University of Edinburgh, School of Mathematics

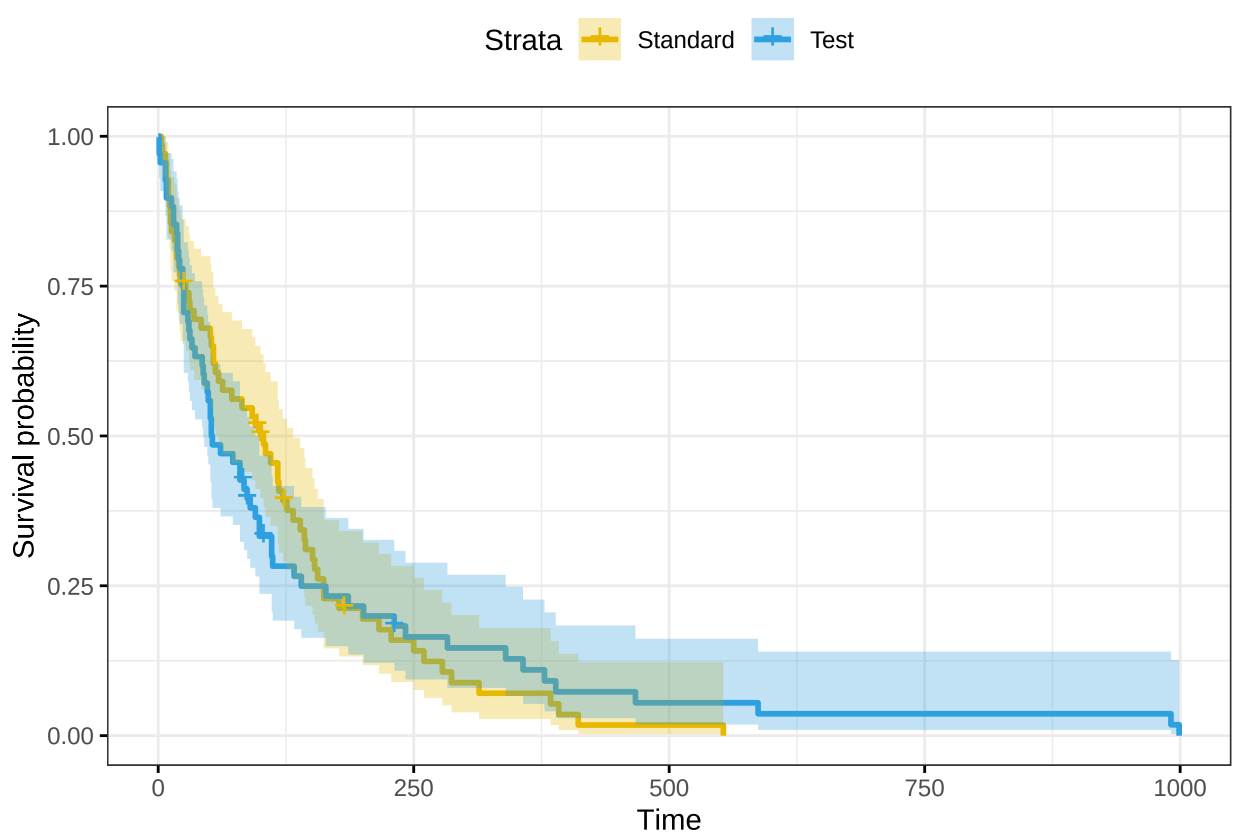
Biostatistics (MATH11230), 2021/2022

Vanda Inácio

We start by reproducing the figure in slide 2.

```
require(survival)
fit_veteran <- survfit(Surv(time, status) ~ trt, data = veteran)

require(survminer)
p <- ggsurvplot(fit_veteran,
data = veteran,
size = 1,
palette = c("#E7B800", "#2E9FDF"),
conf.int = TRUE,
legend.labs =  c("Standard", "Test"),
ggtheme = theme_bw()
)
print(p)
```



We now reproduce the results of the toy example and also illustrate the use of the `survdiff` function.

```
time <- c(3.1, 6.8, 9, 9, 11.3, 16.2, 8.7, 9, 10.1, 12.1, 18.7, 23.1)
status <- c(1, 0, 1, 1, 0, 1, 1, 1, 0, 0, 1, 0)
group <- c(rep(1, 6), rep(2, 6))
res_toy <- survdiff(Surv(time, status) ~ group)
res_toy
```

```
## Call:
## survdiff(formula = Surv(time, status) ~ group)
##
##         N Observed Expected (O-E)^2/E (O-E)^2/V
## group=1 6        4     2.57     0.800      1.62
## group=2 6        3     4.43     0.463      1.62
##
##  Chisq= 1.6  on 1 degrees of freedom, p= 0.2
```

