

# Multistate models:

Occurrence rates, cumulative risks, competing risks, state probabilities with multiple states and time scales in Register Research with R and Epi::Lexis

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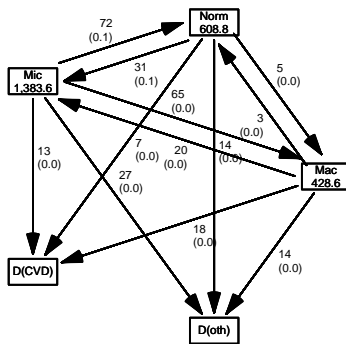
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# Examples of time-to-event measurements

- ▶ Time from diagnosis of cancer to death.
- ▶ Time from randomisation to death in a cancer clinical trial
- ▶ Time from HIV infection to AIDS.
- ▶ Time from marriage to 1st child birth.
- ▶ Time from marriage to divorce.
- ▶ Time to re-offending after being released from jail

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## A multistate model

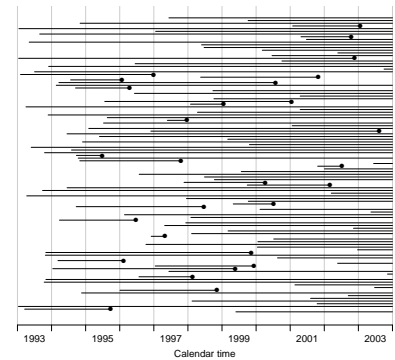


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Each line a person

Each blob a death

Study ended at 31 Dec. 2003



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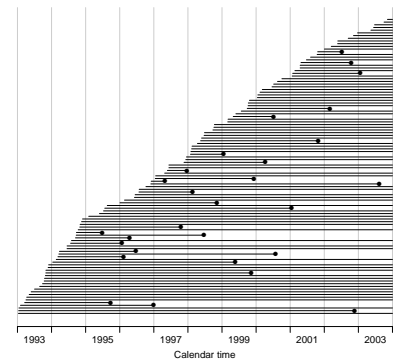
## A multistate model

- ▶ Not really a model
- ▶ What is the data:
  - ▶ Sequence of transitions: (when, from, to)
  - ... same as:
  - ▶ sequence of: (state time, next state)
- ▶ What are the target parameters:
  - ▶ Rates (the arrows)
  - ▶ State probabilities (of being in a state at a given time)
  - ▶ Survival probability
  - ▶ Sojourn times (how long time do you spend in a state)
  - ▶ Probability of ever visiting a state

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Ordered by date of entry

Most likely the order in your database.



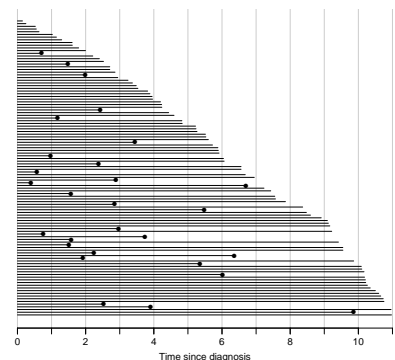
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## What is a statistical model

- ▶ Specification of a statistical machinery that could have generated data
- ▶ ... so when we have a statistical model we can simulate a data set
- ▶ The basis for the likelihood of data is the statistical model
  - ⇒ Estimation of parameters in the model
- ▶ Parameter estimates needed for prediction of rates (hazards)

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Timescale changed to "Time since diagnosis".



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## Survival data

Persons enter the study at some date.

Persons exit at a later date, either dead or alive.

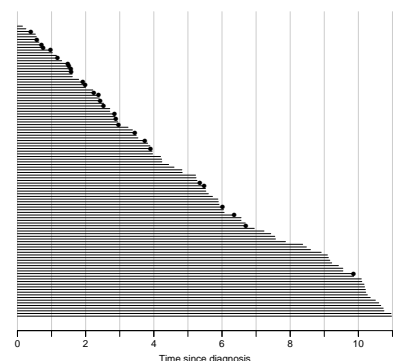
Observation:

Actual time span to death ("event")

or

Some time alive ("at least this long")

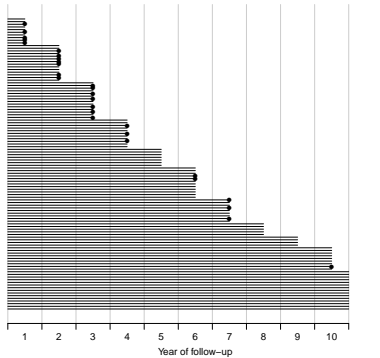
Patients ordered by survival time.



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Survival times grouped into bands of survival.



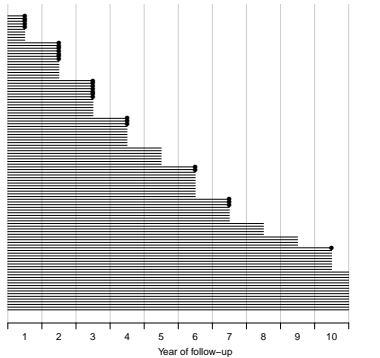
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## Prerequisites

```
> library(Epi)
> library(popEpi)
> # popEpi::splitMulti returns a data.frame rather than a data.table
> options("popEpi.datatable" = FALSE)
```

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Patients ordered by survival status within each band.



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## The lung data set

```
> library(survival)
> data(lung)
> lung$sex <- factor(lung$sex,
+                   levels = 1:2,
+                   labels = c("M", "W"))
> lung$time <- lung$time / (365.25/12)
> head(lung)

  inst  time status age sex ph.ecog ph.karno pat.karno meal.cal wt.loss
1    3 10.053388    2  74  M     1     90     100    1175    NA
2    3 14.948665    2  68  M     0     90     90    1225    15
3    3 33.182752    1  56  M     0     90     90     NA    15
4    5  6.899384    2  57  M     1     90     60    1150    11
5    1 29.010267    2  60  M     0    100     90     NA     0
6   12 33.577002    1  74  M     1     50     80     513     0
```

