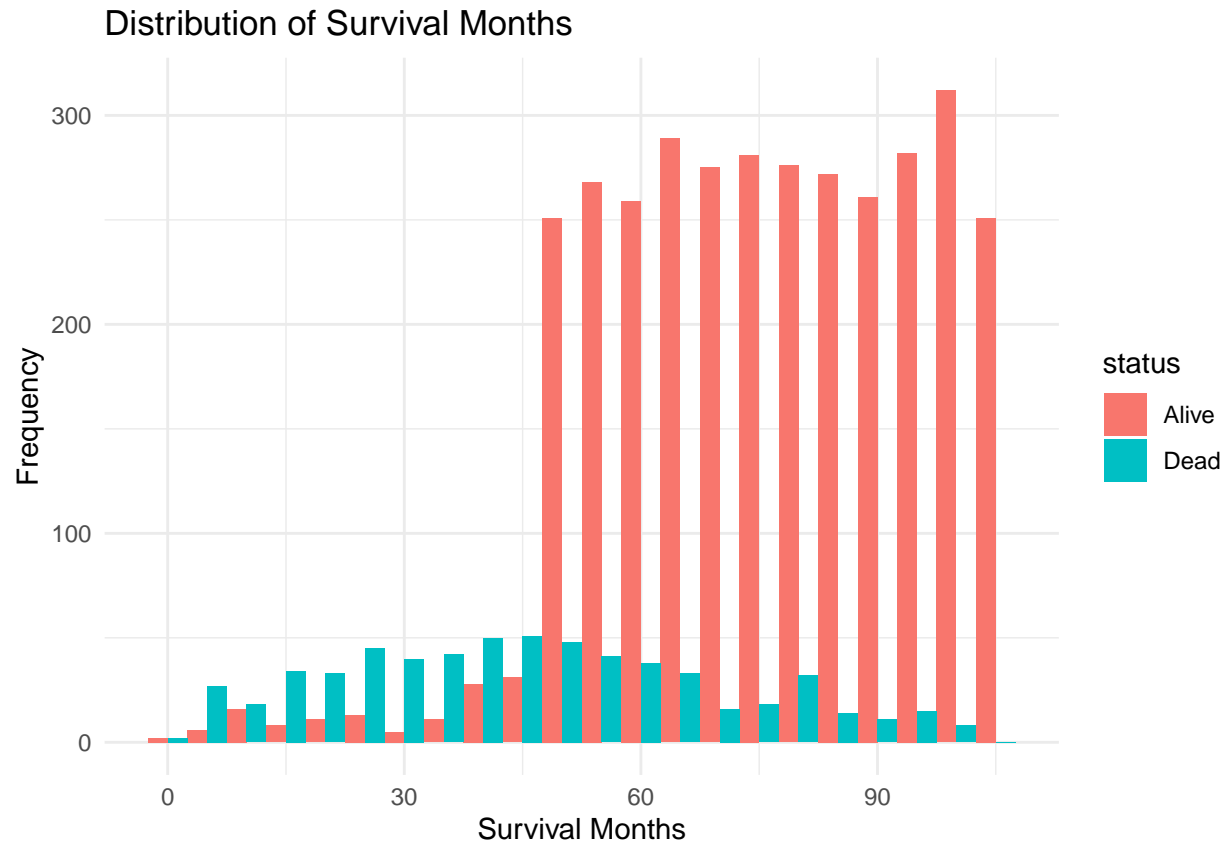
The Dead group is concentrated in the shorter survival months, while the Alive group is predominant in longer survival months, particularly beyond 60 months.

## The distribution of the tumor sizes by t_stage

```
ggplot(survival_df, aes(x = tumor_size, y = t_stage)) +
  geom_boxplot(fill = "light blue") +
  scale_x_continuous(breaks = seq(0, max(survival_df$tumor_size, na.rm = TRUE), by = 10)) +
  labs(
    title = "Distribution of Tumor Sizes by T_stage",
    x = "Tumor Sizes",
    y = "T_stage"
  )
```

Distribution of 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. There are some outliers both ar T1 stage and T3 stage.

