

from PhD Course  
**Advanced Biostatistics**

# Survival Analysis

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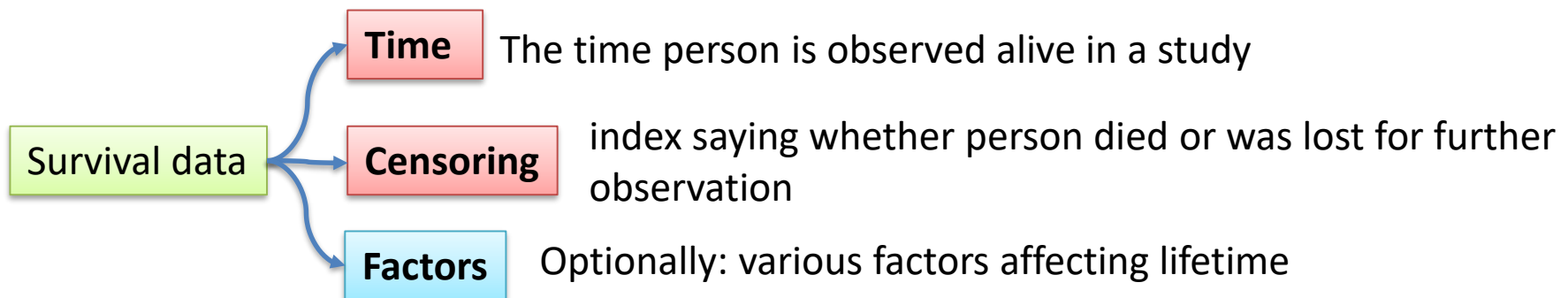
## Survival Data

### Survival analysis

is a branch of statistics which deals with analysis of time to events, such as death in biological organisms and failure in mechanical systems (i.e. **reliability theory** in engineering).

Survival analysis attempts to answer questions such as:

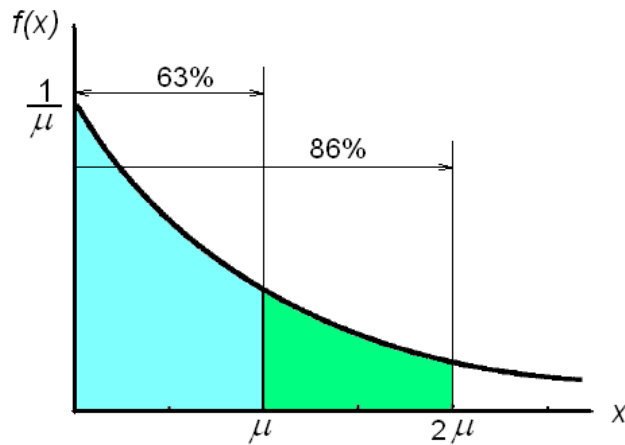
- What is the proportion of a population which will survive past a certain time?
- Of those that survive, at what rate will they die or fail?
- Can multiple causes of death or failure be taken into account?
- How do particular circumstances or characteristics increase or decrease the probability of survival?



<http://www.partek.com/webinars/survival-analysis-partek-genomics-suite-software>

## Cox's Survival Model

$$f(x) = \frac{1}{\mu} e^{-\frac{x}{\mu}} \quad \text{for } x \geq 0, \mu > 0$$



$$h(t) = h_0(t) e^{\beta_1 x_1 + \beta_2 x_2 + \dots + \beta_n x_n}$$

$h(t)$  – hazard function

$h_0(t)$  – basic hazard

$x_1 \dots x_n$  – variables (expression of gene X) and covariates  
(age, smoking,) which are time-independent!

$\beta_1 \dots \beta_n$  – fitted parameters

$$HR = \frac{h_i(t)}{h_j(t)} = \exp\{\beta_1(x_{i1} - x_{j1}) + \dots + \beta_n(x_{in} - x_{jn})\}$$

To identify significantly involved covariate: partial likelihood is calculated

```
library(survival)
str(lung)
```

```
## create a survival object
## lung$status: 1-censored, 2-dead
sData = Surv(lung$time, event = lung$status == 2)
print(sData)
```

```
## Let's visualize it
fit = survfit(sData~1)
plot(fit)
```

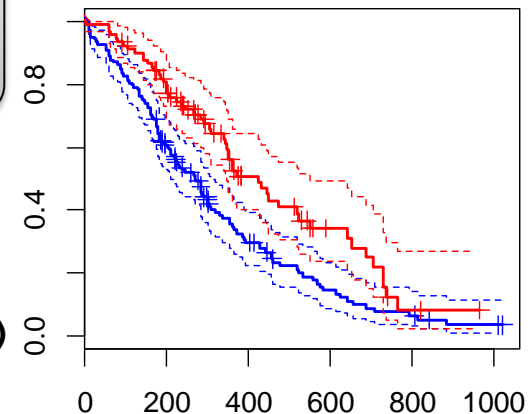
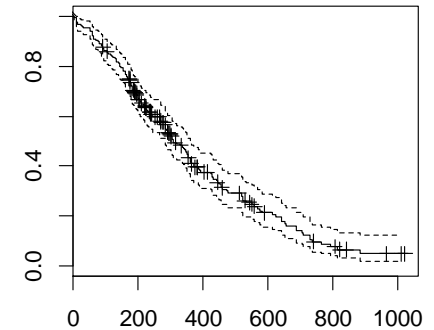
```
## Let's visualize it for male/female
fit.sex = survfit(sData ~ lung$sex)
plot(fit.sex, col=c("blue","red"), conf.int = TRUE)
```

```
## Rank test for survival data
dif.sex = survdiff(sData ~ lung$sex)
dif.sex
```

```
## build Cox regression model
mod = coxph(sData ~ sex + age, data=lung)
summary(mod)
```

## Example: Lung

“event” should be:  
0 – for censored  
1 – for dead patients



ovarian