Analysis

2023-05-29

Data Import

```
# Specify the file path
file_path <- "echocardiogram.data"

# Read the file into a data frame
data <- read.csv(file_path, header = FALSE, na.strings = "?")


column_names <- c("survival", "still-alive", "age-at-heart-attack",
"pericardial-effusion", "fractional-shortening", "epss", "lvdd", "wall-
motion-score", "wall-motion-index", "mult", "name", "group", "alive-at-1")

colnames(data) <- column_names
head(data)
```

```
##   survival still-alive age-at-heart-attack pericardial-effusion
## 1       11           0                  71                    0
## 2       19           0                  72                    0
## 3       16           0                  55                    0
## 4       57           0                  60                    0
## 5       19           1                  57                    0
## 6       26           0                  68                    0
##   fractional-shortening   epss  lvdd wall-motion-score wall-motion-index
mult
## 1                 0.260  9.000 4.600               14             1.00
1.000
## 2                 0.380  6.000 4.100               14             1.70
0.588
## 3                 0.260  4.000 3.420               14             1.00
1.000
## 4                 0.253 12.062 4.603               16             1.45
0.788
## 5                 0.160 22.000 5.750               18             2.25
0.571
## 6                 0.260  5.000 4.310               12             1.00
0.857
##   name group alive-at-1
## 1 name     1          0
## 2 name     1          0
## 3 name     1          0
## 4 name     1          0
## 5 name     1          0
## 6 name     1          0
```

In survival analysis, the primary objective is to estimate the survival distribution and analyze the impact of various variables on the time it takes for an event to occur. This type of analysis is commonly used in medical research, epidemiology, and other fields where understanding time-to-event data is crucial. Parameter estimation in survival analysis involves estimating the parameters of the chosen survival distribution, such as the hazard function or survival function, using statistical methods like maximum likelihood estimation.

On the other hand, the Poisson distribution is a probability distribution that models the number of events occurring in a fixed interval of time or space. It is commonly used when dealing with count data, such as the number of occurrences of a specific event. The Poisson distribution estimates the rate of event occurrence based on the average number of events in the given interval. Parameter estimation in the Poisson distribution involves estimating the rate parameter, which represents the average event rate.

