# Survival Analysis

## Lecture 4

Marta Fiocco[1,2] & Hein Putter [1]

(1) Department of Medical Statistics and Bioinformatics
Leiden University Medical Center
(2) Mathematical Institute Leiden University

# Outline

KMsurv packages

CI S(t)

R code

Confidence intervals

Confidence bands

Mean and median $S(t)$
- Example

Follow-up
- Descriptives
- Reverse Kaplan-Meier

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- A lot of functions (and data sets) for survival analysis are in the package survival
- we need to load it at first

```
>  library(survival) #load library
>  library(help=survival) # list of available functions and data sets
```

- data sets from Klein and Moeschberger

```
> library(KMsurv)
> library(help=KMsurv)
> # look at a specific data set in the library
> data(lung)
> # print the first 6 rows of data set lung
> head(lung)
  time death time2 death2
1  139     1   139      1
2  304     1   304      1
3  193     1   193      1
4  248     1   248      1
5   27     1    27      1
6  210     1   210      1
```

# Some R code to begin with

- look at the time to event in the data set **aml** with function `Surv`

```
> ?Surv # see the help
> Surv(aml$time, aml$status)
 [1]   9    13   13+  18   23   28+  31   34   45+  48  161+   5    5
[16]  12   16+  23   27   30   33   43   45
```

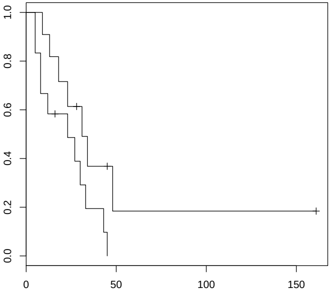
- Kaplan-Meier and Nelson-Aalen estimator obtained with the R function `survfit()`
- estimate the distribution of lifetimes non-parametrically, based on right censored observations
- use Kaplan-Meier estimator; the R function to perform this is `survfit()`

```
> #estimate survival curve for aml data
> fit <- survfit(Surv(time, status) ~ x, data = aml)

> summary(fit)
Call: survfit(formula = Surv(time, status) ~ x, data = aml)

                x=Maintained
 time n.risk n.event survival std.err lower 95% CI upper 95% CI
    9     11       1    0.909  0.0867       0.7541        1.000
   13     10       1    0.818  0.1163       0.6192        1.000
   18      8       1    0.716  0.1397       0.4884        1.000
   23      7       1    0.614  0.1526       0.3769        0.999
   31      5       1    0.491  0.1642       0.2549        0.946
   34      4       1    0.368  0.1627       0.1549        0.875
   48      2       1    0.184  0.1535       0.0359        0.944
```

- output from `summary(fit)`

```
                x=Nonmaintained
time n.risk n.event survival std.err lower 95% CI upper 95% CI
   5     12       2   0.8333  0.1076       0.6470        1.000
   8     10       2   0.6667  0.1361       0.4468        0.995
  12      8       1   0.5833  0.1423       0.3616        0.941
  23      6       1   0.4861  0.1481       0.2675        0.883
  27      5       1   0.3889  0.1470       0.1854        0.816
  30      4       1   0.2917  0.1387       0.1148        0.741
  33      3       1   0.1944  0.1219       0.0569        0.664
  43      2       1   0.0972  0.0919       0.0153        0.620
  45      1       1   0.0000     NaN           NA           NA
```

```
> # to know what has been estimated with survfit
> names(summary(fit))
 [1] "surv"          "time"          "n.risk"        "n.event"
 [5] "conf.int"      "type"          "table"         "std.err"
 [9] "lower"         "upper"         "strata"        "rmean.endtime"
[13] "call"
> # plot Kaplan-Meier estimator, ticks for the censored observations.
> plot(fit)
```



# Standard errors in R

- look at the standard error from `survfit` and `summary.survit(fit)`

```
> fit$std.err
 [1] 0.09534626 0.14213381 0.19508758 0.24873417 0.24873417 0.33446777
 [7] 0.44181673 0.44181673 0.83378775 0.83378775 0.12909944 0.20412415
[13] 0.24397502 0.24397502 0.30472470 0.37796447 0.47559487 0.62678317
[19] 0.94491118        Inf
>
> sfit$std.err
 [1] 0.08667842 0.11629130 0.13966497 0.15263233 0.16419327 0.16266889
 [7] 0.15349275 0.10758287 0.13608276 0.14231876 0.14813006 0.14698618
[13] 0.13871517 0.12187451 0.09186636        NaN
```

