

survival package

(AST405) Lifetime data analysis

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Lecture Outline

Subsection 1

Introduction to R package survival

Time-to-event data

- Time-to-event data are defined as $\{(t_i, \delta_i), i = 1, \dots, n\}$
 - ▶ $t_i \rightarrow$ observed time
 - ▶ $\delta_i \rightarrow$ censoring indicator (1=failure, 0=censored)

Time-to-event data

- Defining time and censoring indicator in R for the following sample of five observations

20, 13⁺, 10, 25, 18⁺

```
dat0 <- tibble(  
  time = c(20, 13, 10, 25, 18),  
  status = c(1, 0, 1, 1, 0)  
)
```

Time-to-event data

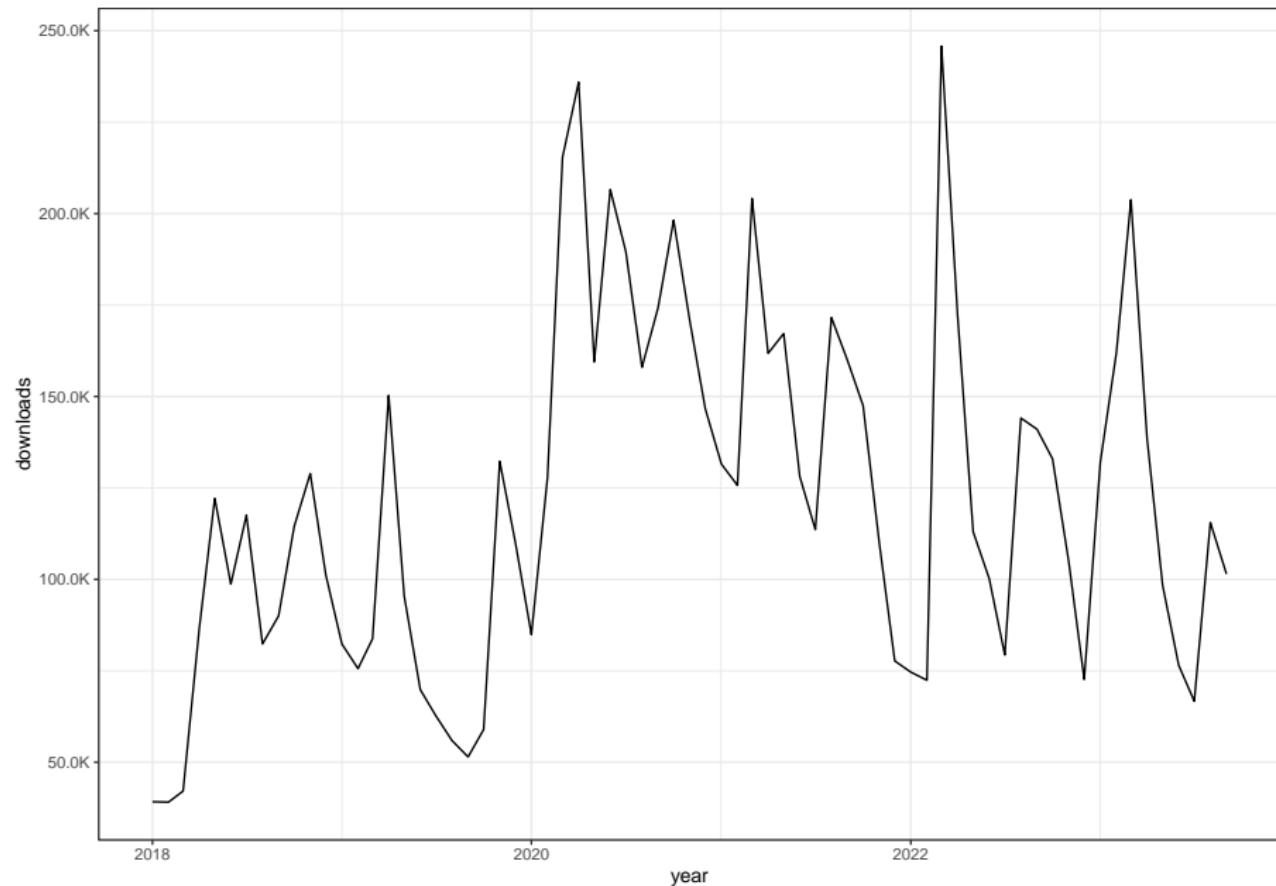
```
dat0
```

```
# A tibble: 5 x 2
  time status
  <dbl>  <dbl>
1     20     1
2     13     0
3     10     1
4     25     1
5     18     0
```