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## Survival after Cervix cancer

| Year | Stage I |   |    | Stage II |    |    |
|------|---------|---|----|----------|----|----|
|      | N       | D | L  | N        | D  | L  |
| 1    | 110     | 5 | 5  | 234      | 24 | 3  |
| 2    | 100     | 7 | 7  | 207      | 27 | 11 |
| 3    | 86      | 7 | 7  | 169      | 31 | 9  |
| 4    | 72      | 3 | 8  | 129      | 17 | 7  |
| 5    | 61      | 0 | 7  | 105      | 7  | 13 |
| 6    | 54      | 2 | 10 | 85       | 6  | 6  |
| 7    | 42      | 3 | 6  | 73       | 5  | 6  |
| 8    | 33      | 0 | 5  | 62       | 3  | 10 |
| 9    | 28      | 0 | 4  | 49       | 2  | 13 |
| 10   | 24      | 1 | 8  | 34       | 4  | 6  |

Life-table estimator of death probability:  $D/(N - L/2)$

Estimated risk of death in year 1 for Stage I women is  $5/107.5 = 0.0465$

Estimated 1 year survival is  $1 - 0.0465 = 0.9535$

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## Survival function

- Use `survfit` to construct the Kaplan-Meier estimator of overall survival:

```
> ?Surv
> ?survfit

> km <- survfit(Surv(time, status == 2) ~ 1, data = lung)
> km

Call: survfit(formula = Surv(time, status == 2) ~ 1, data = lung)

      n events median 0.95LCL 0.95UCL
228.00  165.00  10.18   9.36  11.93

> # summary(km) # very long output
```

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## Survival after Cervix cancer

| Year | Stage I |   |   | Stage II |    |    |
|------|---------|---|---|----------|----|----|
|      | N       | D | L | N        | D  | L  |
| 1    | 110     | 5 | 5 | 234      | 24 | 3  |
| 2    | 100     | 7 | 7 | 207      | 27 | 11 |
| 3    | 86      | 7 | 7 | 169      | 31 | 9  |

Estimated risk in year 1 for Stage I women is  $5/107.5 = 0.0465$

Estimated risk in year 2 for Stage I women is  $7/96.5 = 0.0725$

Estimated risk in year 3 for Stage I women is  $7/82.5 = 0.0848$

Estimated 1 year survival is  $1 - 0.0465 = 0.9535$

Estimated 2 year survival is  $0.9535 \times (1 - 0.0725) = 0.8843$

Estimated 3 year survival is  $0.8843 \times (1 - 0.0848) = 0.8093$

This is the life-table estimator.

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We can plot the survival curve—this is the default plot for a `survfit` object:

```
> plot(km)
```

What is the median survival? What does it mean? Explore if survival patterns between men and women are different:

```
> kms <- survfit(Surv(time, status == 2) ~ sex, data = lung)
> kms

Call: survfit(formula = Surv(time, status == 2) ~ sex, data = lung)

      n events median 0.95LCL 0.95UCL
sex=M 138   112  8.87   6.97  10.2
sex=W  90    53 14.00  11.43  18.1
```

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- No need to use 1 year intervals
- Very small intervals will leave at most 1 censoring or 1 death in each
- Interval with 1 death and  $n_t$  persons at risk:  $P\{\text{Death}\} = 1/n_t$
- corresponding death probability  $(n_t - 1)/n_t$
- if you multiply these over times with event:

$$S(t) = \prod_{t \text{ with event}} (n_t - 1)/n_t$$

... you have the **Kaplan-Meier estimator**

- looks complicated but just a question of book keeping

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We see that men have worse survival than women, but they are also a bit older (age is age at diagnosis of lung cancer):

```
> with(lung, tapply(age, sex, mean))

      M      W
63.34058 61.07778
```

Formally there is a significant difference in survival between men and women

```
> survdiff(Surv(time, status==2) ~ sex, data = lung)

Call:
survdiff(formula = Surv(time, status == 2) ~ sex, data = lung)

      N Observed Expected (O-E)^2/E (O-E)^2/V
sex=M 138   112   91.6     4.55    10.3
sex=W  90    53   73.4     5.68    10.3

      Chisq= 10.3 on 1 degrees of freedom, p= 0.001
```

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## Rates and rate-ratios

### ► Occurrence rate:

$$\lambda(t) = \lim_{h \rightarrow 0} P \{ \text{event in } (t, t+h] \mid \text{alive at } t \} / h$$

—measured in probability per time: time<sup>-1</sup>

- observation in a survival study: (exit status, time alive)
- empirical rate  $(d, y) = (\text{deaths}, \text{time})$
- the Cox model is a model for rates as function of time  $(t)$  and covariates  $(x_1, x_2)$ :

$$\lambda(t, x) = \lambda_0(t) \exp(\beta_1 x_1 + \beta_2 x_2)$$

—mortality depends on the person's sex and age, say.

- Data looks like data for a K-M analysis **plus** covariate values

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Sex and age effects are quite close between the Poisson and the Cox models.

Poisson model has an intercept term, the estimate of the (assumed) constant underlying mortality.

The risk time part of the response (second argument in the `cbind`) was entered in units of months (remember we rescaled in the beginning?), the `(Intercept)` (taken from the `ci.exp`) is a rate per 1 person-month.

What age and sex does the `(Intercept)` refer to?

```
> ci.exp(p1) # Poisson
              exp(Est.)      2.5%      97.5%
(Intercept) 0.03255152 0.01029228 0.1029511
sexW         0.61820515 0.44555636 0.8577537
age          1.01574132 0.99777446 1.0340317
```

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## Rates and rate-ratios: Simple Cox model

Now explore how sex and age (at diagnosis) influence the mortality—note that in a Cox-model we are addressing the mortality rate and not the survival:

```
> c0 <- coxph(Surv(time, status == 2) ~ sex, data = lung)
> c1 <- coxph(Surv(time, status == 2) ~ sex + age, data = lung)
> summary(c1)
> ci.exp(c0)
> ci.exp(c1)
```

What variables from `lung` are we using?