- the former is the standard error for the estimated cumulative hazards $\widehat{H}(t)$
- the latter is the standard error for the survival $\widehat{S}(t)$

# Cumulative hazard function

- The cumulative hazard function and the survival function are related in the following way for continuous data:

$$S(t) = exp(-H(t))$$

- $H(t)$ may be obtained by the inverse transformation of the Kaplan-Meier estimate

$$\hat{H}(t) = -\log \hat{S}(t)$$

- Another method to estimate $H(t)$ is the Nelson-Aalen estimator:

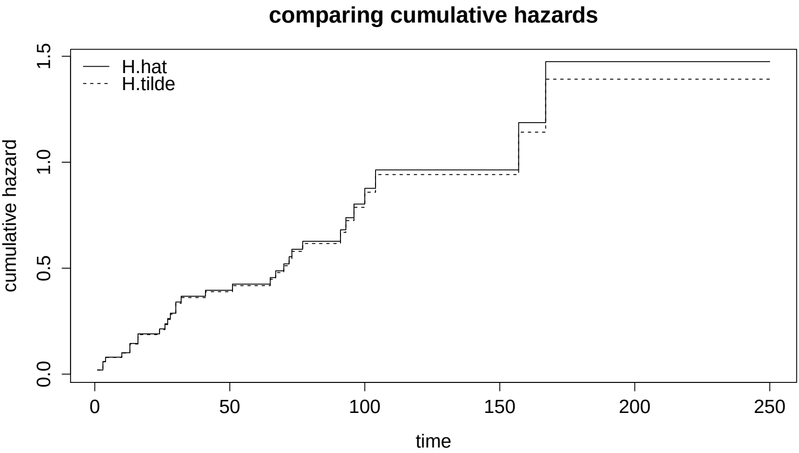
$$\tilde{H}(t) = \sum_{t_i \leq t} \frac{d_i}{Y_i}, \quad \sigma_H^2 = \sum_{t_i \leq t} \frac{d_i}{Y_i^2}$$

- no function in the survival package calculates either form automatically, the object returned by `summary(survfit())` can be used to calculate the estimates

```
data(tongue); attach(tongue)
my.surv <- Surv(time[type==1], delta[type==1])
my.fit <- summary(survfit(my.surv ~ 1))
H.hat <- -log(my.fit$surv)
H.hat <- c(H.hat, tail(H.hat, 1))
```

- construct Nelson-Aalen

```
h.sort.of <- my.fit$n.event / my.fit$n.risk
H.tilde <- cumsum(h.sort.of)
H.tilde <- c(H.tilde, tail(H.tilde, 1))
plot(c(my.fit$time, 250), H.hat, xlab="time", ylab="cumulative hazard"
main="comparing cumulative hazards", ylim=range(c(H.hat, H.tilde)),
type="s")
points(c(my.fit$time, 250), H.tilde, lty=2, type="s")
legend("topleft", legend=c("H.hat","H.tilde"), lty=1:2, bty="n")
detach(tongue)
```


comparing cumulative hazards
H.hat
H.tilde
cumulative hazard
0.0
0.5
1.0
1.5
time
0
50
100
150
200
250

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# Pointwise confidence intervals for $\widehat{S}(t)$

- Product-Limit estimator provides an estimate of the survival
- the corresponding standard error provides some limited information about the precision of the estimate
- use these estimators to provide confidence intervals for the survival function at a fixed time $t_0$
- construct the intervals to assure, with a given confidence level $1-\alpha$ that the true value of the survival function, at a predetermined time $t_0$ falls in this interval
- most common used confidence interval

$$\hat{S}(t_o) - Z_{1-\alpha/2}\sigma_S(t_o)\hat{S}(t_o)\,,\, \hat{S}(t_o) + Z_{1-\alpha/2}\sigma_S(t_o)\hat{S}(t_o)$$