The distribution of survival months by a_stage based on status(alive/dead)

```
ggplot(survival_df, aes(x = survival_months, y = a_stage)) +
  geom_boxplot(fill = "light blue") +
  scale_x_continuous(breaks = seq(0, max(survival_df$survival_months, na.rm = TRUE), by = 10)) +
  labs(
    title = "Distribution of Survival Months by A_stage",
    x = "Survival Months",
    y = "A_stage"
  ) +
  facet_grid(~ status)
```

Distribution of Survival Months by A_stage
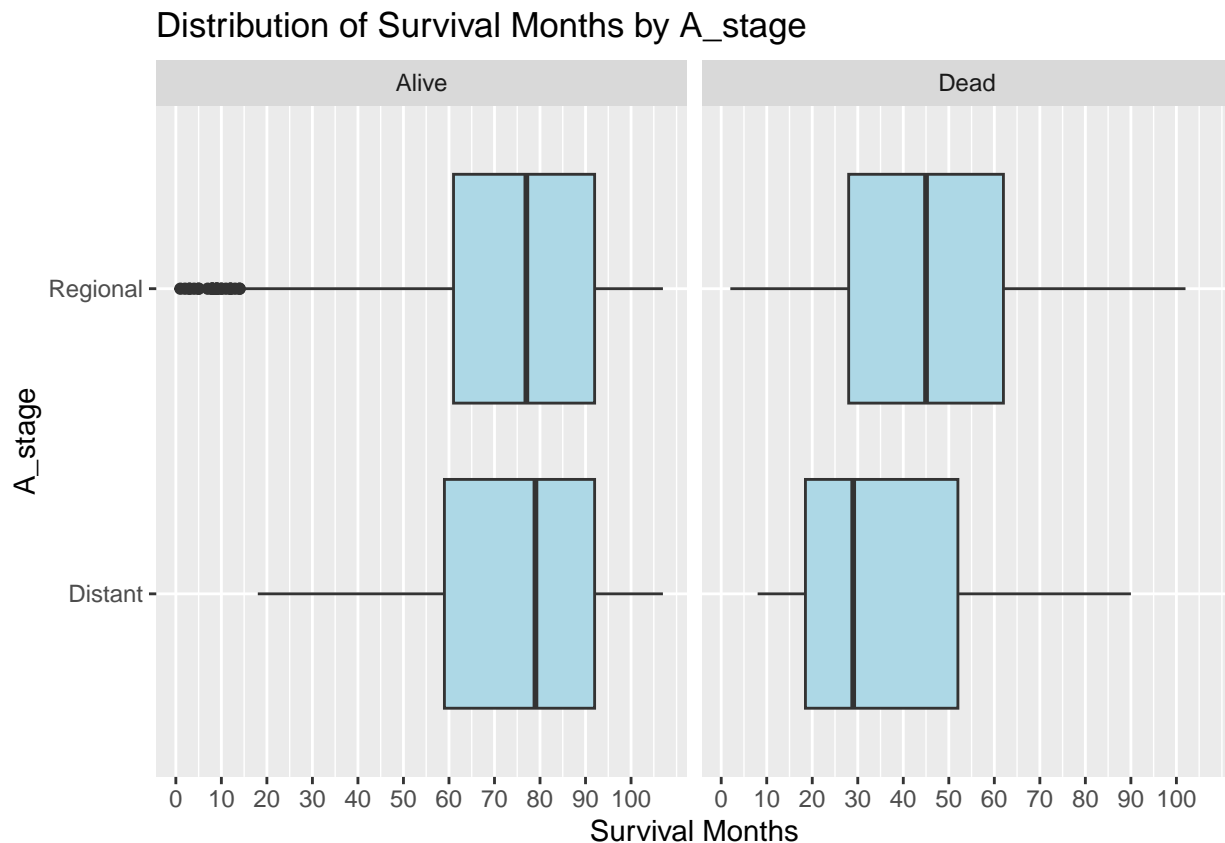
Through this plot, we can find that subjects with Distant stage have fewer survival months than subjects with Regional stage. However, the IQR of the survival months of subjects with Distant stage is much larger than subjects with Regional stage.

Distribution of Estrogen Status by Tumor Size Based on race

```
ggplot(survival_df, aes(x = progesterone_status, y = tumor_size)) +
  geom_boxplot(fill = "light blue") +
  labs(
    title = "Distribution of Estrogen Status by Tumor Size",
    x = "Estrogen Status",
    y = "Tumor Size"
  ) +
  facet_grid(~ race)
```