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## poisreg and poisson

```
poisreg: cbind(d,y) ~ ...
```

```
> p1 <- glm(cbind(status == 2, time) ~ sex + age,
+          family = poisreg,
+          data = lung)
```

```
poisson: d ~ ... + offset(log(y))
```

```
> px <- glm(status == 2 ~ sex + age + offset(log(time)),
+          family = poisson,
+          data = lung)
+ ## or:
> px <- glm(status == 2 ~ sex + age,
+          offset = log(time),
+          family = poisson,
+          data = lung)
```

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```
> c0 <- coxph(Surv(time, status == 2) ~ sex, data = lung)
> c1 <- coxph(Surv(time, status == 2) ~ sex + age, data = lung)
> summary(c1)
```

```
Call:
coxph(formula = Surv(time, status == 2) ~ sex + age, data = lung)
```

```
n = 228, number of events = 165

              coef exp(coef) se(coef)      z Pr(>|z|)
sexW -0.513219  0.598566  0.167458 -3.065  0.00218
age   0.017045  1.017191  0.009223  1.848  0.06459
```

```
              exp(coef) exp(-coef) lower .95 upper .95
sexW    0.5986    1.6707    0.4311    0.8311
age     1.0172    0.9831    0.9990    1.0357
```

```
Concordance = 0.603 (se = 0.025)
Likelihood ratio test = 14.12 on 2 df, p = 9e-04
Wald test = 13.47 on 2 df, p = 0.001
Score (logrank) test = 13.72 on 2 df, p = 0.001
```

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## Representation of follow-up: Lexis object

```
> L1 <- Lexis(exit = list(tfl = time),
+           exit.status = factor(status,
+                               levels = 1:2,
+                               labels = c("Alive", "Dead")),
+           data = lung)
```

```
NOTE: entry.status has been set to "Alive" for all.
NOTE: entry is assumed to be 0 on the tfl timescale.
```

```
> head(L1)
```

|   | tfl | lex.dur   | lex.Cst | lex.Xst | lex.id | inst | time      | status | age | sex | ph.ecog | ph.k |
|---|-----|-----------|---------|---------|--------|------|-----------|--------|-----|-----|---------|------|
| 1 | 0   | 10.053388 | Alive   | Dead    | 1      | 3    | 10.053388 | 2      | 74  | M   | 1       | 1    |
| 2 | 0   | 14.948665 | Alive   | Dead    | 2      | 3    | 14.948665 | 2      | 68  | M   | 0       | 0    |
| 3 | 0   | 33.182752 | Alive   | Alive   | 3      | 3    | 33.182752 | 1      | 56  | M   | 0       | 0    |
| 4 | 0   | 6.899384  | Alive   | Dead    | 4      | 5    | 6.899384  | 2      | 57  | M   | 1       | 0    |
| 5 | 0   | 29.010267 | Alive   | Dead    | 5      | 1    | 29.010267 | 2      | 60  | M   | 0       | 1    |
| 6 | 0   | 33.577002 | Alive   | Alive   | 6      | 12   | 33.577002 | 1      | 74  | M   | 0       | 1    |

|   | meal.cal | wt.loss |
|---|----------|---------|
| 1 | 1175     | NA      |
| 2 | 1225     | 15      |
| 3 | NA       | 15      |

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```
> ci.exp(c0)
```

```
              exp(Est.)      2.5%      97.5%
sexW  0.5980028 0.4237178 0.8159848
```

```
> ci.exp(c1)
```

```
              exp(Est.)      2.5%      97.5%
sexW  0.598566 0.4310936 0.8310985
age   1.017191 0.9989686 1.0357467
```

What do these estimates mean?

$$\lambda(t, x) = \lambda_0(t) \exp(\beta_1 x_1 + \beta_2 x_2)$$

Where is  $\beta_1$ ? Where is  $\beta_2$ ? Where is  $\lambda_0(t)$ ?

What is the mortality RR for a 10 year age difference?

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## New variables in Lexis object

`tfl`: time from lung cancer **at the time of entry**, therefore it is 0 for all persons; the entry time is 0 from the entry time.

`lex.dur`: the **length** of time a person is in state `lex.Cst`, here measured in months, because `time` is.

`lex.Cst`: Current state, the state in which the `lex.dur` time is spent.

`lex.Xst`: eXit state, the state to which the person moves after the `lex.dur` time in `lex.Cst`.

`lex.id`: an id of each record in the source dataset. Can be explicitly set by `id=`.

Overkill?

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If mortality is assumed constant ( $\lambda(t) = \lambda$ ), then the likelihood for the Cox-model is equivalent to a Poisson likelihood, which can be fitted using the `poisreg` family from the `Epi` package:

```
> ?poisreg
```

```
> p1 <- glm(cbind(status == 2, time) ~ sex + age,
+          family = poisreg,
+          data = lung)
> ci.exp(p1) # Poisson
```

```
              exp(Est.)      2.5%      97.5%
(Intercept) 0.03255152 0.01029228 0.1029511
sexW         0.61820515 0.44555636 0.8577537
age          1.01574132 0.99777446 1.0340317
```

```
> ci.exp(c1) # Cox
```

```
              exp(Est.)      2.5%      97.5%
sexW  0.598566 0.4310936 0.8310985
age   1.017191 0.9989686 1.0357467
```

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## Lexis object: Overview of FU

```
> summary(L1)
```

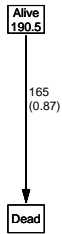
```
Transitions:
```

|  | To    | From  | Alive | Dead | Records | Events | Risk time | Persons |
|--|-------|-------|-------|------|---------|--------|-----------|---------|
|  | Alive | Alive | 63    | 165  | 228     | 165    | 2286.42   | 228     |

What is the average follow-up time for persons?

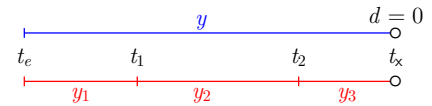
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```
> boxes(L1, boxpos = TRUE, scale.Y = 12, digits.R = 2)
```



Explain the numbers in the graph.

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Probability

$$P(\text{surv } t_e \rightarrow t_x | \text{entry } t_e)$$

$$= P(\text{surv } t_e \rightarrow t_1 | \text{entry } t_e)$$

$$\times P(\text{surv } t_1 \rightarrow t_2 | \text{entry } t_1)$$

$$\times P(\text{surv } t_2 \rightarrow t_x | \text{entry } t_2)$$

log-Likelihood

$$0 \log(\lambda) - \lambda y$$

$$= 0 \log(\lambda) - \lambda y_1$$

$$+ 0 \log(\lambda) - \lambda y_2$$

$$+ 0 \log(\lambda) - \lambda y_3$$

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Cox model using the Lexis-specific variables:

```
> c1 <- coxph(Surv(tfl,
+             tfl + lex.dur,
+             lex.Xst == "Dead") ~ sex + age,
+             data = L1)
```

Surv(from-time, to-time, event indicator)

Using the Lexis features:

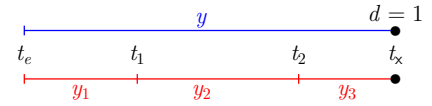
```
> cL <- coxph.Lexis(L1, tfl ~ sex + age)
```

```
survival::coxph analysis of Lexis object L1:
Rates for the transition Alive->Dead
Baseline timescale: tfl
```

```
> round(cbind(ci.exp(cL),
+             ci.exp(c1)), 3)
```

|      | exp(Est.) | 2.5%  | 97.5% | exp(Est.) | 2.5%  | 97.5% |
|------|-----------|-------|-------|-----------|-------|-------|
| sexW | 0.599     | 0.431 | 0.831 | 0.599     | 0.431 | 0.831 |
| age  | 1.017     | 0.999 | 1.036 | 1.017     | 0.999 | 1.036 |

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Probability

$$P(\text{event at } t_x | \text{entry } t_e)$$

$$= P(\text{surv } t_e \rightarrow t_1 | \text{entry } t_e)$$

$$\times P(\text{surv } t_1 \rightarrow t_2 | \text{entry } t_1)$$

$$\times P(\text{event at } t_x | \text{entry } t_2)$$

log-Likelihood

$$1 \log(\lambda) - \lambda y$$

$$= 0 \log(\lambda) - \lambda y_1$$

$$+ 0 \log(\lambda) - \lambda y_2$$

$$+ 1 \log(\lambda) - \lambda y_3$$

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The crude Poisson model:

```
> pc <- glm(cbind(lex.Xst == "Dead", lex.dur) ~ sex + age,
+           family = poisreg,
+           data = L1)
```

or even simpler, by using the Lexis features:

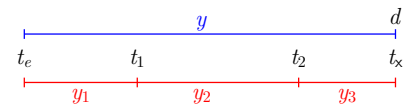
```
> pL <- glm.Lexis(L1, ~ sex + age)
```

```
stats::glm Poisson analysis of Lexis object L1 with log link:
Rates for the transition: Alive->Dead
```

```
> round(cbind(ci.exp(pL),
+             ci.exp(pc)), 3)
```

|             | exp(Est.) | 2.5%  | 97.5% | exp(Est.) | 2.5%  | 97.5% |
|-------------|-----------|-------|-------|-----------|-------|-------|
| (Intercept) | 0.033     | 0.010 | 0.103 | 0.033     | 0.010 | 0.103 |
| sexW        | 0.618     | 0.446 | 0.858 | 0.618     | 0.446 | 0.858 |
| age         | 1.016     | 0.998 | 1.034 | 1.016     | 0.998 | 1.034 |

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Probability

$$P(d \text{ at } t_x | \text{entry } t_e)$$

$$= P(\text{surv } t_e \rightarrow t_1 | \text{entry } t_e)$$

$$\times P(\text{surv } t_1 \rightarrow t_2 | \text{entry } t_1)$$

$$\times P(d \text{ at } t_x | \text{entry } t_2)$$

log-Likelihood

$$d \log(\lambda) - \lambda y$$

$$= 0 \log(\lambda) - \lambda y_1$$

$$+ 0 \log(\lambda) - \lambda y_2$$

$$+ d \log(\lambda) - \lambda y_3$$

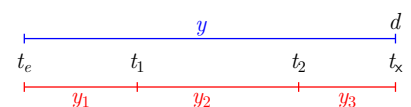
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## Likelihood and records

Suppose a person is alive from  $t_e$  (entry) to  $t_x$  (exit) and that the person's status at  $t_x$  is  $d$ , where  $d = 0$  means alive and  $d = 1$  means dead. If we choose, say, two time points,  $t_1, t_2$  between  $t_e$  and  $t_x$ , standard use of conditional probability (formally, repeated use of Bayes' formula) gives

$$P\{d \text{ at } t_x | \text{entry at } t_e\} = P\{\text{survive } (t_e, t_1) | \text{alive at } t_e\} \times \\ P\{\text{survive } (t_1, t_2) | \text{alive at } t_1\} \times \\ P\{\text{survive } (t_2, t_3) | \text{alive at } t_2\} \times \\ P\{d \text{ at } t_x | \text{alive at } t_3\}$$

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Probability

$$P(d \text{ at } t_x | \text{entry } t_e)$$

$$= P(\text{surv } t_e \rightarrow t_1 | \text{entry } t_e)$$

$$\times P(\text{surv } t_1 \rightarrow t_2 | \text{entry } t_1)$$

$$\times P(d \text{ at } t_x | \text{entry } t_2)$$

log-Likelihood

$$d \log(\lambda) - \lambda y$$

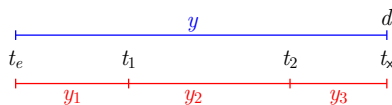
$$= 0 \log(\lambda_1) - \lambda_1 y_1$$

$$+ 0 \log(\lambda_2) - \lambda_2 y_2$$

$$+ d \log(\lambda_3) - \lambda_3 y_3$$

— allows different rates ( $\lambda_i$ ) in each interval

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Probability

$$P(d \text{ at } t_x | \text{entry } t_e)$$

$$= P(\text{surv } t_e \rightarrow t_1 | \text{entry } t_e)$$

$$\times P(\text{surv } t_1 \rightarrow t_2 | \text{entry } t_1)$$

$$\times P(d \text{ at } t_x | \text{entry } t_2)$$

log-Likelihood

$$d \log(\lambda) - \lambda y$$

$$= 0 \log(\lambda) - \lambda y_1$$

$$+ 0 \log(\lambda) - \lambda y_2$$

$$+ d \log(\lambda) - \lambda y_3$$

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## Baseline hazard: splitting time

```
> S1 <- splitMulti(L1, tfl = 0:36)
> summary(L1)
```

Transitions:

| From  | Alive | Dead | Records: | Events: | Risk time: | Persons: |
|-------|-------|------|----------|---------|------------|----------|
| Alive | 63    | 165  | 228      | 165     | 2286.42    | 228      |