# Pointwise confidence intervals for $\widehat{S}(t)$

- $\sigma^2_S(t) = \widehat{V}[\widehat{S}(t)]/\widehat{S}^2(t)$
- recall $\widehat{V}[\widehat{S}(t)] = \widehat{S}(t)^2 \sum_{t_i \le t} \frac{d_i}{Y_i(Y_i - d_i)}$
- $Z_{1-\alpha/2}$: $1 - \alpha/2$ percentile of a $N(0,1)$ distribution
- this is the confidence interval constructed by most statistical packages
- better confidence intervals can be constructed by first transforming $\widehat{S}(t_0)$
- The "log"-transformed confidence interval is based on first finding a confidence interval for the log of the cumulative hazard function (called log-log transformed interval since the cumulative hazard function is the negative log of the survival function $H(t) = -\log(S(t))$)

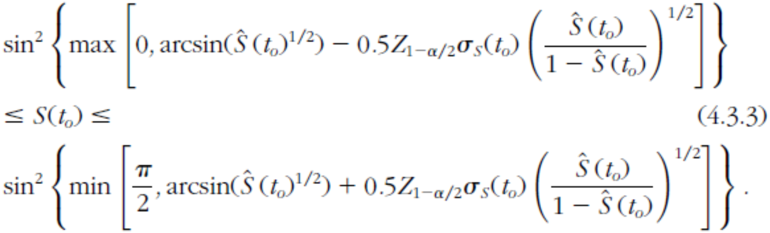
# Pointwise confidence intervals for $\widehat{S}(t)$

- the $100 \times (1-\alpha)\%$ log-transformed confidence interval for the survival function at $t_0$ is given by

$$[\widehat{S}(t_0)^{1/\theta}, \widehat{S}(t_0)^{\theta}], \quad \theta = \exp\{\frac{Z_{1-\alpha/2}\sigma_S^2(t_0)}{\log[\widehat{S}(t_0)]}\}$$

- the second transformation is an arcsine-square root transformation of the survival function; this yields the following $100 \times (1-\alpha)\%$ confidence interval for the survival function

# Second transformation for the confidence intervals



$$\sin^2\left\{\max\left[0, \arcsin(\hat{S}(t_o)^{1/2}) - 0.5Z_{1-\alpha/2}\sigma_S(t_o)\left(\frac{\hat{S}(t_o)}{1-\hat{S}(t_o)}\right)^{1/2}\right]\right\}$$
$$\le S(t_o) \le \qquad (4.3.3)$$
$$\sin^2\left\{\min\left[\frac{\pi}{2}, \arcsin(\hat{S}(t_o)^{1/2}) + 0.5Z_{1-\alpha/2}\sigma_S(t_o)\left(\frac{\hat{S}(t_o)}{1-\hat{S}(t_o)}\right)^{1/2}\right]\right\}.$$

# "Plain" intervals

- confidence intervals can be computed on the scale of $S(t)$ as

$$\widehat{S}(t) \pm 1.96\sqrt{\mathrm{var}[\widehat{S}(t)]}$$

- where the variance is computed with the Greenwood's formula
- it has been shown the inferiority of the "plain" intervals in the sense that intervals may extend below zero or above 1
- the plain scale interval has poor coverage properties
- therefore it is better to avoid them

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# Some R code

```
> library(survival)
> data(lung)
kfit <- survfit(Surv(time2,death2) ~1, data=lung)
> print(kfit)
Call: survfit(formula = Surv(time2, death2) ~ 1, data = lung)

records   n.max n.start  events  median 0.95LCL 0.95UCL
     25      25      25      13     210     144      NA
```

- the left-hand side of the formula declares the response variable to be a survival object
- the right-hand side $\sim$ 1 is a null model,

```
>  plot(kfit, col="blue") #ticks for the censored observations
# make the plot a bit nicer...
plot(kfit, mark.time=F, xscale=365.25, xlab="Years", ylab="Survival")
# in the plot command mark.time=F prevents "+" marks from being added
#at the censoring times
# if you want to see censored observations
plot(kfit, mark.time=T, xscale=365.25, xlab="Years", ylab="Survival")
```