Distribution of Estrogen Status by Tumor Size
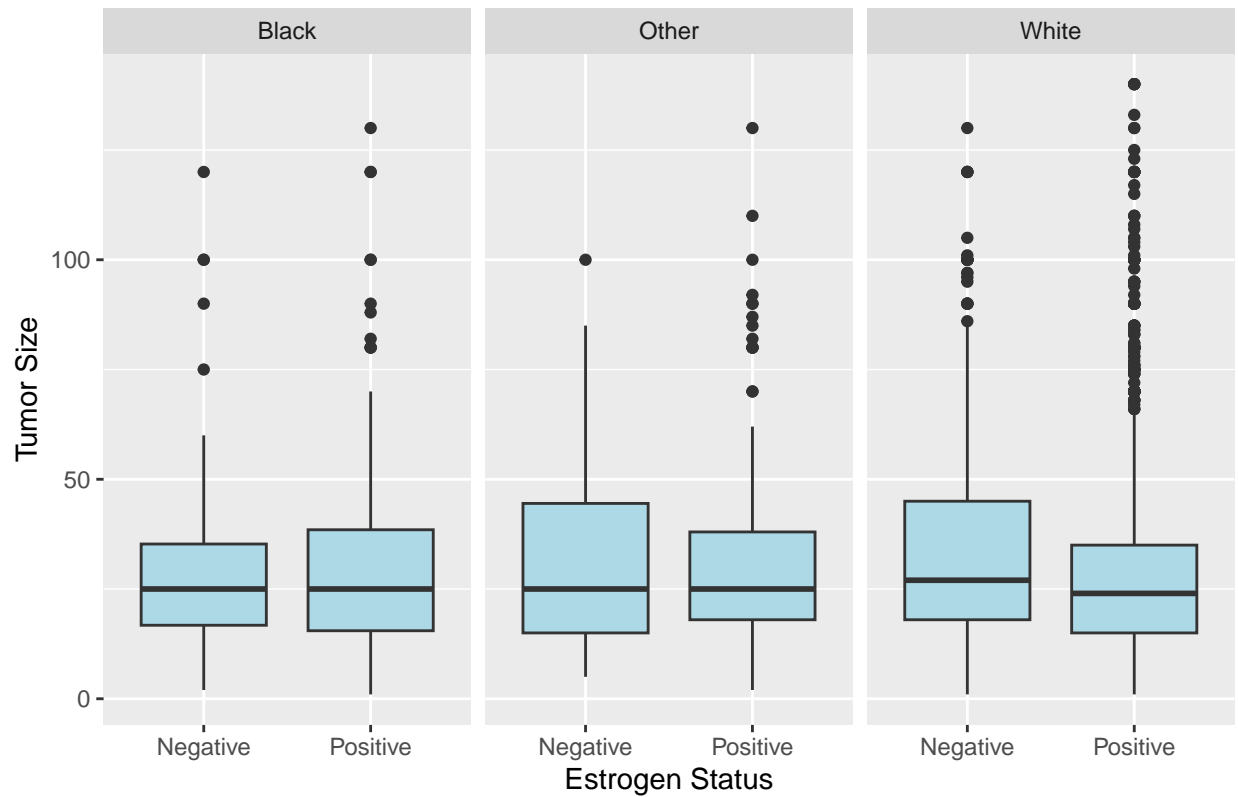
While the overall patterns are consistent, with Negative estrogen status generally associated with slightly larger tumor sizes, the variability and prevalence of outliers differ between groups. The White group shows the greatest spread in tumor size, while the Other group displays the least variability.

Tumor Size Distribution by Grade

```
ggplot(survival_df, aes(x = grade, y = tumor_size)) +
  geom_boxplot(fill = "lightblue") +
  labs(title = "Tumor Size Distribution by Grade",
       x = "Grade",
       y = "Tumor Size (mm)") +
  theme_minimal()
```