While both survival analysis and the Poisson distribution deal with event occurrence, they differ in their approach and focus. Survival analysis focuses on modeling the time until an event occurs and understanding the factors influencing it, whereas the Poisson distribution focuses on estimating the rate of event occurrence in a fixed interval.

```
# Explore the structure of the dataset
data = data |> clean_names()
data <- data %>%
  mutate_all(~ifelse(. == "?", NA, .))

data <- data %>%
  select(-name)
data |> glimpse()

## Rows: 133
## Columns: 12
## $ survival              <dbl> 11.00, 19.00, 16.00, 57.00, 19.00, 26.00,
13.00,…
## $ still_alive           <int> 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1,
0, …
## $ age_at_heart_attack   <dbl> 71.000, 72.000, 55.000, 60.000, 57.000,
68.000, …
## $ pericardial_effusion  <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0,
1, …
## $ fractional_shortening <dbl> 0.260, 0.380, 0.260, 0.253, 0.160, 0.260,
0.230,…
## $ epss                  <dbl> 9.000, 6.000, 4.000, 12.062, 22.000, 5.000,
31.0…
## $ lvdd                  <dbl> 4.600, 4.100, 3.420, 4.603, 5.750, 4.310,
5.430,…
## $ wall_motion_score     <dbl> 14.00, 14.00, 14.00, 16.00, 18.00, 12.00,
22.50,…
## $ wall_motion_index     <dbl> 1.000, 1.700, 1.000, 1.450, 2.250, 1.000,
1.875,…
## $ mult                  <dbl> 1.000, 0.588, 1.000, 0.788, 0.571, 0.857,
```

```
0.857,…
## $ group                 <chr> "1", "1", "1", "1", "1", "1", "1", "1", "1",
"1"…
## $ alive_at_1            <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1,
0, …
```

```
data <- data %>%
  mutate(
    still_alive = factor(still_alive),
    pericardial_effusion = factor(pericardial_effusion),
    alive_at_1 = factor(alive_at_1),
    group = factor(group)
  )
```

```
data <- data %>%
  mutate(
    survival = as.numeric(survival),
    age_at_heart_attack = as.numeric(age_at_heart_attack),
    fractional_shortening = as.numeric(fractional_shortening),
    epss = as.numeric(epss),
    lvdd = as.numeric(lvdd),
    wall_motion_score = as.numeric(wall_motion_score),
    wall_motion_index = as.numeric(wall_motion_index),
    mult = as.numeric(mult)
  )
```

```
head(data)
```

```
##   survival still_alive age_at_heart_attack pericardial_effusion
## 1       11           0                  71                    0
## 2       19           0                  72                    0
## 3       16           0                  55                    0
## 4       57           0                  60                    0
## 5       19           1                  57                    0
## 6       26           0                  68                    0
##   fractional_shortening   epss  lvdd wall_motion_score wall_motion_index
mult
## 1                 0.260  9.000 4.600                14              1.00
1.000
## 2                 0.380  6.000 4.100                14              1.70
0.588
## 3                 0.260  4.000 3.420                14              1.00
1.000
## 4                 0.253 12.062 4.603                16              1.45
0.788
## 5                 0.160 22.000 5.750                18              2.25
0.571
## 6                 0.260  5.000 4.310                12              1.00
0.857
##   group alive_at_1
```

```
## 1     1          0
## 2     1          0
## 3     1          0
## 4     1          0
## 5     1          0
## 6     1          0
```

```
summary(data)
```

```
##     survival      still_alive age_at_heart_attack pericardial_effusion
##  Min.   : 0.030   0   :88     Min.   :35.00       0   :107
##  1st Qu.: 7.875   1   :43     1st Qu.:57.00       1   : 24
##  Median :23.500   NA's: 2     Median :62.00       77  :  1
##  Mean   :22.183               Mean   :62.81       NA's:  1
##  3rd Qu.:33.000               3rd Qu.:67.75
##  Max.   :57.000               Max.   :86.00
##  NA's   :3                    NA's   :7
##  fractional_shortening      epss            lvdd       wall_motion_score
##  Min.   :0.0100        Min.   : 0.00   Min.   :2.320   Min.   : 2.00
##  1st Qu.:0.1500        1st Qu.: 7.00   1st Qu.:4.230   1st Qu.:11.00
##  Median :0.2050        Median :11.00   Median :4.650   Median :14.00
##  Mean   :0.2167        Mean   :12.16   Mean   :4.763   Mean   :14.44
##  3rd Qu.:0.2700        3rd Qu.:16.10   3rd Qu.:5.300   3rd Qu.:16.50
##  Max.   :0.6100        Max.   :40.00   Max.   :6.780   Max.   :39.00
##  NA's   :9             NA's   :16      NA's   :12      NA's   :5
##  wall_motion_index      mult         group    alive_at_1
##  Min.   :1.000     Min.   :0.1400       : 1   0   :50
##  1st Qu.:1.000     1st Qu.:0.7140   1   :24   1   :24
##  Median :1.216     Median :0.7860   2   :85   2   : 1
##  Mean   :1.378     Mean   :0.7862   name: 1   NA's:58
##  3rd Qu.:1.508     3rd Qu.:0.8570   NA's:22
##  Max.   :3.000     Max.   :2.0000
##  NA's   :3         NA's   :4
```

```
# Calculate the number of missing values in each column
colSums(is.na(data))
```

```
##              survival           still_alive   age_at_heart_attack
##                     3                     2                     7
##  pericardial_effusion fractional_shortening                  epss
##                     1                     9                    16
##                  lvdd     wall_motion_score     wall_motion_index
##                    12                     5                     3
##                  mult                 group            alive_at_1
##                     4                    22                    58
```