# R code

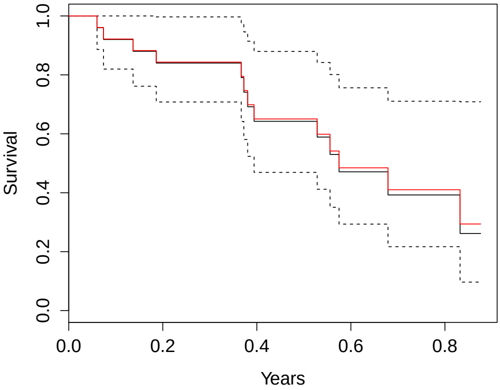
- estimate the survival as suggested by Breslow (1972) $\widetilde{S}(t) = \exp(-\widetilde{H}(t))$

```
> ffit <- survfit(Surv(time2,death2) ~1, data=lung,
type="fleming-harrington")
```

- plot the two estimates along with a 95% confidence interval for the K-M

```
> plot(kfit, mark.time=F, xscale=365.25, xlab="Years",
ylab="Survival")
> lines(ffit,mark.time=F, xscale=365.25, col= "red")
```

# Kaplan-Meier (dark line) and Nelson-Aalen estimates for the lung data set



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# Computation of confidence intervals

- use the estimated disease-free survival function and cumulative hazard rate for ALL patients in Section 1.3 $\widehat{S}(365) = 0.5492$ $\widehat{V}[\widehat{S}(365)] = 0.0812^2$

$$\sigma_S^2(365) = (\frac{0.0812}{0.5492})^2 = 0.1479^2$$

- 95% confidence interval for the survival function at one year $0.5492 \pm 1.96 \times 0.1479 \times 0.5492 = (0.3900, 0.7084)$

# Computation of confidence intervals

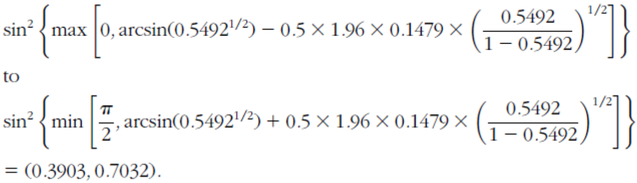
- 95% log-transformed confidence interval for the one year survival function:

$$\theta = \exp\left\{\frac{Z_{1-\alpha/2}\sigma_S^2(t)}{\log[\widehat{S}(t_0)]}\right\} = \exp\left\{\frac{1.96 \times 0.1479}{\log[0.5492]}\right\} = 0.6161$$

- CI: $(0.549211^{1/0.6165}, 0.5492^{0.6165}) = (0.3783, 0.6911)$

# Computation of confidence intervals

- 95% arcsine-square root transformation confidence interval for the one year survival function



$$\sin^2\left\{\max\left[0, \arcsin(0.5492^{1/2}) - 0.5 \times 1.96 \times 0.1479 \times \left(\frac{0.5492}{1-0.5492}\right)^{1/2}\right]\right\}$$

to

$$\sin^2\left\{\min\left[\frac{\pi}{2}, \arcsin(0.5492^{1/2}) + 0.5 \times 1.96 \times 0.1479 \times \left(\frac{0.5492}{1-0.5492}\right)^{1/2}\right]\right\}$$

$$= (0.3903, 0.7032).$$

- three ways of computing pointwise confidence intervals

- how R compute the standard error for the survival?
- use bmt data in library KMsur

```
# estimate disease free survival for ALL group
> resALLDFS <- survfit(Surv(t2,d3) ~1, data=ALL)
> sresALLDFS <- summary(resALLDFS)
> sresALLDFS std.err
 [1] 0.02596722 0.03622354 0.04374408 0.04978449 0.05483610 0.05915279
 [7] 0.06288607 0.06613483 0.07143378 0.07357035 0.07540531 0.07696022
[13] 0.07825178 0.07952180 0.08050884 0.08122321 0.08167208 0.08185981
[19] 0.08178820 0.08145656 0.08086170 0.08026005 0.07929563
```

- R uses Greenwood's formula to estimate the variance of the product-limit estimator
- note that variance can be found with `summary.survfit(survival)`