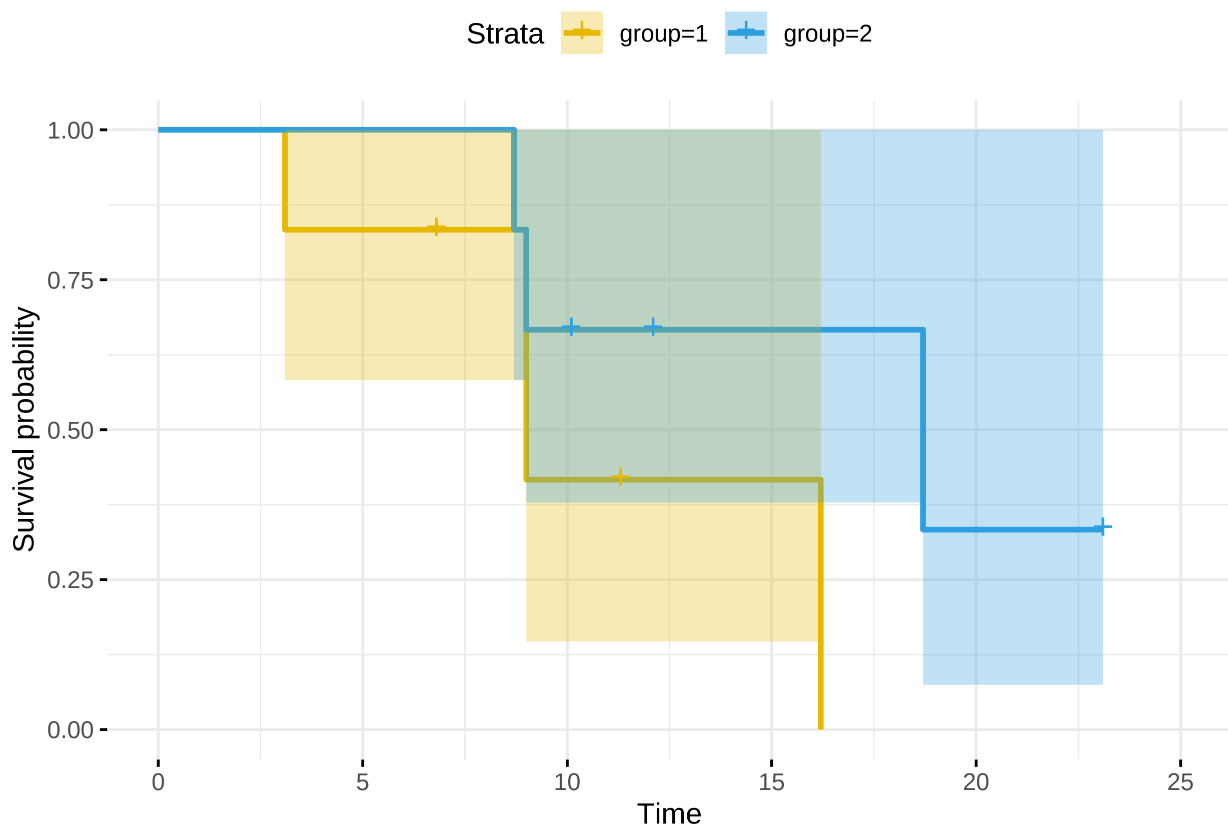
```
#observed number events across all timepoints
o <- 4
#expected number events across all timepoints
e <- (6/12) + (4/10) + (12/9) + (1/3)
#variance  of the U_L statistic
v <- (6*6*11)/((12^2)*11) + (4*6*9)/((10^2)*9) +
     (4*5*3*6)/((9^2)*8) + (1*2*1*2)/((3^2)*2) + 0
((o-e)^2)/v
```

```
## [1] 1.620508
```

```
#p-value
pchisq(((o-e)^2)/v, df = 1, lower.tail = FALSE)
```

```
## [1] 0.2030209
```

```
require(survminer)
toy_data <- data.frame("time" = time, "status" = status, "group" = group)
fit_toy <- survfit(Surv(time, status) ~ group, data = toy_data)
ggsurvplot(fit_toy,
           conf.int = 0.95,
           palette = c("#E7B800", "#2E9FDF"),
           ggtheme = theme_minimal(),
           data = toy_data
           )
```