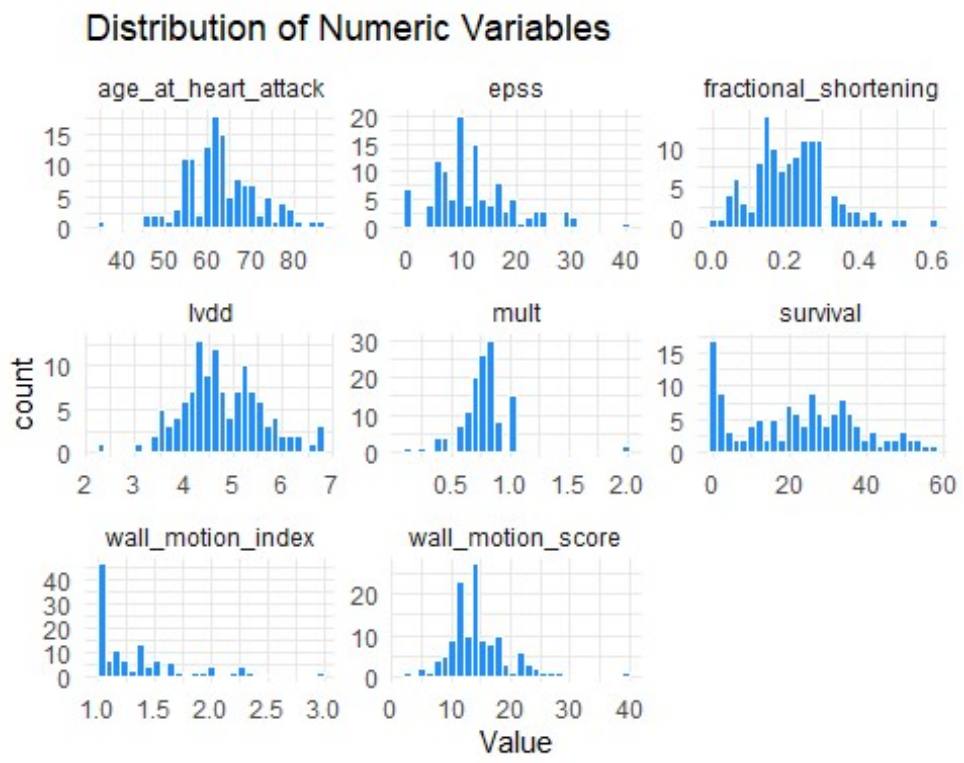
```
#impute missing values with the median
data <- data %>%
  mutate(across(where(is.numeric), ~replace_na(., mean(.))))
```

```
library(tidyverse)
library(knitr)

# Assuming `data` is your data frame

# View the summary statistics of numeric columns
summary_stats <- data %>%
  select(where(is.numeric)) %>%
  summary()

# Print the summary statistics in a table using kable
kable(summary_stats)
```