## Implement formula (4.2.2) Greenwood's variance for $S(t)$

```
> # number of events
> d<-sresALLDFS$n.event
> # number at risk
> y<-sresALLDFS$n.risk
> # estimate S(t) the product limit estimator
> S<- cumprod(1-d/y)
> # estimate the standard error with formula (4.2.2)
> varS<-S^2*cumsum(d/(y*(y-d)))
> # standard error for S(t)
> sqrt(varS)
 [1] 0.02596722 0.03622354 0.04374408 0.04978449 0.05483610 0.05915279
 [7] 0.06288607 0.06613483 0.07143378 0.07357035 0.07540531 0.07696022
[13] 0.07825178 0.07952180 0.08050884 0.08122321 0.08167208 0.08185981
[19] 0.08178820 0.08145656 0.08086170 0.08026005 0.07929563
```

- R uses Greenwood's formula to estimate the standard error of $S(t)$

```
> sresALLDFS std.err
 [1] 0.02596722 0.03622354 0.04374408 0.04978449 0.05483610 0.05915279
 [7] 0.06288607 0.06613483 0.07143378 0.07357035 0.07540531 0.07696022
[13] 0.07825178 0.07952180 0.08050884 0.08122321 0.08167208 0.08185981
[19] 0.08178820 0.08145656 0.08086170 0.08026005 0.07929563
```

- results from formula (4.2.2) implemented

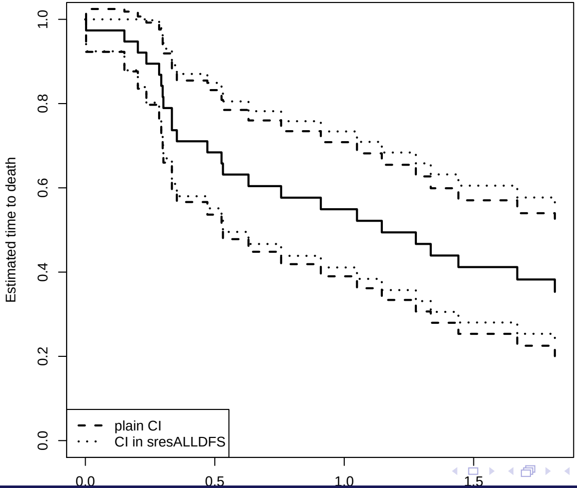
```
> sqrt(varS)
 [1] 0.02596722 0.03622354 0.04374408 0.04978449 0.05483610 0.05915279
 [7] 0.06288607 0.06613483 0.07143378 0.07357035 0.07540531 0.07696022
[13] 0.07825178 0.07952180 0.08050884 0.08122321 0.08167208 0.08185981
[19] 0.08178820 0.08145656 0.08086170 0.08026005 0.07929563
```

- use library `km.ci` to look at different CI

```
> library(km.ci)
> library(help=km.ci)
> CI.ALLDFS <-km.ci(resALLDFS , conf.level=0.95, tl=NA, tu=NA,
 method="log")
# compare with results in sresALLDF
> unique(CI.ALLDFS$upper)
 [1] 1.0259327 1.0210933 1.0109066 0.9978320 0.9828316 0.9664027
 [7] 0.9488421 0.9303438 0.8910352 0.8703953 0.8491781 0.8274268
[13] 0.8051752 0.7819310 0.7581542 0.7338670 0.7090860 0.6838229
[19] 0.6580849 0.6318752 0.6051932 0.5770646 0.5483048
> sresALLDFS$upper
 [1] 1.0000000 1.0000000 1.0000000 0.9978320 0.9828316 0.9664027
 [7] 0.9488421 0.9303438 0.8910352 0.8703953 0.8491781 0.8274268
[13] 0.8051752 0.7819310 0.7581542 0.7338670 0.7090860 0.6838229
[19] 0.6580849 0.6318752 0.6051932 0.5770646 0.5483048
```

- implement formula (4.3.1) and (4.3.2) page 105 to look at the different values for CI