```
> summary(S1)
```

Transitions:

| From  | Alive | Dead | Records: | Events: | Risk time: | Persons: |
|-------|-------|------|----------|---------|------------|----------|
| Alive | 2234  | 165  | 2399     | 165     | 2286.42    | 228      |

What happened to no. records?

What happened to amount of risk time?

What happened to no. events?

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```

> wh <- names(L1)[1:10] # names of variables in some order
> subset(L1, lex.id == 10)[,wh]

  tfl lex.dur lex.Cst lex.Xst lex.id inst   time status age sex
10   0 5.453799  Alive   Dead    10    7 5.453799   2 61  M

> subset(S1, lex.id == 10)[,wh]

  tfl lex.dur lex.Cst lex.Xst lex.id inst   time status age sex
163  0 1.0000000  Alive   Alive    10    7 5.453799   2 61  M
164  1 1.0000000  Alive   Alive    10    7 5.453799   2 61  M
165  2 1.0000000  Alive   Alive    10    7 5.453799   2 61  M
166  3 1.0000000  Alive   Alive    10    7 5.453799   2 61  M
167  4 1.0000000  Alive   Alive    10    7 5.453799   2 61  M
168  5 0.4537988  Alive   Dead    10    7 5.453799   2 61  M

```

In `S1` each record now represents a small interval of follow-up for a person, so each person has many records.

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## Survival function and hazard function

$$S(t) = \exp\left(-\int_0^t \lambda(u) du\right)$$

Simple, but the CI for  $S(t)$  not so simple...

Implemented in the `ci.surv` function

Arguments: 1:model, 2:prediction data frame, 3:equidistance

Prediction data frame must correspond to a sequence of equidistant time points:

```

> matshade(prf$tfl, ci.surv(ps, prf, intl = 0.2),
+ plot = TRUE, ylim = 0:1, lwd = 3)
> lines(prf$tfl, ci.surv(pc, prf, intl = 0.2)[,1], col="blue")
> lines(survfit(c1, newdata = data.frame(sex = "W", age = 60)),
+ lwd = 2, lty = 1, col="magenta")

```

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## Natural splines for baseline hazard

```

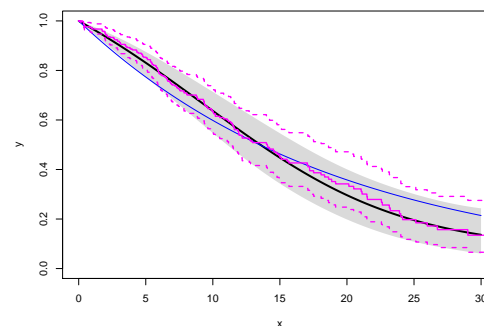
> ps <- glm(cbind(lex.Xst == "Dead", lex.dur)
+ ~ Ns(tfl, knots = seq(0, 36, 12)) + sex + age,
+ family = poisreg,
+ data = S1)
or even simpler:
> ps <- glm.Lexis(S1, ~ Ns(tfl, knots = seq(0, 36, 12)) + sex + age)
stats::glm Poisson analysis of Lexis object S1 with log link:
Rates for the transition: Alive->Dead
> ci.exp(ps)

      exp(Est.)      2.5%      97.5%
(Intercept) 0.0189837 0.005700814 0.06321569
Ns(tfl, knots = seq(0, 36, 12))1 2.4038681 0.809442081 7.13896863
Ns(tfl, knots = seq(0, 36, 12))2 4.1500822 0.436273089 39.47798357
Ns(tfl, knots = seq(0, 36, 12))3 0.8398973 0.043928614 16.05849662
sexW      0.5987171 0.431232662 0.83124998
age      1.0165872 0.998377104 1.03512945

```

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## Survival functions



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Comparing with estimates from the Cox-model and from the model with constant baseline:

```

> round(cbind(ci.exp(c1),
+ ci.exp(ps, subset = c("sex", "age")),
+ ci.exp(pc, subset = c("sex", "age"))), 3)

      exp(Est.)  2.5% 97.5% exp(Est.)  2.5% 97.5% exp(Est.)  2.5% 97.5%
sexW    0.599 0.431 0.831    0.599 0.431 0.831    0.618 0.446 0.858
age     1.017 0.999 1.036    1.017 0.998 1.035    1.016 0.998 1.034

```

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## Hazard and survival functions

```

> par(mfrow = c(1,2), mar=c(3,3,1,1), mgp=c(3,1,0)/1.6)
> # hazard scale
> matshade(prf$tfl, ci.pred(ps, prf),
+ plot = TRUE, log = "y", lwd = 3)
> matshade(prf$tfl, ci.pred(pc, prf), lty = 3, lwd = 3)
> # survival
> matshade(prf$tfl, ci.surv(ps, prf, intl = 0.2),
+ plot = TRUE, ylim = 0:1, lwd = 3)
> lines(survfit(c1, newdata = data.frame(sex = "W", age = 60)),
+ col = "forestgreen", lwd = 3, conf.int = FALSE)
> lines(survfit(c1, newdata = data.frame(sex = "W", age = 60)),
+ col = "forestgreen", lwd = 1, lty = 1)

```

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## But where is the baseline hazard?

`ps` is a model for the hazard so we can predict the value of it at defined values for the covariates in the model:

```

> prf <- data.frame(tfl = seq(0, 30, 0.2),
+ sex = "W",
+ age = 60)

```

We can over-plot with the predicted rates from the model where mortality rates are constant, the only change is the model (`pc` instead of `ps`):

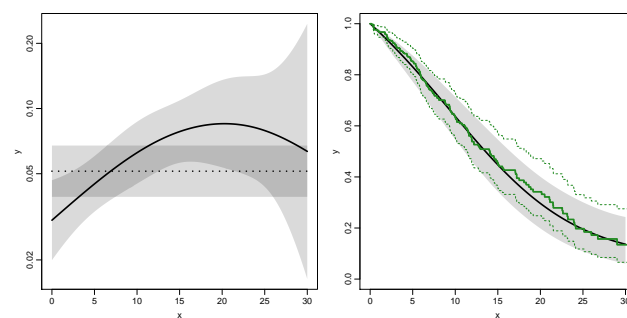
```

> matshade(prf$tfl, ci.pred(ps, prf),
+ plot = TRUE, log = "y", lwd = 3)
> matshade(prf$tfl, ci.pred(pc, prf), lty = 3, lwd = 3)

```

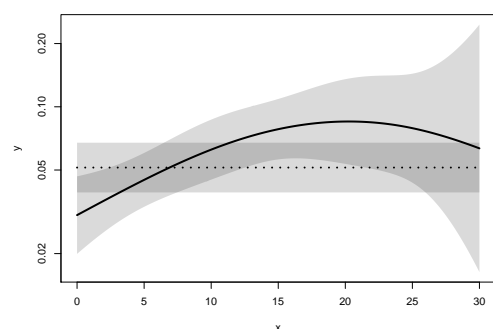
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## Hazard and survival functions



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## Here is the baseline hazard!