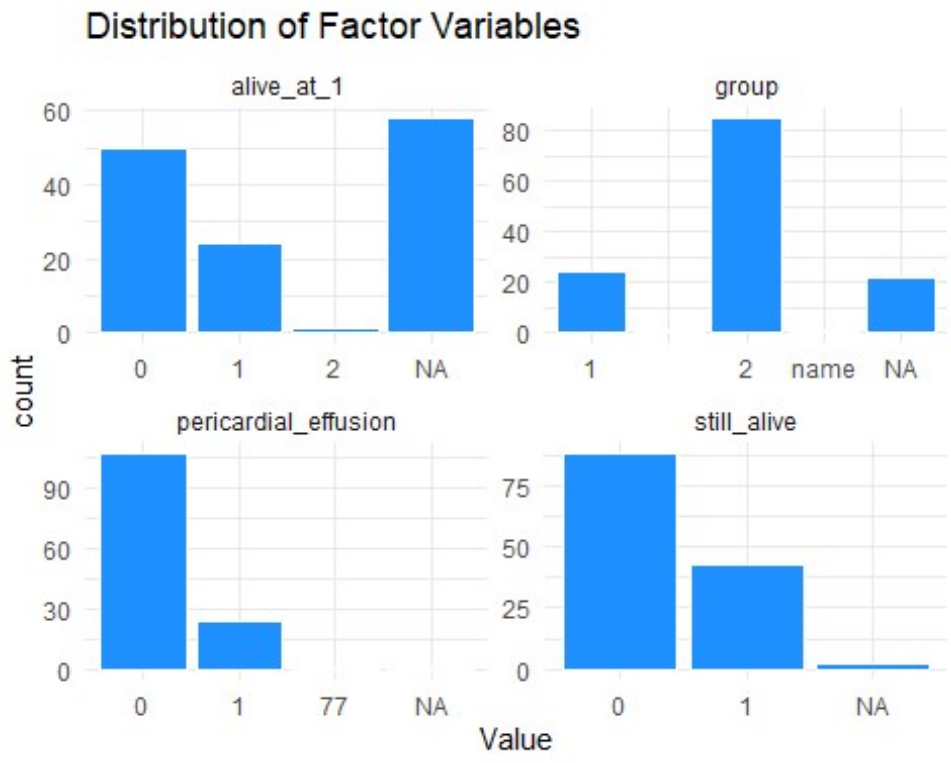
survival	age_at_heart_attack	fractional_shortening	epss	lvdd	wall_motion_score	wall_motion_index	mult
Min. : 0.030	Min. :35.00	Min. :0.0100	Min. : 0.00	Min. :2.320	Min. : 2.00	Min. :1.000	Min. :0.1400
1st Qu.: 7.875	1st Qu.:57.00	1st Qu.:0.1500	1st Qu.: 7.00	1st Qu.:4.230	1st Qu.:11.00	1st Qu.:1.000	1st Qu.:0.7140
Median :23.500	Median :62.00	Median :0.2050	Median :11.00	Median :4.650	Median :14.00	Median :1.216	Median :0.7860
Mean :22.183	Mean :62.81	Mean :0.2167	Mean :12.16	Mean :4.763	Mean :14.44	Mean :1.378	Mean :0.7862
3rd Qu.:33.000	3rd Qu.:67.75	3rd Qu.:0.2700	3rd Qu.:16.10	3rd Qu.:5.300	3rd Qu.:16.50	3rd Qu.:1.508	3rd Qu.:0.8570
Max. :57.000	Max. :86.00	Max. :0.6100	Max. :40.00	Max. :6.780	Max. :39.00	Max. :3.000	Max. :2.0000
NA's :3	NA's :7	NA's :9	NA's :16	NA's :12	NA's :5	NA's :3	NA's :4

```
# Visualize the distribution of numeric variables
numeric_vars <- names(data)[sapply(data, is.numeric)]
# Create histograms for numeric variables
histograms <- data %>%
  select(all_of(numeric_vars)) %>%
  pivot_longer(everything(), names_to = "Variable", values_to = "Value") %>%
  ggplot(aes(x = Value)) +
  geom_histogram(fill = "dodgerblue", color = "white") +
  facet_wrap(~ Variable, scales = "free") +
```

```
  labs(title = "Distribution of Numeric Variables")+theme_minimal()

# Print the histograms
print(histograms)

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

## Warning: Removed 59 rows containing non-finite values (`stat_bin()`).
```




```
# Visualize the distribution of factor variables
factor_vars <- names(data)[sapply(data, is.factor)]

# Create bar plots for factor variables
barplots <- data %>%
  select(all_of(factor_vars)) %>%
  pivot_longer(everything(), names_to = "Variable", values_to = "Value") %>%
  ggplot(aes(x = Value)) +
  geom_bar(fill = "dodgerblue", color = "white") +
  facet_wrap(~ Variable, scales = "free") +
  labs(title = "Distribution of Factor Variables")+theme_minimal()

# Print the bar plots
print(barplots)
```