survival package

- There are a number of R packages available for analyzing time-to-event data
- The survival package will be used for the course, the current (January 2025) version of survival package is 3.8-3
- Author, contributors, and maintainer of survival package
 - ▶ Terry M Therneau [aut, cre]
 - ▶ Thomas Lumley
 - ▶ Atkinson Elizabeth
 - ▶ Crowson Cynthia
- So far there are about 8.41 millions downloads of the survival package (between the years 2015 and 2023)

survival package



PL estimate

- `survival::survfit()` function is used to obtain non-parametric estimate survivor function

```
survfit(Surv(time, time2, event) ~ x, data)
```

- `Surv` → creates a survival object, which has arguments such as, `time`, `time2`, `event`, and `type` (censoring type “right”, “left”, “interval”, etc.)
- `time` → observed time (numeric object)
- `event` → censoring status (1=failure, 0=censored)
- `x` → strata (categorical variable), `x=1` when stratified analysis is not required (single curve)

PL estimate

- Some important arguments of `survfit()` function
 - ▶ `stype` → 1 (direct estimation of survivor function), 2 (survivor function estimated from cumulative hazard function)
 - ▶ `ctype` → method used to estimate cumulative hazard function (1=Nelson Aalen, 2=Fleming-Harrington)
 - ▶ `conf.type` → available options include ("none", "plain", "log" (default), "log-log", and "logit")

Example |

```
dim(gehan65)
```

```
[1] 42 3
```

```
print(gehan65, n = 6)
```

```
# A tibble: 42 x 3
  time status drug
  <dbl>   <dbl> <chr>
1     6     1  6-MP
2     6     1  6-MP
3     6     1  6-MP
4     6     0  6-MP
5     7     1  6-MP
6     9     0  6-MP
# i 36 more rows
```

Example |

```
gehan65 %>%  
  count(drug, status)
```

```
# A tibble: 3 x 3  
  drug     status     n  
  <chr>    <dbl> <int>  
1 6-MP        0     12  
2 6-MP        1      9  
3 placebo     1     21
```

Example |

```
dat6MP <- gehan65 %>%
  filter(drug == "6-MP")
```

```
mod1 <- survfit(Surv(time = time, event = status) ~ 1,
                  conf.type = "plain",
                  data = dat6MP)
```

- Default `conf.type` is `log`

Example |

```
names(mod1)
```

```
[1] "n"          "time"        "n.risk"       "n.event"      "n.censor"
[7] "std.err"     "cumhaz"       "std.chaz"     "type"         "logse"
[13] "conf.type"   "lower"        "upper"        "t0"           "call"
```

Example |

```
head(mod1$time)
```

```
[1] 6 7 9 10 11 13
```

```
head(mod1$n.risk)
```

```
[1] 21 17 16 15 13 12
```

```
head(mod1$n.event)
```

```
[1] 3 1 0 1 0 1
```

```
head(mod1$surv)
```

```
[1] 0.8571429 0.8067227 0.8067227 0.7529412 0.7529412 0.690196
```

Example |

```
names(summary(mod1))
```

```
[1] "n"                  "time"                "n.risk"              "n.event"  
[5] "n.censor"           "surv"                 "std.err"              "cumhaz"  
[9] "std.chaz"            "type"                 "logse"                "conf.int"  
[13] "conf.type"           "lower"                "upper"                "t0"  
[17] "call"                "table"                "rmean.endtime"
```