What are the units on the  $y$ -axis? Describe the mortality rates

45/97

## K-M estimator and smooth Poisson model

Kaplan-Meier estimator and compared to survival from corresponding Poisson-model, which is one with time (`tfl`) as the only covariate:

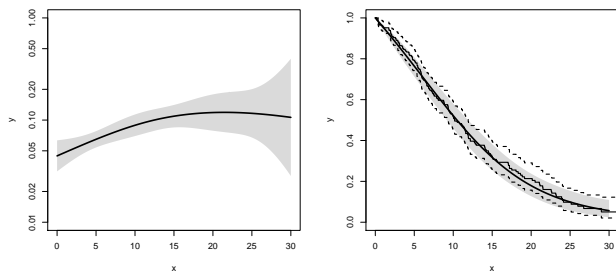
```

> par(mfrow=c(1,2))
> pk <- glm(cbind(lex.Xst == "Dead",
+ lex.dur) ~ Ns(tfl, knots = seq(0, 36, 12)),
+ family = poisreg,
+ data = S1)
> # hazard
> matshade(prf$tfl, ci.pred(pk, prf),
+ plot = TRUE, log = "y", lwd = 3, ylim = c(0.01,1))
> # survival from smooth model
> matshade(prf$tfl, ci.surv(pk, prf, intl = 0.2),
+ plot = TRUE, lwd = 3, ylim = 0:1)
> # K-M estimator
> lines(km, lwd = 2)

```

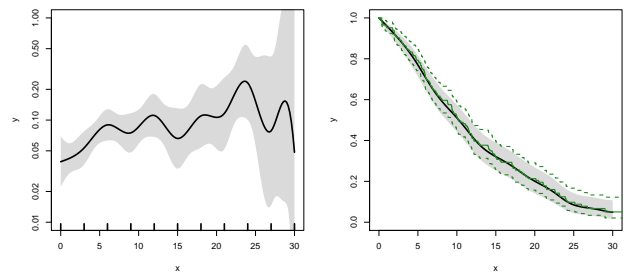
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## K-M estimator and smooth Poisson model



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## K-M estimator and smooth Poisson model



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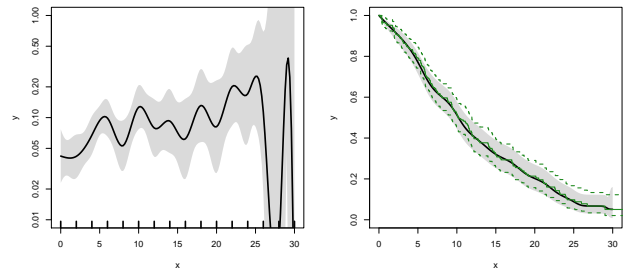
## K-M estimator and smooth Poisson model

We can explore how the tightness of the knots in the smooth model influence the underlying hazard and the resulting survival function:

```
> zz <- function(dk) # distance between knots
+ {
+   par(mfrow=c(1,2))
+   kn <- seq(0, 36, dk)
+   pk <- glm(cbind(lex.Xst == "Dead",
+                 lex.dur) ~ Ns(tfl, knots = kn),
+           family = poisreg,
+           data = S1)
+   matshade(prf$tfl, ci.pred(pk, prf),
+           plot = TRUE, log = "y", lwd = 3, ylim = c(0.01,1))
+   rug(kn, lwd=3)
+   matshade(prf$tfl, ci.surv(pk, prf, int1 = 0.2) ,
+           plot = TRUE, lwd = 3, ylim = 0:1)
+   lines(kn, lwd = 2, col = "forestgreen")
+ }
> zz(12)
```

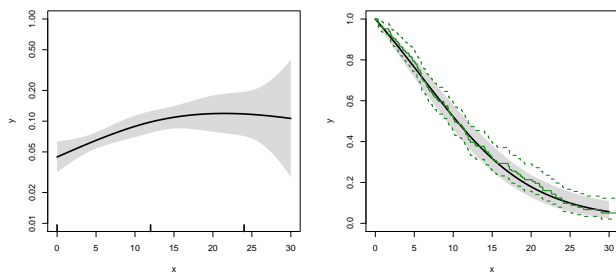
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## K-M estimator and smooth Poisson model



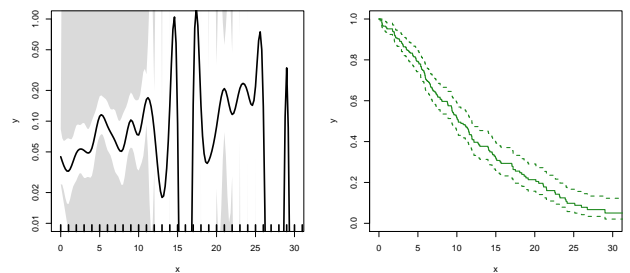
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## K-M estimator and smooth Poisson model



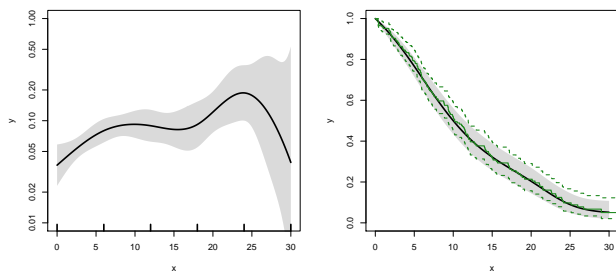
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## K-M estimator and smooth Poisson model



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## K-M estimator and smooth Poisson model