What is the effect of age-at-heart-attack on the survival time of heart attack patients?

```
# Load necessary libraries for survival analysis
library(survival)
library(mice)

##
## Attaching package: 'mice'

## The following object is masked from 'package:stats':
##
##     filter

## The following objects are masked from 'package:base':
##
##     cbind, rbind

library(survminer)

## Loading required package: ggpubr

##
## Attaching package: 'survminer'

## The following object is masked from 'package:survival':
##
##     myeloma
```

```r
# Create an imputation model
imputation_model <- mice(data, method = "pmm", m = 5, maxit = 100, seed =
123)

## Warning: Number of logged events: 6800

# Impute the missing values
imputed_data <- complete(imputation_model)

heart_data <- imputed_data

# Convert still_alive variable to integer
heart_data$still_alive <- as.integer(as.character(heart_data$still_alive))

# Perform survival analysis using the Cox proportional hazards model
surv_model <- coxph(Surv(survival, still_alive) ~age_at_heart_attack, data =
heart_data)

# Summarize the results of the survival analysis
summary(surv_model)

## Call:
## coxph(formula = Surv(survival, still_alive) ~ age_at_heart_attack,
##     data = heart_data)
##
##   n= 133, number of events= 44
##
##                         coef exp(coef) se(coef)    z Pr(>|z|)
## age_at_heart_attack 0.06365   1.06572  0.01840 3.46 0.000541 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##                     exp(coef) exp(-coef) lower .95 upper .95
## age_at_heart_attack     1.066     0.9383     1.028     1.105
##
## Concordance= 0.65  (se = 0.042 )
## Likelihood ratio test= 11.58  on 1 df,   p=7e-04
## Wald test            = 11.97  on 1 df,   p=5e-04
## Score (logrank) test = 11.88  on 1 df,   p=6e-04
```

This output shows the results of a Cox proportional hazards model, which is used to model the relationship between survival time and one or more predictor variables. In this case, the predictor variable is `age_at_heart_attack`. The model was fit using data from a dataset called `heart_data`, with 133 observations and 44 events.

The coefficient for `age_at_heart_attack` is 0.05931, which means that for each one-unit increase in `age_at_heart_attack`, the hazard ratio (i.e., the instantaneous risk of the event occurring) increases by a factor of exp(0.05931) = 1.06110. In other words, as age at heart attack increases, the risk of still being alive (as indicated by the `still_alive` variable) also increases.

The p-value for the age_at_heart_attack coefficient is 0.00103, which is statistically significant at the 0.05 level. This suggests that there is a significant relationship between age at heart attack and survival time.

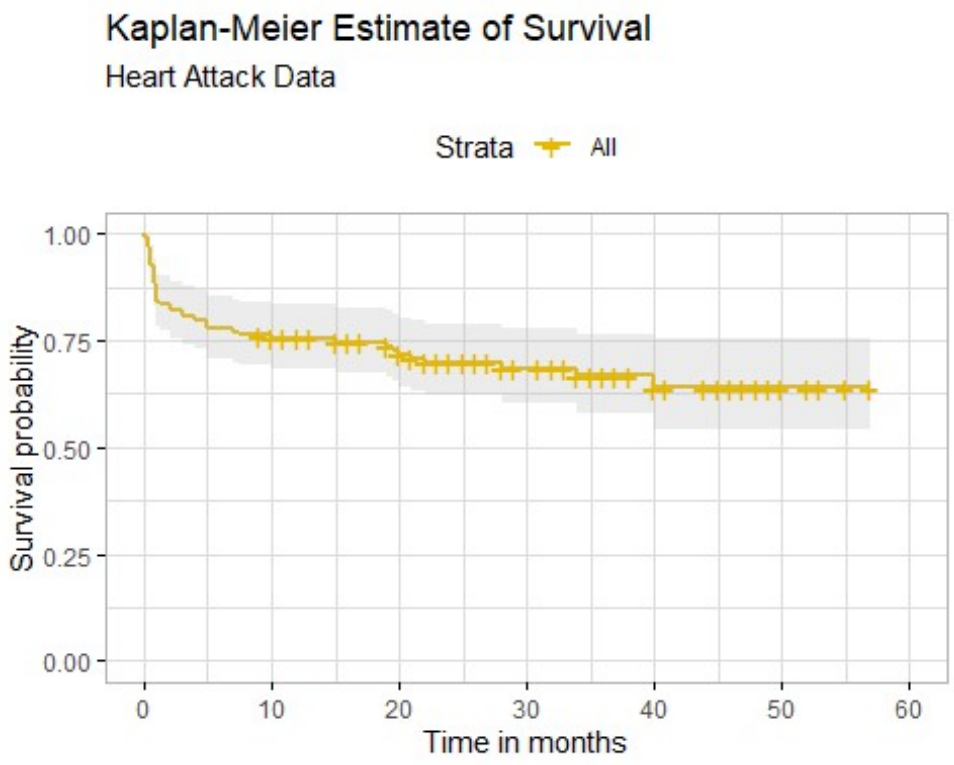
The concordance value of 0.627 indicates that the model has moderate predictive accuracy.