## Tumor Size Distribution by Grade
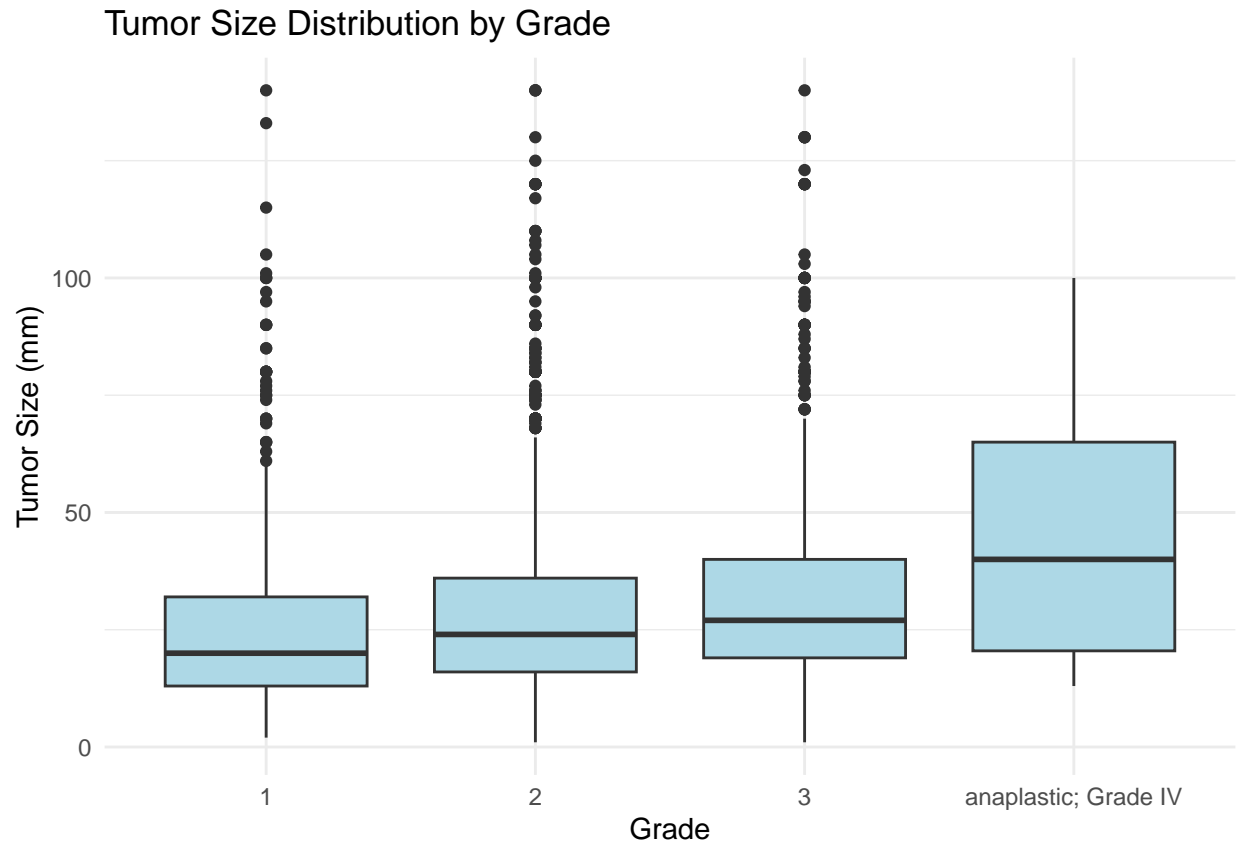
Lower grades (1–3) exhibit comparable tumor size distributions, with slight increases in variability as the grade increases.

Grade IV stands out due to its higher median and broader range, suggesting that more aggressive tumor grades are associated with larger tumor sizes.

## Proportion of Grade by Estrogen Status

```
ggplot(survival_df, aes(x = grade, fill = estrogen_status)) +
    geom_bar(position = "fill") +
    labs(title = "Proportion of Grade by Estrogen Status",
        x = "Grade",
        y = "Proportion",
        fill = "Race") +
    theme_minimal()
```