Let us now compare the log-rank test and its corresponding weighted versions using the veteran dataset.

```
res_veteran <- survdiff(Surv(time, status) ~ trt, data = veteran)
res_veteran
```

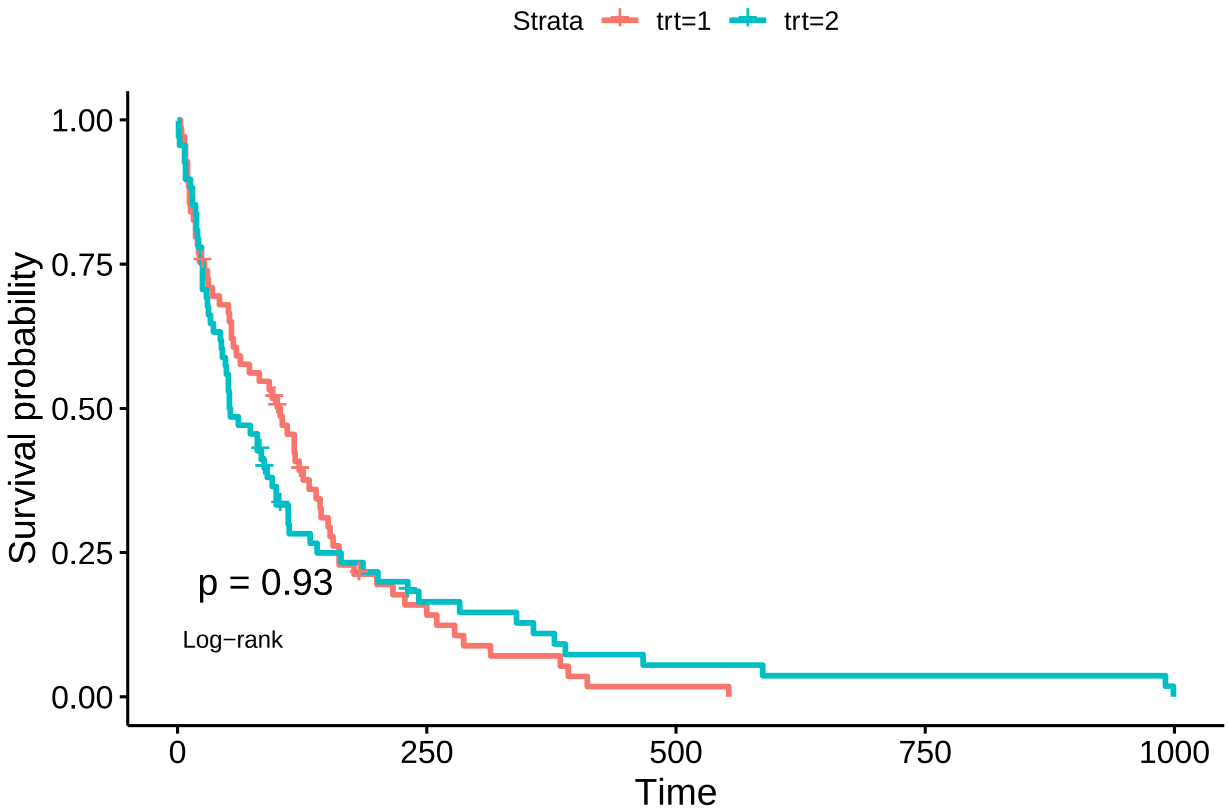
```
## Call:
## survdiff(formula = Surv(time, status) ~ trt, data = veteran)
##
##         N Observed Expected (O-E)^2/E (O-E)^2/V
## trt=1 69       64     64.5   0.00388   0.00823
## trt=2 68       64     63.5   0.00394   0.00823
##
##  Chisq= 0  on 1 degrees of freedom, p= 0.9
```

```
res_veteran_peto <- survdiff(Surv(time, status) ~ trt, data = veteran, rho = 1)
res_veteran_peto
```