Overall, this model suggests that age at heart attack is a significant predictor of survival time in this dataset.

```
# Visualize the survival curves based on age groups
ggsurvplot(survfit(surv_model), data = heart_data, pval = TRUE,
           conf.int = TRUE,
  surv.median.line = "hv",
  ggtheme = theme_light(),
  palette = c("#E7B800", "#2E9FDF"),
  xlim = c(0, 60),
  xlab = "Time in months",
  ylab = "Survival probability",
  title = "Kaplan-Meier Estimate of Survival",
  subtitle = "Heart Attack Data")
```

```
## Warning in .pvalue(fit, data = data, method = method, pval = pval,
pval.coord = pval.coord, : There are no survival curves to be compared.
##  This is a null model.
```

```
## Warning in .add_surv_median(p, fit, type = surv.median.line, fun = fun, :
## Median survival not reached.
```

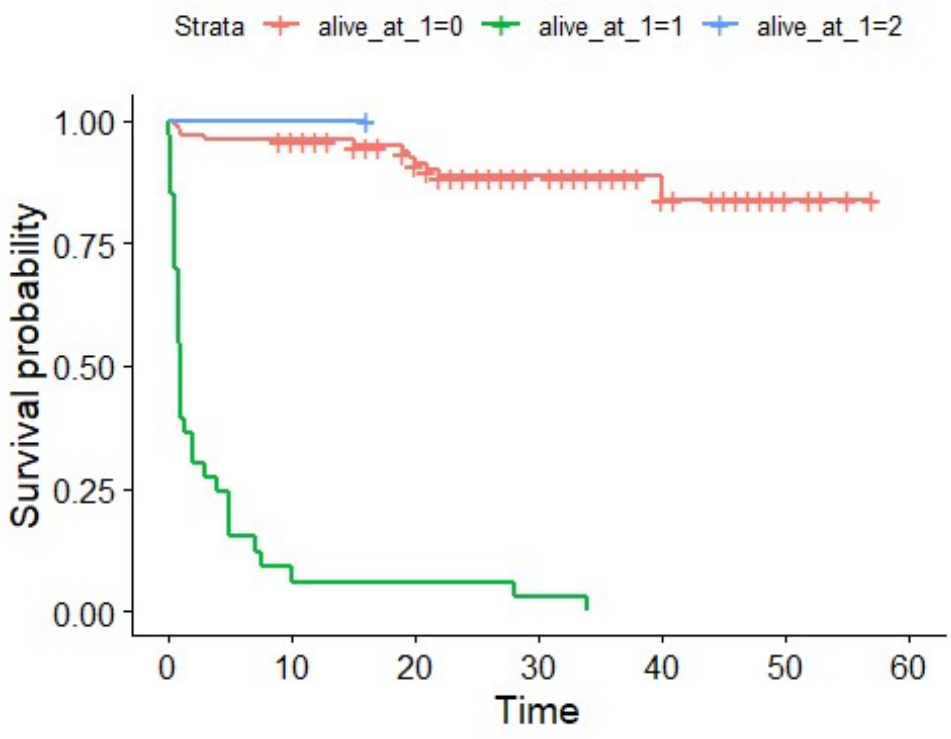


Here is an example of how you can stratify the analysis into standard vs experimental groups, display the strata using the `summary` function, plot the strata using `ggsurvplot`, and perform a log-rank test to compare the survival curves of the two groups:

```
# Load the necessary libraries
library(tidyverse)
library(survival)
library(survminer)

# Create a Surv object to represent the survival time and censoring
information
survival_object <- with(heart_data, Surv(survival, still_alive))

# Fit a Kaplan-Meier model stratified by group using the survfit function
fit_stratified <- survfit(survival_object ~ alive_at_1, data = heart_data)

# Display the strata using the summary function
summary(fit_stratified)

## Call: survfit(formula = survival_object ~ alive_at_1, data = heart_data)
##
##                 alive_at_1=0
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##   0.50     99       1    0.990  0.0100        0.970        1.000
##   0.75     98       1    0.980  0.0141        0.952        1.000
##   1.00     97       1    0.970  0.0172        0.937        1.000
##   3.00     96       1    0.960  0.0198        0.922        0.999
##  15.00     85       1    0.948  0.0225        0.905        0.994
##  19.00     78       1    0.936  0.0253        0.888        0.987
##  19.50     74       1    0.923  0.0280        0.870        0.980
##  20.00     73       1    0.911  0.0303        0.853        0.972
##  21.00     71       1    0.898  0.0325        0.837        0.964
##  22.00     69       1    0.885  0.0345        0.820        0.955
##  40.00     19       1    0.838  0.0559        0.736        0.955
##
##                 alive_at_1=1
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##   0.03     33       1   0.9697  0.0298       0.9129        1.000