Proportion of Grade by Estrogen Status
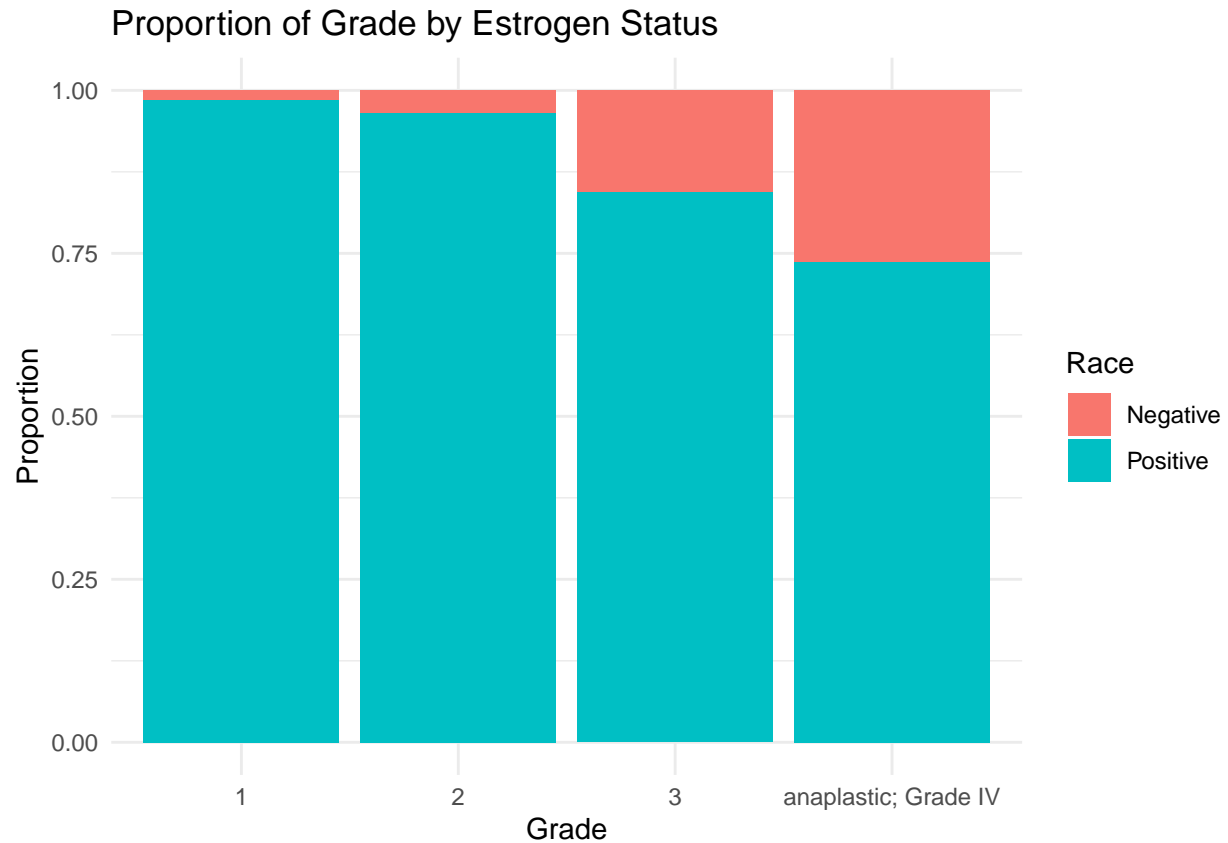
As tumor grade increases, the proportion of Negative estrogen status gradually increases, becoming more prominent in the anaplastic Grade IV category. Conversely, the dominance of the Positive estrogen status decreases with higher tumor grades.

Proportion of Grade by Marital Status

```
ggplot(survival_df, aes(x = grade, fill = marital_status)) +
    geom_bar(position = "fill") +
    labs(title = "Proportion of Grade by Marital Status",
        x = "Grade",
        y = "Proportion",
        fill = "Race") +
    theme_minimal()
```

Proportion of Grade by Marital Status
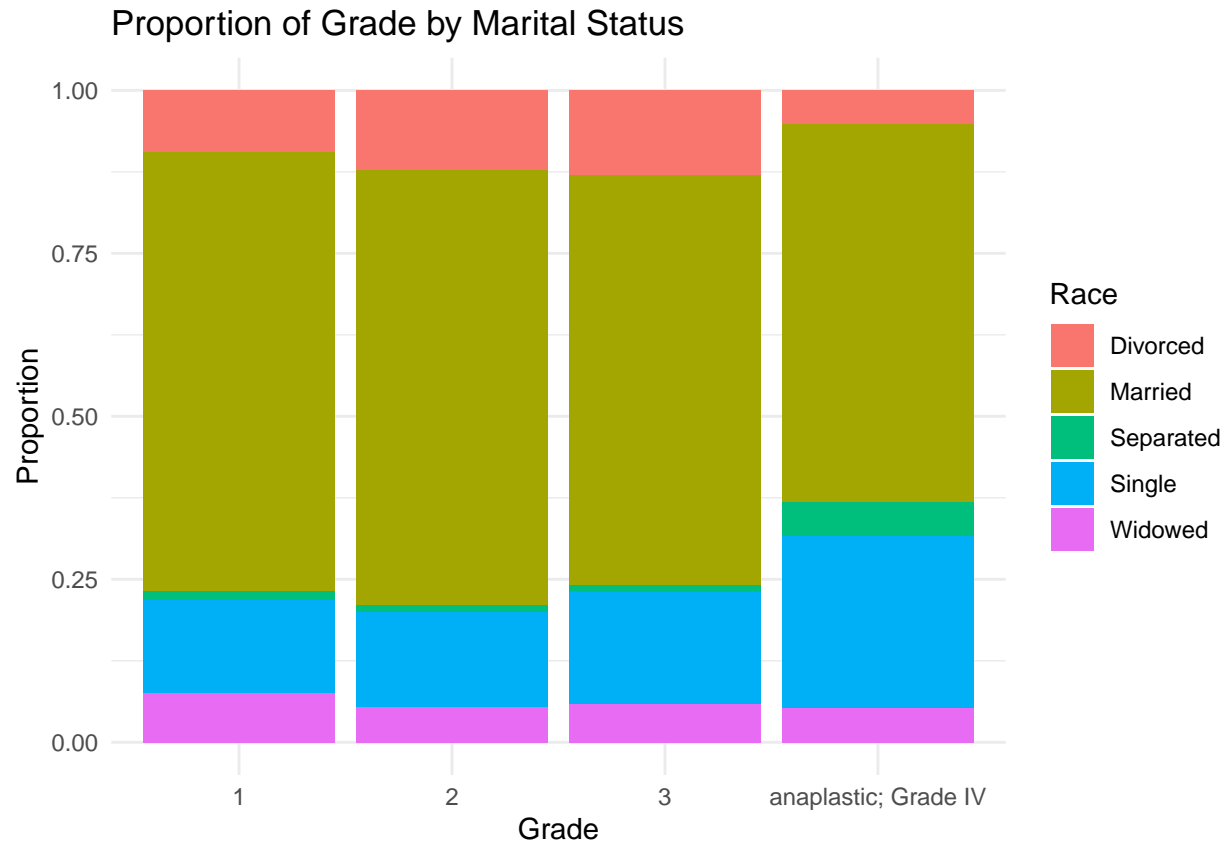
Across all grades, the "Married" group consistently constitutes the largest proportion of individuals, dominating every tumor grade category.