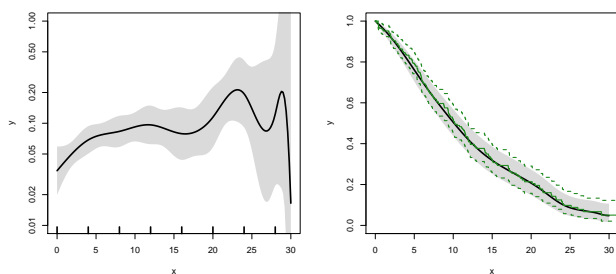
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## Survival analysis summary

- ▶ 1 to 1 correspondence between hazard function and survival function
- ▶ K-M and Cox use a very detailed baseline hazard (omits it)
- ▶ Smooth parametric hazard function more credible:
  - ▶ Define `Lexis` object
  - ▶ Split along time
  - ▶ Fit Poisson model
  - ▶ Prediction data frame
  - ▶ `ci.pred` to get baseline rates
  - ▶ `ci.surv` to get baseline survival

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## K-M estimator and smooth Poisson model



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```
> data(lung)
> lung$sex <- factor(lung$sex, labels=c("M", "F"))
> Lx <- Lexis(exit = list(tfe=time),
+           exit.status = factor(status, labels = c("Alive", "Dead")),
+           data = lung)
> sL <- splitMulti(Lx, tfe=seq(0, 1200, 10))
```

Smooth parametric hazard function

```
> m0 <- glm.Lexis(sL, ~ Ns(tfe, knots = seq(0, 30, 6) * 30) + sex + age)
```

Prediction data frame

```
> nd <- data.frame(tfe = seq(0, 900, 20) + 10, sex = "M", age = 65)
```

Predictions

```
> rate <- ci.pred(m0, nd) * 365.25 # per year, not per day
```

```
> surv <- ci.surv(m0, nd, int = 20)
```

Plot the rates

```
> matshade(nd$tfe, rate, log = "y", plot = TRUE)
```

Plot the survival function

```
> matshade(nd$tfe - 10, surv, ylim = c(0, 1), plot = TRUE)
```

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```

> library(survival)
> library(Epi)
> library(popEpi)
> # popEpi::splitMulti returns a data.frame rather than a data.table
> options("popEpi.datatable" = FALSE)
> library(tidyverse)
> clear()

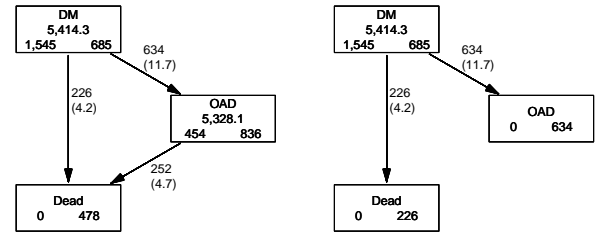
> data(DMlate)
> # str(DMlate)
> set.seed(1952)
> DMlate <- DMlate[sample(1:nrow(DMlate), 2000),]
> str(DMlate)

'data.frame': 2000 obs. of 7 variables:
 $ sex : Factor w/ 2 levels "M","F": 2 1 2 1 1 1 1 1 1 1 ...
 $ doth: num 1964 1944 1957 1952 1952 ...
 $ dodm: num 2003 2006 2008 2007 2003 ...
 $ dothd: num NA NA NA NA NA NA NA NA NA NA ...
 $ dooad: num NA 2006 NA 2007 2006 ...
 $ doins: num NA NA NA 2008 NA ...
 $ dox : num 2010 2010 2010 2010 2010 ...

```

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## Transitions in Cdm and Adm



66/97

## Lexis object from DM to Death

```

> Ldm <- Lexis(entry = list(per = dodm,
+                           age = dodm - doth,
+                           tfd = 0),
+             exit = list(per = dox,
+                         exit.status = factor(!is.na(doth),
+                                             labels = c("DM", "Dead")),
+                         data = DMlate)

NOTE: entry.status has been set to "DM" for all.
NOTE: Dropping 1 rows with duration of follow up < tol
> summary(Ldm)

Transitions:
To
From DM Dead Records: Events: Risk time: Persons:
DM 1521 478 1999 478 10742.34 1999

```

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## Survival function?

$$S(t) = \exp\left(-\int_0^t \lambda(u) + \mu(u) du\right)$$

$$S(t) = \exp\left(-\int_0^t \lambda(u) du\right)$$

$$S(t) = \exp\left(-\int_0^t \mu(u) du\right)$$

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## Cut follow-up at the date of OAD

```

> Cdm <- cutLexis(Ldm,
+                cut = Ldm$dooad,
+                timescale = "per",
+                new.state = "OAD")
> summary(Cdm)

Transitions:
To
From DM OAD Dead Records: Events: Risk time: Persons:
DM 685 634 226 1545 860 5414.3 1545
OAD 0 836 252 1088 252 5328.1 1088
Sum 685 1470 478 2633 1112 10742.3 1999

```

63/97

## Survival function?

- ▶ Regarding either Dead or OAD as censorings — or neither?
- ▶ **Simple survival:** what is the probability of being in each of the states Alive and Dead —depends on **one** rate, Alive → Dead
- ▶ **Competing risks:** what is the probability of being in each of the states DM, OAD and Dead —depends on **two** rates, DM → OAD and DM → Dead

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## Cut follow-up at the date of OAD, dooad

```

> subset(Ldm, lex.id %in% c(2:3,20))[,c(1:7,12)]
  per age tfd lex.dur lex.Cst lex.Xst lex.id dooad
235221 2005.6 61.517 0 4.3532 DM DM 2 2005.8
230872 2007.9 51.097 0 2.1109 DM DM 3 NA
114618 2006.0 73.183 0 3.7919 DM Dead 20 2007.0

> subset(Cdm, lex.id %in% c(2:3,20))[,c(1:7,12)]
  per age tfd lex.dur lex.Cst lex.Xst lex.id dooad
2 2005.6 61.517 0.00000 0.13415 DM OAD 2 2005.8
2001 2005.8 61.651 0.13415 4.21903 OAD OAD 2 2005.8
3 2007.9 51.097 0.00000 2.11088 DM DM 3 NA
20 2006.0 73.183 0.00000 1.01848 DM OAD 20 2007.0
2019 2007.0 74.201 1.01848 2.77344 OAD Dead 20 2007.0