Example |

```
summary(mod1$table)
```

records	n.max	n.start	events	rmean	se(rmean)	
21.000000	21.000000	21.000000	9.000000	23.287395	2.827468	23
0.95UCL						
NA						

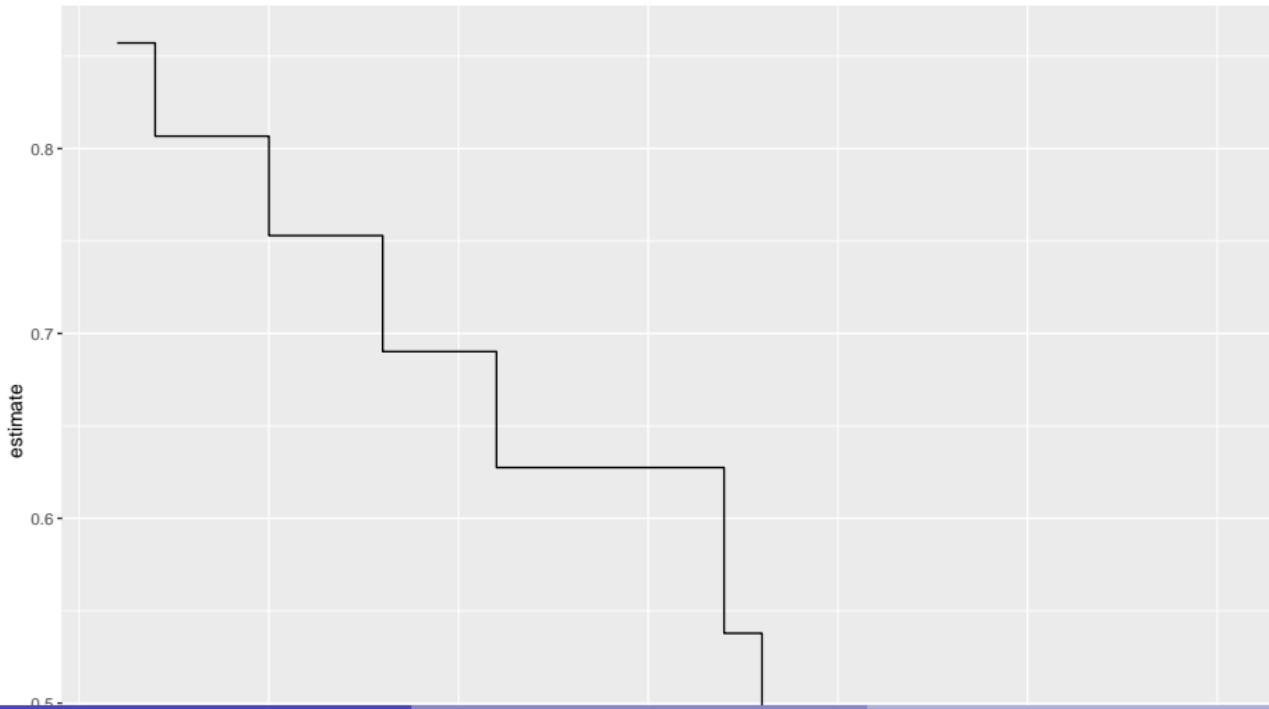
Example |

```
# broom::tidy(mod1)
print(broom::tidy(mod1), n = 6)

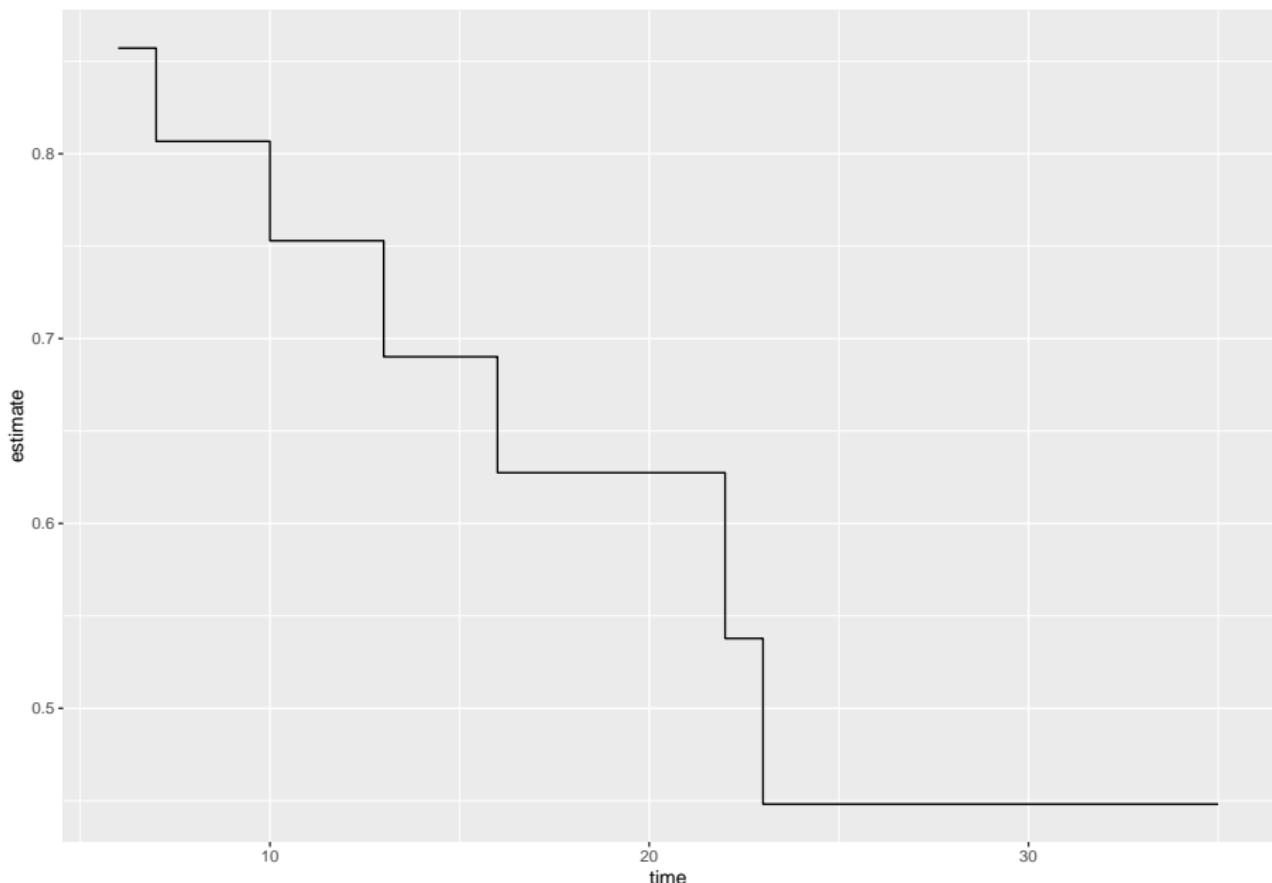
# A tibble: 16 x 8
  time n.risk n.event n.censor estimate std.error conf.high conf.low
  <dbl>   <dbl>   <dbl>   <dbl>     <dbl>     <dbl>      <dbl>      <dbl>
1     6     21      3       1     0.857    0.0891     1
2     7     17      1       0     0.807    0.108     0.977
3     9     16      0       1     0.807    0.108     0.977
4    10     15      1       1     0.753    0.128     0.942
5    11     13      0       1     0.753    0.128     0.942
6    13     12      1       0     0.690    0.155     0.900
# i 10 more rows
```

Plot of survivor function

```
broom::tidy(mod1) %>%
  ggplot() +
  geom_step(aes(time, estimate))
```