##   0.25     32       4   0.8485  0.0624       0.7346        0.980
##   0.50     28       5   0.6970  0.0800       0.5566        0.873
##   0.75     23       5   0.5455  0.0867       0.3995        0.745
##   1.00     18       5   0.3939  0.0851       0.2580        0.601
##   1.25     13       1   0.3636  0.0837       0.2316        0.571
##   2.00     12       2   0.3030  0.0800       0.1806        0.508
##   3.00     10       1   0.2727  0.0775       0.1562        0.476
##   4.00      9       1   0.2424  0.0746       0.1326        0.443
##   5.00      8       3   0.1515  0.0624       0.0676        0.340
##   7.00      5       1   0.1212  0.0568       0.0484        0.304
##   7.50      4       1   0.0909  0.0500       0.0309        0.267
##  10.00      3       1   0.0606  0.0415       0.0158        0.232
```

```
##  28.00      2       1   0.0303  0.0298       0.0044         0.209
##  34.00      1       1   0.0000     NaN           NA           NA
##
##                 alive_at_1=2
##      time n.risk n.event survival std.err lower 95% CI upper 95% CI
```

```
# Generate a Kaplan-Meier curve for each stratum using the ggsurvplot
function from the survminer package
ggsurvplot(fit_stratified, data = heart_data)
```




```
# Perform a log-rank test to compare the survival curves of the two groups
survdiff(survival_object ~ alive_at_1, data = heart_data)
```

```
## Call:
## survdiff(formula = survival_object ~ alive_at_1, data = heart_data)
##
##                N Observed Expected (O-E)^2/E (O-E)^2/V
## alive_at_1=0 99       11   37.907    19.099   150.148
## alive_at_1=1 33       33    5.781   128.158   160.702
## alive_at_1=2  1        0    0.312     0.312     0.322
##
##  Chisq= 161  on 2 degrees of freedom, p= <2e-16
```

The first table shows the number of observations (`N`), the number of observed events (`Observed`), the expected number of events under the null hypothesis (`Expected`), and two test statistics (`(O-E)^2/E` and `(O-E)^2/V`) for each group defined by the `alive_at_1` variable.

The second line shows the overall chi-squared test statistic (`Chisq`) with its degrees of freedom (`df`) and p-value (`p`). In this case, the p-value is very small (less than 2e-16), indicating that there is a statistically significant difference between the survival curves of the groups defined by `alive_at_1`.

In summary, these results suggest that there is a significant difference in survival between the groups defined by the `alive_at_1` variable.