# Comparison CI



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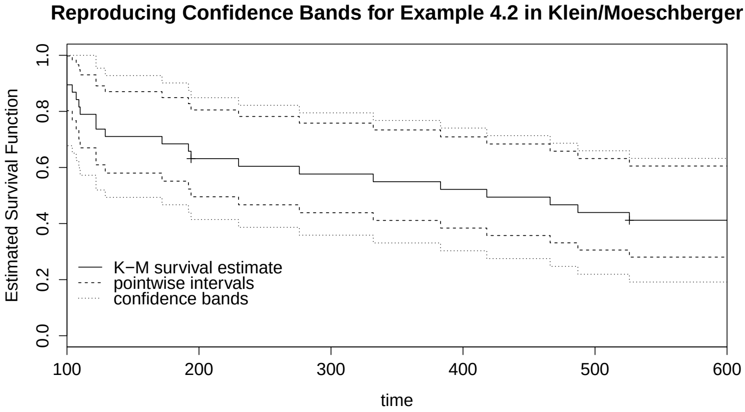
- Pointwise confidence intervals apply to a single point in the time scale
- look at simultaneous confidence bands (or confidence bands for short), which are valid for the entire range of time values simultaneously
- A 95% confidence band, for example, will capture the entire true survival curve about 19 out of 20 times.
- While the survival package doesn't offer tools for confidence bands, they may be calculated using `confBands` from the `OIsurv` library

```
 data(bmt); attach(bmt)
 my.surv <- Surv(t2[group==1], d3[group==1])
 my.cb <- confBands(my.surv, confLevel=0.95, type="hall")
 plot(survfit(my.surv ~ 1), xlim=c(100, 600), xlab="time",
        ylab="Estimated Survival Function",
        main="Confidence Bands for Example 4.2 in Klein/Moeschberger")

lines(my.cb$time, my.cb$lower, lty=3, type="s")
lines(my.cb$time, my.cb$upper, lty=3, type="s")
legend(100, 0.3, legend=c("K-M survival estimate",
      "pointwise intervals","confidence bands"), lty=1:3, bty="n")
 detach(bmt)
```


Reproducing Confidence Bands for Example 4.2 in Klein/Moeschberger
Estimated Survival Function
0.0
0.2
0.4
0.6
0.8
1.0
100
200
300
400
500
600
time
K−M survival estimate
pointwise intervals
confidence bands

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- the mean time to the event $\mu$ is given by $\mu = \int_0^\infty S(t)dt$
- estimator of $\mu$ obtained by substituting $\widehat{S}(t)$ for $S(t)$: $\hat{\mu} = \int_0^\infty \hat{S}(t)dt$ (compute the area under the KM curve)
- this estimator is appropriate only when the largest observation corresponds to a death
- in other cases, the product-limit estimator is not defined beyond the largest observation
- several solutions to this problem are available
- *solution 1*: changes the largest observed time to a death if it was a censored observation
- estimate the mean restricted to the interval 0 to $t_{max}$

- *solution 2*: estimate the meanlifetime restricted to some preassigned interval $[0, \tau]$
- $\tau$ is chosen by the investigator to be the longest possible time to which anyone could survive
- the estimated mean restricted to the interval $[0, \tau]$ in both cases is

$$\hat{\mu}_\tau = \int_0^\tau \widehat{S}(t)dt$$

# Estimates of the variance and CI for the mean survival time

- variance for the mean survival time

$$\widehat{V}[\hat{\mu}_\tau] = \sum_{i=1}^{D} \left[ \int_{t_i}^{\tau} \widehat{S}(t)dt \right]^2 \frac{d_i}{Y_i(Y_i - d_i)}$$

- confidence interval for the mean

$$\hat{\mu}_\tau \pm Z_{1-\alpha/2} \sqrt{\widehat{V}[\hat{\mu}_\tau]}$$

## Example

- Consider, for example, a sample of right censored life times $1, 1, 1^+, 2.5, 5^+, 7^+$
- The censored observation $7^+$ will be treated as a 7 (true failure) for computing the Kaplan-Meier estimator so that $\hat{S}(7) = 0$
- Computations for KM

| $t_i$ | $d_i$ | $Y_i$ | $\hat{S}(t)$ |
|---|---|---|---|
| 1 | 2 | 6 | 2/3 |
| 2.5 | 1 | 3 | 4/9 |
| 7 | 1 | 1 | 0 |

## Example

- estimated mean

$$\hat{\mu} = 1 \times (1 - 0) + \frac{2}{3} \times (2.5 - 1) + \frac{4}{9} \times (7 - 2.5) = 4$$