The "Single" group is the second-largest proportion in most grades, particularly Grades 2 and 3.

The "Widowed" group and "Divorced" group make up smaller proportions across all tumor grades.

Relationship Between Age and Tumor Size across status

```
ggplot(survival_df, aes(x = age, y = tumor_size, color = status)) +
   geom_point(alpha = 0.5, size = 0.6) +
  geom_smooth(method = "lm", color = "green") +
  facet_wrap(~ status) +
   labs(title = "Relationship Between Age and Tumor Size",
        x = "Age (years)",
        y = "Tumor Size (mm)",
        color = "Status") +
   theme_minimal()
```

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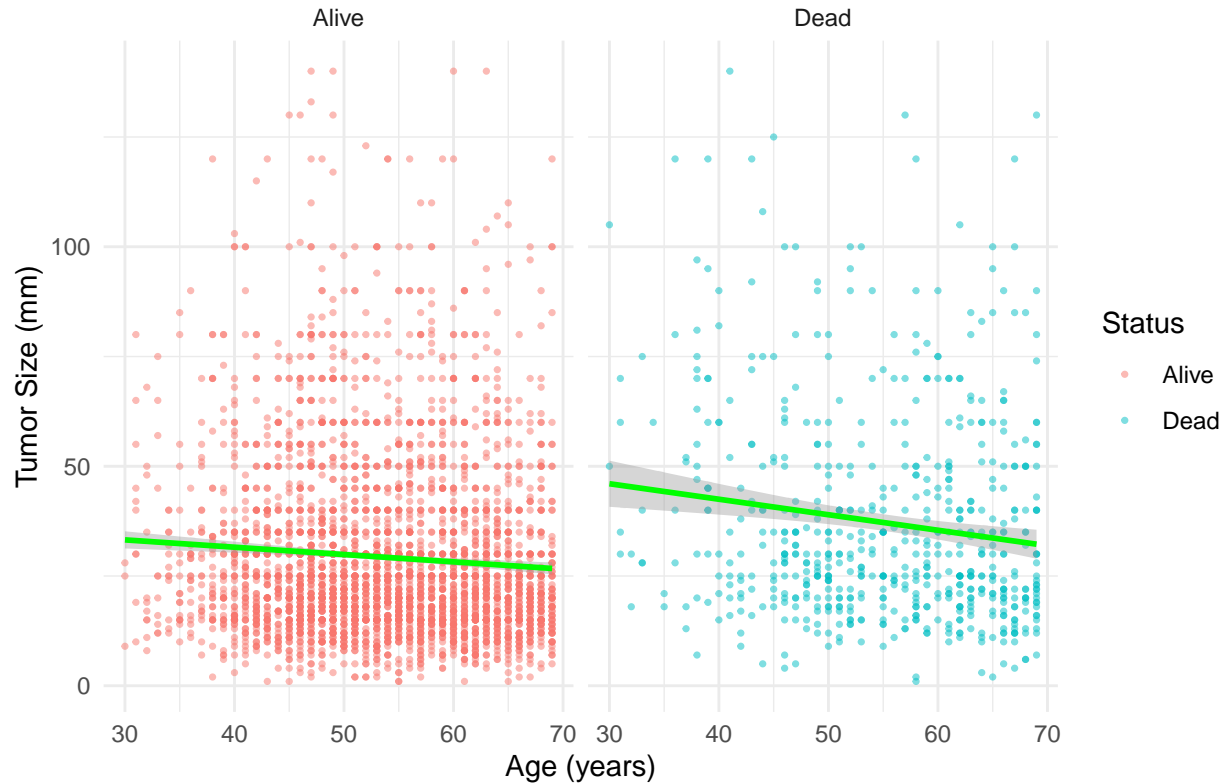
This figure highlights the differences in tumor size distribution and trends with age between individuals who are alive and those who are deceased. While the "Alive" group shows no significant relationship between age and tumor size, the "Dead" group exhibits a pattern where larger tumors are associated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