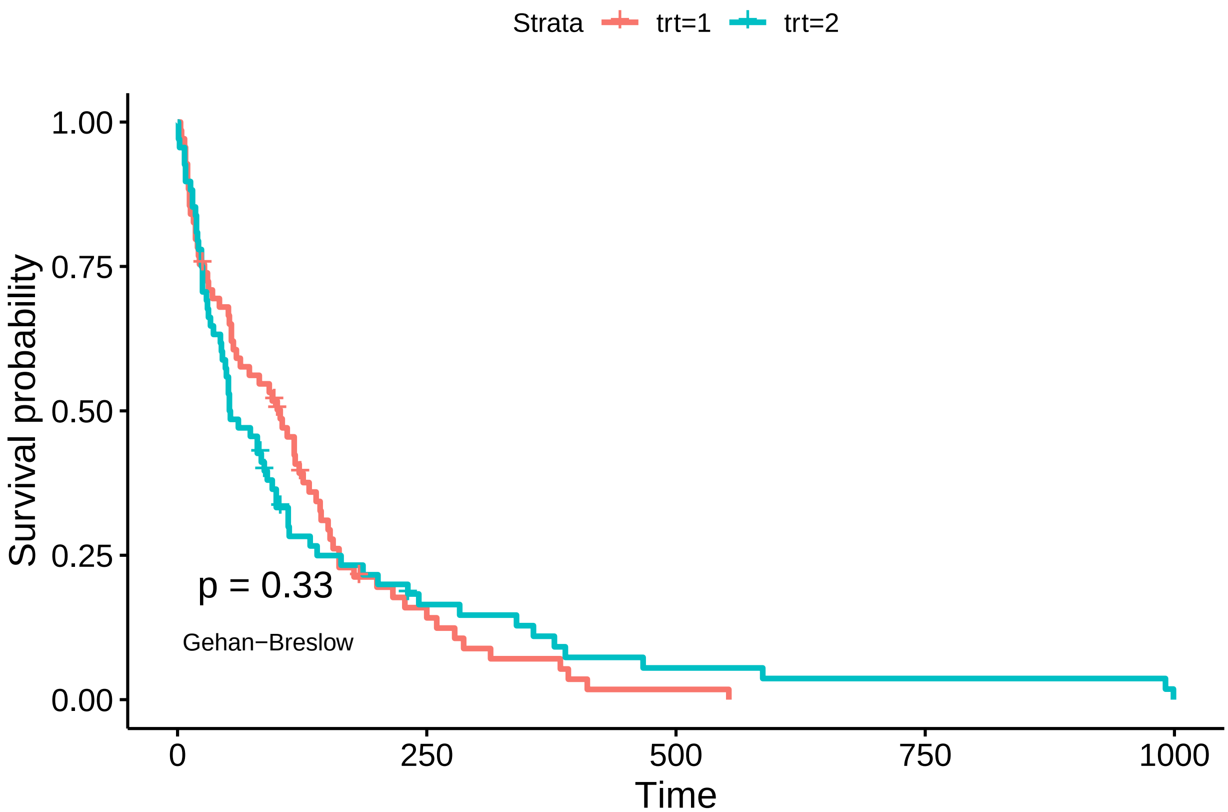
```
## Call:
## survdiff(formula = Surv(time, status) ~ trt, data = veteran,
##     rho = 1)
##
##         N Observed Expected (O-E)^2/E (O-E)^2/V
## trt=1 69     32.2     35.4     0.279     0.871
## trt=2 68     35.2     32.1     0.308     0.871
##
##  Chisq= 0.9  on 1 degrees of freedom, p= 0.4
```

```
#p-value in the plot corresponds to log rank test
ggsurvplot(fit_veteran,
           data = veteran,
```