- in general: let $\tau_1 < \ldots < \tau_m$ be the distinct event (failure or censoring) times

$$\hat{\mu} = \sum_{i=1}^{n} \Delta\tau_i \hat{S}(\tau_{i-1})$$

- where $\tau_0 = 0$, $\Delta\tau_i = \tau_i - \tau_{i-1}$

# Median survival time

- the Product-Limit estimator can be used to provide estimates of quantiles of the distribution of the time-to-event distribution
- p*th* quantile: $x_p = \inf\{t : S(t) \leq 1 - p\}$ ($x_p$: smallest time at which the survival function is less than or equal to $1 - p$)
- $p = 1/2$; $x_p$ is the median time to the event of interest
- estimate $x_p$: $\hat{x}_p = \inf\{t : \widehat{S}(t) \leq 1 - p\}$
- the standard error of $x_p$ is difficult to compute because it requires an estimate of the density function of $X$ at $x_p$
- The median survival time is the time at which half of the population has died and half are still alive

- If $S_i(t_{Max}) > 0.5$: the median survival time cannot be estimated directly from the data
- there are methods to approximate the median survival time beyond the duration of follow-up based on geometric and linear growth in death rates
- The median and its 95% confidence interval may be estimated using `survfit()`

```
> data(drug6mp); attach(drug6mp)
> my.surv <- Surv(t1, rep(1, 21)) # all placebo patients observed
> survfit(my.surv ~ 1)
Call: survfit(formula = my.surv ~ 1)

records   n.max n.start  events  median 0.95LCL 0.95UCL
     21      21      21      21       8       4      12
```

## Example

- Using `survfit()` together with `print()`, the mean survival time and its standard error may be obtained:

```
> print(survfit(my.surv ~ 1), print.rmean=TRUE)
Call: survfit(formula = my.surv ~ 1)

   records      n.max    n.start     events     *rmean *se(rmean)
     21.00      21.00      21.00      21.00       8.67       1.38
    * restricted mean with upper limit =  23
> detach(drug6mp)
```

- The `print.rmean=TRUE` argument is used to obtain the mean and its standard error, and $\tau$ is automatically set as the largest observed or censored time. Alternatively, $\tau$ may be specified using the `rmean` argument

# Outline

KMsurv packages

CI S(t)

R code

Confidence intervals

Confidence bands

Mean and median $S(t)$

Example

**Follow-up**

Descriptives

Reverse Kaplan-Meier

# Why follow-up?

- Why should we be bothered with follow-up?
- If we want to know 5-years survival after surgery for breast cancer for instance
- Would we be comfortable in reporting this if we have followed patients for three years?
- Follow-up tells you something about the maturity of the data, hence about the reliability of your results
- In reality, for instance in clinical trials, not all patients have been followed for the same length of time
- The first patient has been included 7 years ago
- The last patient has been included 2 years ago
- The follow-up is different from person to person
- So there is a follow-up *distribution*

# How to calculate median follow-up?

## Wrong way

- Calculate the median of the follow-up times
- Why is this wrong?

# How to calculate median follow-up?

## Wrong way

- Calculate the median of the follow-up times
- Why is this wrong?

## Better

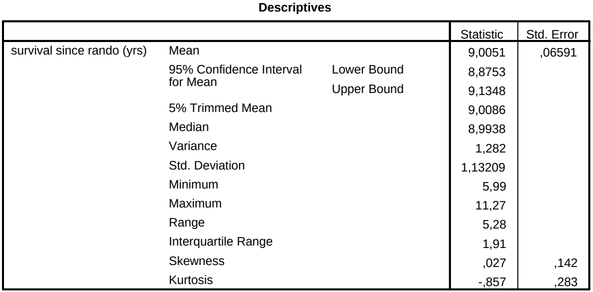
- Calculate the median of the follow-up times
- Exclude the patients that have died
- This is often done in practice

# Example

- Dutch Gastric Cancer Trial
- First patient died after 5 days; highest follow-up time: 11.27 years (alive)
- Removing dead patients: minimum follow-up 5.99 years, maximum 11.27 years, median follow-up 8.99 years