Age vs. Tumor Size Across Grades

```
ggplot(survival_df, aes(x = age, y = tumor_size)) +
    geom_point(color = "lightblue", size = 0.8, alpha = 0.5) +
  geom_smooth(method = "lm") +
    facet_wrap(~ marital_status) +
    labs(title = "Age vs. Tumor Size Across Grades",
        x = "Age (years)",
        y = "Tumor Size (mm)") +
    theme_minimal()
```

Age vs. Tumor Size Across Grades
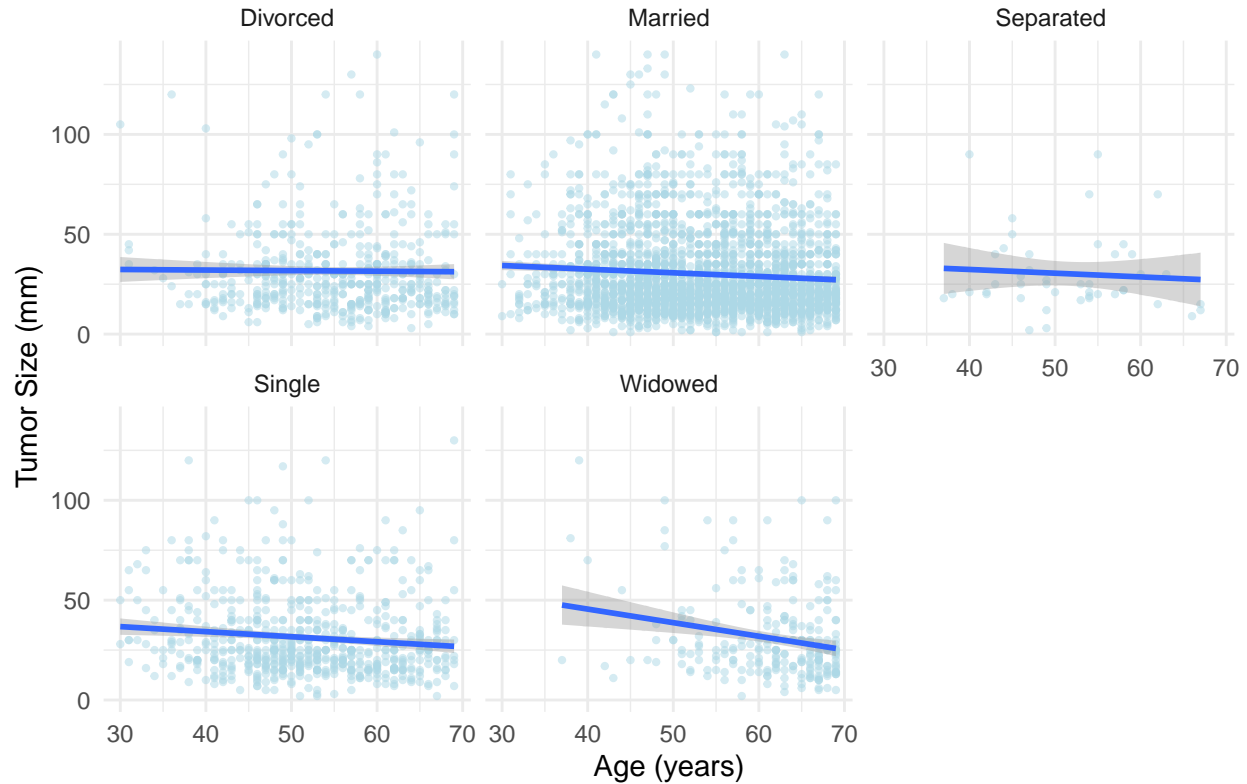
Divorced: Tumor size seems to remain fairly constant with age, as the trend line is relatively flat.