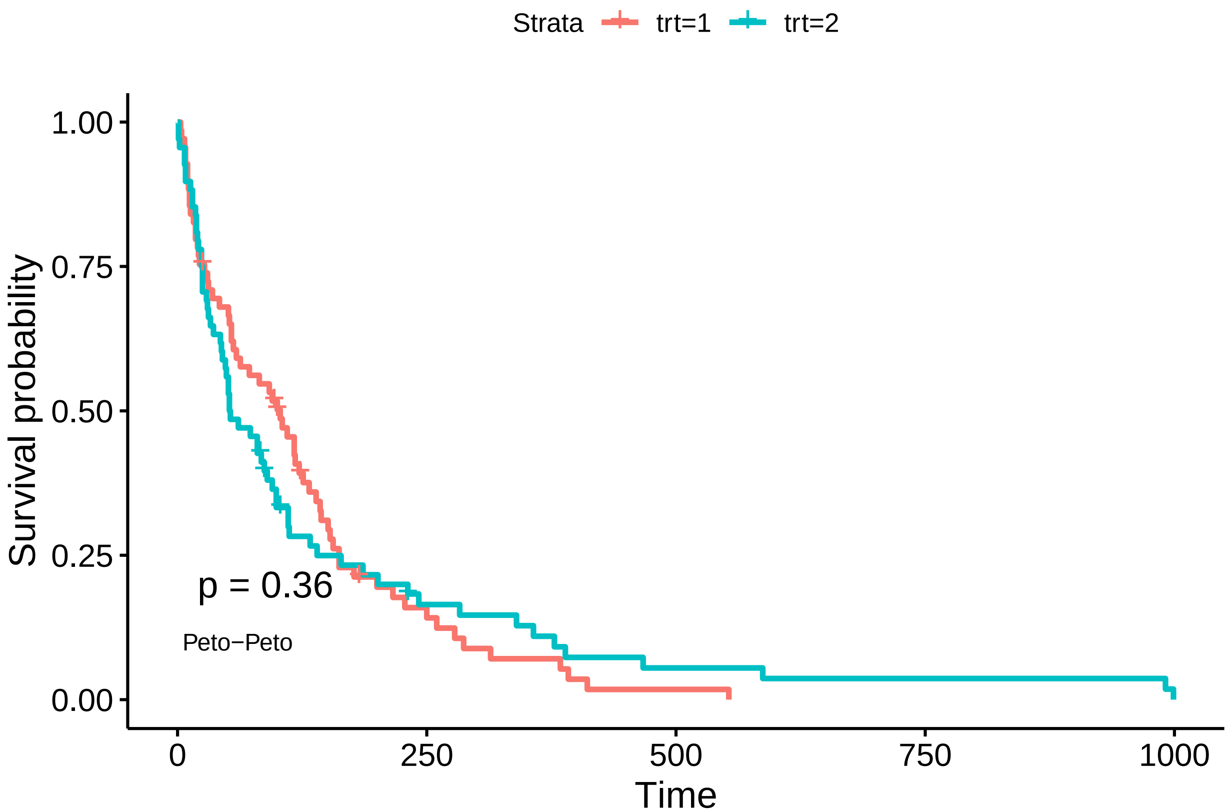
```
          pval = TRUE,
          pval.method = TRUE,
          log.rank.weights = "1",
          pval.method.coord = c(5, 0.1),
          pval.method.size = 3)
```




```
#p-value in the plot corresponds to Gehan-Breslow test
ggsurvplot(fit_veteran,
          data = veteran,
          pval = TRUE,
          pval.method = TRUE,
          log.rank.weights = "n",
          pval.method.coord = c(5, 0.1),
          pval.method.size = 3)
```




```
#p-value in the plot corresponds to Peto test
ggsurvplot(fit_veteran,
           data = veteran,
           pval = TRUE,
           pval.method = TRUE,
           log.rank.weights = "S1",
           pval.method.coord = c(5, 0.1),
           pval.method.size = 3)
```



To illustrate the extension of the log rank test for the comparison of multiple survival curves let us use the veteran dataset again but now comparing the survival experience for the different cell types (1=squamous, 2=smallcell, 3=adeno, 4=large).

```
res_veteran_multiple <- survdiff(Surv(time, status) ~ celltype, data = veteran)
res_veteran_multiple
```

```
## Call:
## survdiff(formula = Surv(time, status) ~ celltype, data = veteran)
##
##                      N Observed Expected (O-E)^2/E (O-E)^2/V
## celltype=squamous   35       31     47.7      5.82     10.53
## celltype=smallcell  48       45     30.1      7.37     10.20
## celltype=adeno      27       26     15.7      6.77      8.19
## celltype=large      27       26     34.5      2.12      3.02
##
##  Chisq= 25.4  on 3 degrees of freedom, p= 1e-05
```

```
#Reconstructing the test statistic manually
U <- res_veteran_multiple$obs[1:3] - res_veteran_multiple$exp[1:3]
V <- res_veteran_multiple$var[1:3, 1:3]
t(U)%*%solve(V)%*%U
```

```
##         [,1]
## [1,] 25.4037
```