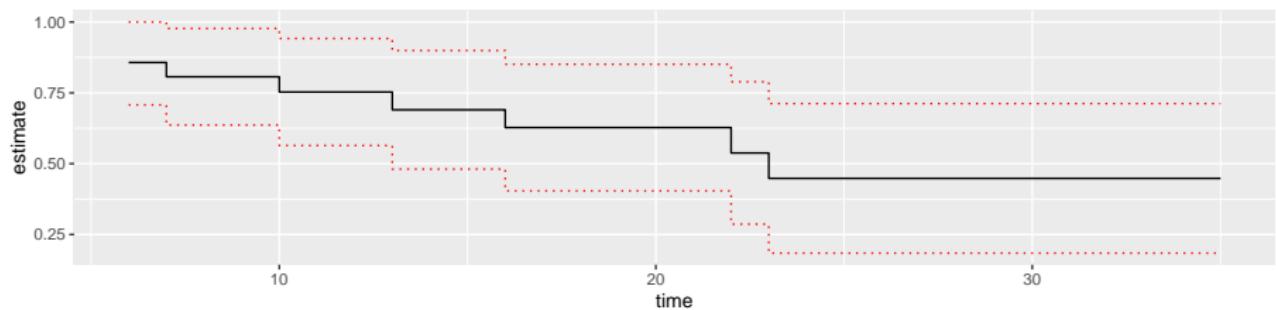


Plot of survivor function

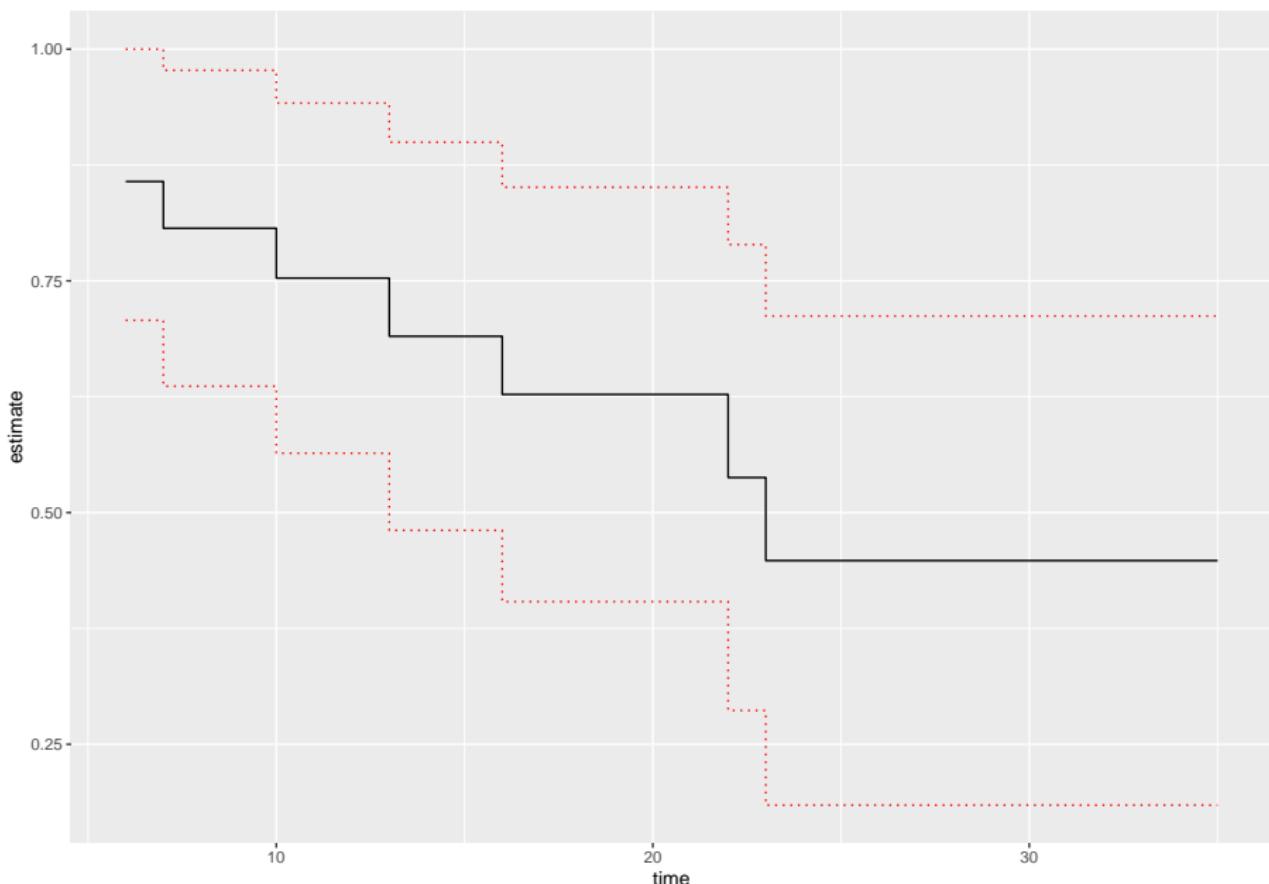


Plot of survivor function

```
tidy(mod1) %>%
  ggplot() +
  geom_step(aes(time, estimate)) +
  geom_step(aes(time, conf.high), linetype = "dotted", col = "red") +
  geom_step(aes(time, conf.low), linetype = "dotted", col = "red")
```



Plot of survivor function



Quantiles

```
qsurv <- function(mod, p) {  
  tmod <- broom::tidy(mod)  
  if (min(tmod$estimate) > (1 - p)) return(NA_real_)  
  else {  
    tmod %>%  
      filter(estimate <= (1 - p)) %>%  
      pull(time) %>%  
      min()  
  }  
}
```

Quantiles

- First quartile

```
qsurv(mod1, .25)
```

```
[1] 13
```

- Median

```
qsurv(mod1, .5)
```

```
[1] 23
```

Example |

```
mod2 <- survfit(  
  Surv(time = time, event = status) ~ drug,  
  data = gehan65,  
  conf.type = "plain"  
)
```

Example |

```
broom::tidy(mod2)
```

```
# A tibble: 28 x 9
  time n.risk n.event n.censor estimate std.error conf.high conf.low strata
  <dbl>   <dbl>   <dbl>   <dbl>     <dbl>    <dbl>     <dbl>    <dbl>   <chr>
1     6     21      3      1     0.857   0.0891     1     0.707 drug=6-MP