Married: A slight negative trend is observable, suggesting that tumor size may decrease marginally with age.

Separated: The data is sparse, but the trend shows a slightly negative relationship, with wide confidence intervals due to fewer observations.

Single: A modest negative trend is observed, indicating a potential decline in tumor size with increasing age.

Widowed: A more apparent negative trend is evident compared to other groups, suggesting a stronger decrease in tumor size with age.

Positive Reginol Node vs Survival Months Across Cancer Grade

```
ggplot(survival_df, aes(x = reginol_node_positive, y = survival_months)) +
  geom_point(color = "light blue", size = 0.5, alpha = 0.5)  +
  facet_wrap(.~grade) +
  geom_smooth(method = "lm") +
  labs(
    title = "Distribution of Positive Reginol Node and Survival Months by Cancer Grade",
    x = "Positive Reginol Node",
    y = "Survival Months"
  ) +
  theme_minimal()
```

Distribution of Positive Reginol Node and Survival Months by Cancer Grade
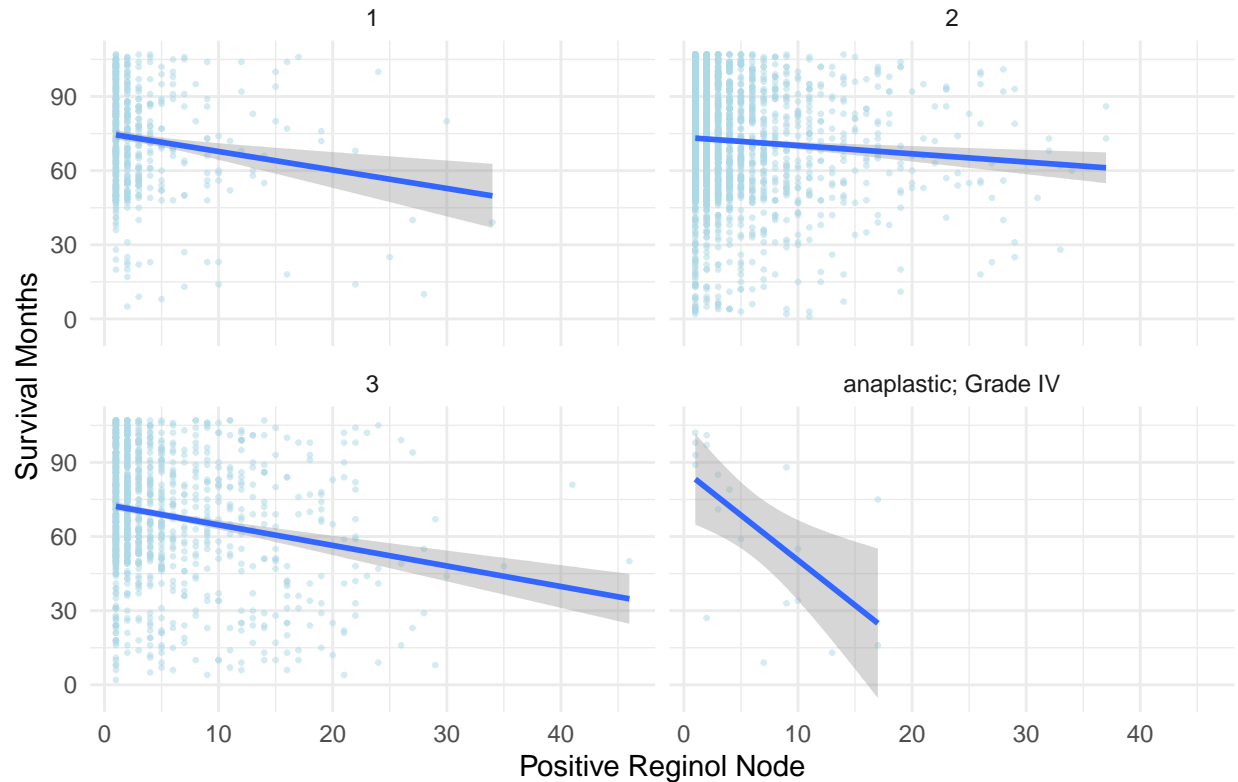
According to the trend lines, as the cancer grade increases, the negative correlation between the number of positive reginol nodes and the survival months becomes stronger. At the Grade IV, the correlation is strong. AS the number of positive reginol nodes increases, the survival months will decrease.

Transformations

```
survival_df = survival_df |>
  mutate(
    log_tumor_size = log(tumor_size),
    log_reginol_node_positive = log(reginol_node_positive)
  )
```

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