# Descriptives

## After removing dead patients

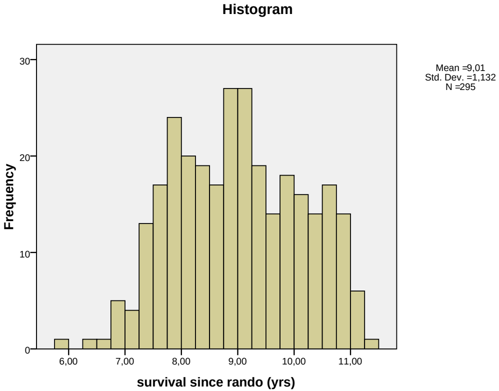


**Descriptives**

| | | | Statistic | Std. Error |
|---|---|---|---|---|
| survival since rando (yrs) | Mean | | 9,0051 | ,06591 |
| | 95% Confidence Interval for Mean | Lower Bound | 8,8753 | |
| | | Upper Bound | 9,1348 | |
| | 5% Trimmed Mean | | 9,0086 | |
| | Median | | 8,9938 | |
| | Variance | | 1,282 | |
| | Std. Deviation | | 1,13209 | |
| | Minimum | | 5,99 | |
| | Maximum | | 11,27 | |
| | Range | | 5,28 | |
| | Interquartile Range | | 1,91 | |
| | Skewness | | ,027 | ,142 |
| | Kurtosis | | -,857 | ,283 |

# Histogram

## After removing dead patients



# Reporting of follow-up

## Often reported

- Median and range (minimum and maximum) follow-up

## Less often reported

- The whole distribution
- Pity, really, but usually there is no space in a paper
- Both minimum and maximum don't tell you very much about maturity
- Especially minimum; there could be one patient who was lost to follow-up very early but last patient was included four years ago

# Estimating the censoring distribution

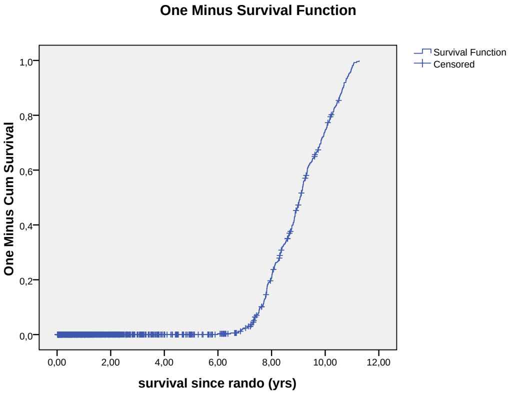
- How long it takes for the number at risk to drop to half the starting value?
- Two reasons for the number at risk to drop over time:
  - A subject can die or his data can be censored
  - If someone dies, you don’t know how long they would have been followed
- From the point of view of tracking follow-up time, the roles of deaths and censoring are sort of reversed
- Idea: run the data through the Kaplan-Meier analysis again, but with the meaning of the status indicator reversed

# Reverse Kaplan-Meier

- The end point is loss to follow-up (which is usually considered censoring)
- If a patient died, you can't know how long he would have been followed
- Death censors the true but unknown observation time of an individual
- Create a Kaplan-Meier curve where loss to follow-up is the event being followed, and a death is treated as censored data

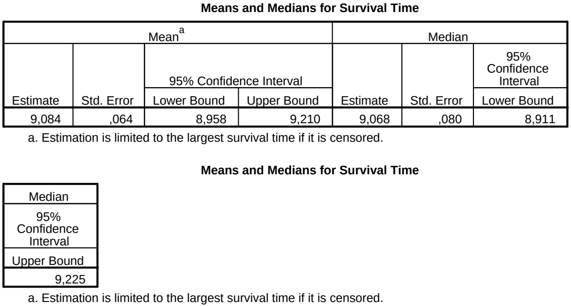
# Follow-up using reverse Kaplan-Meier

## One-minus-survival curve



# Follow-up using reverse Kaplan-Meier

## Mean and median table



**Means and Medians for Survival Time**

| Mean[a] | | | | Median | | | |
|---|---|---|---|---|---|---|---|
| | | 95% Confidence Interval | | | | 95% Confidence Interval | 95% Confidence Interval |
| Estimate | Std. Error | Lower Bound | Upper Bound | Estimate | Std. Error | Lower Bound | Upper Bound |
| 9,084 | ,064 | 8,958 | 9,210 | 9,068 | ,080 | 8,911 | 9,225 |

a. Estimation is limited to the largest survival time if it is censored.

**Means and Medians for Survival Time**

a. Estimation is limited to the largest survival time if it is censored.