2     7     17      1      0     0.807   0.108    0.977   0.636 drug=6-MP
3     9     16      0      1     0.807   0.108    0.977   0.636 drug=6-MP
4    10     15      1      1     0.753   0.128    0.942   0.564 drug=6-MP
5    11     13      0      1     0.753   0.128    0.942   0.564 drug=6-MP
6    13     12      1      0     0.690   0.155    0.900   0.481 drug=6-MP
7    16     11      1      0     0.627   0.182    0.851   0.404 drug=6-MP
8    17     10      0      1     0.627   0.182    0.851   0.404 drug=6-MP
9    19      9      0      1     0.627   0.182    0.851   0.404 drug=6-MP
10   20      8      0      1     0.627   0.182    0.851   0.404 drug=6-MP
# i 18 more rows
```

Example |

```
broom::tidy(mod2) %>%
  select(time, estimate, strata)

# A tibble: 28 x 3
  time   estimate strata
  <dbl>     <dbl> <chr>
1     6     0.857 drug=6-MP
2     7     0.807 drug=6-MP
3     9     0.807 drug=6-MP
4    10     0.753 drug=6-MP
5    11     0.753 drug=6-MP
6    13     0.690 drug=6-MP
7    16     0.627 drug=6-MP
8    17     0.627 drug=6-MP
9    19     0.627 drug=6-MP
10   20     0.627 drug=6-MP
# i 18 more rows
```

Example |

```
broom:::tidy(mod2) %>%
  ggplot() +
  geom_step(aes(time, estimate, col = strata))
```