```

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## Survival function and Cumulative risk function

survfit does the trick; the requirements are:

1. (start, stop, event) arguments to `Surv`
2. the third argument to the `Surv` function is a factor
3. an `id` argument is given, pointing to an id variable that links together records belonging to the same person.
4. the initial state (DM) must be the first level of the factor `lex.Xst`

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## Restrict to those alive in DM

```

> Adm <- subset(Cdm, lex.Cst == "DM")
> summary(Adm)

Transitions:
To
From DM OAD Dead Records: Events: Risk time: Persons:
DM 685 634 226 1545 860 5414.3 1545

> par(mfrow=c(1,2))
> boxes(Cdm, boxpos = TRUE, scale.R = 100, show.BE = TRUE)
> boxes(Adm, boxpos = TRUE, scale.R = 100, show.BE = TRUE)

```

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## Survival function and Cumulative risk function

```

> levels(Adm$lex.Xst)
[1] "DM" "OAD" "Dead"

> m3 <- survfit(Surv(tfd, tfd + lex.dur, lex.Xst) ~ 1,
+              id = lex.id,
+              data = Adm)
> # names(m3)
> m3$states
[1] "(s0)" "OAD" "Dead"

> head(cbind(time = m3$time, m3$pstate))
  time
[1,] 0.0027379 0.99871 0.0012945 0.00000000
[2,] 0.0054757 0.99288 0.0064725 0.00064725
[3,] 0.0082136 0.98900 0.0090615 0.00194175
[4,] 0.0109514 0.98770 0.0097087 0.00258900
[5,] 0.0136893 0.98382 0.0135922 0.00258900
[6,] 0.0164271 0.98058 0.0168285 0.00258900

```

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## Survival function and cumulative risks—formulae

$$S(t) = \exp\left(-\int_0^t \lambda(u) + \mu(u) du\right)$$

$$R_{\text{Dead}}(t) = \int_0^t \mu(u) S(u) du$$

$$R_{\text{OAD}}(t) = \int_0^t \lambda(u) S(u) du$$

$$= \int_0^t \lambda(u) \exp\left(-\int_0^u \lambda(s) + \mu(s) ds\right) du$$

$$S(t) + R_{\text{OAD}}(t) + R_{\text{Dead}}(t) = 1, \quad \forall t$$

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## Survival function and cumulative risks—don't

```
> m2 <- survfit(Surv(tfd,
+                 tfd + lex.dur,
+                 lex.Xst == "OAD" ) ~ 1,
+               data = Adm)
> M2 <- survfit(Surv(tfd,
+                 tfd + lex.dur,
+                 lex.Xst == "Dead" ) ~ 1,
+               data = Adm)
> par(mfrow = c(1,2))
> mat2pol(m3$pstate, c(2,3,1), x = m3$time,
+         col = c("red", "black", "transparent"),
+         xlim=c(0,15), xaxs="i",
+         yaxs = "i", xlab = "time since DM", ylab = "" )
> lines(m2$time, 1 - m2$surv, lwd = 3, col = "red" )
> mat2pol(m3$pstate, c(3,2,1), x = m3$time, yaxs = "i",
+         col = c("black", "red", "transparent"),
+         xlim=c(0,15), xaxs="i",
+         yaxs = "i", xlab = "time since DM", ylab = "" )
> lines(M2$time, 1 - M2$surv, lwd = 3, col = "black" )
```

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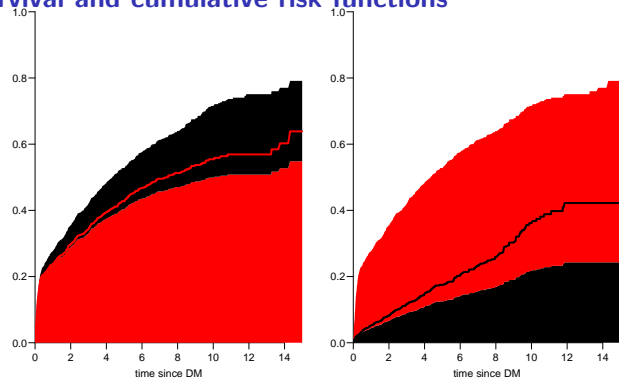
## Survival function and cumulative risks

```
> par( mfrow=c(1,2) )
> matplot(m3$time, m3$pstate,
+         type="s", lty=1, lwd=4,
+         col=c("ForestGreen","red", "black"),
+         xlim=c(0,15), xaxs="i",
+         ylim=c(0,1), yaxs="i" )
> stackedCIF(m3, lwd=3, xlim=c(0,15), xaxs="i", yaxs="i" )
> text(rep(12,3), c(0.9,0.3,0.6), levels(Cdm))
> box(bty="o")

> par( mfrow = c(1,2) )
> matshade(m3$time, cbind(m3$pstate,
+                         m3$lower,
+                         m3$upper)[,c(1,4,7,2,5,8,3,6,9)],
+         plot = TRUE, lty = 1, lwd = 4,
+         col = c("ForestGreen", "red", "black"),
+         xlim=c(0,15), xaxs="i",
+         ylim = c(0,1), yaxs="i" )
> stackedCIF(m3, lwd=3, xlim=c(0,15), xaxs="i", yaxs="i" )
> text(rep(12,3), c(0.9,0.3,0.6), levels(Cdm))
> box(bty="o")
```

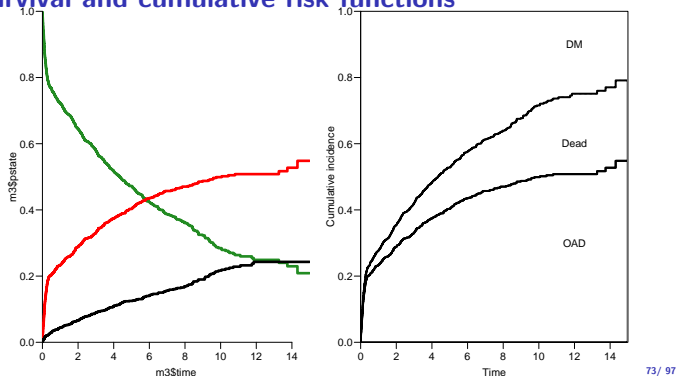
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## Survival and cumulative risk functions



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## Survival and cumulative risk functions



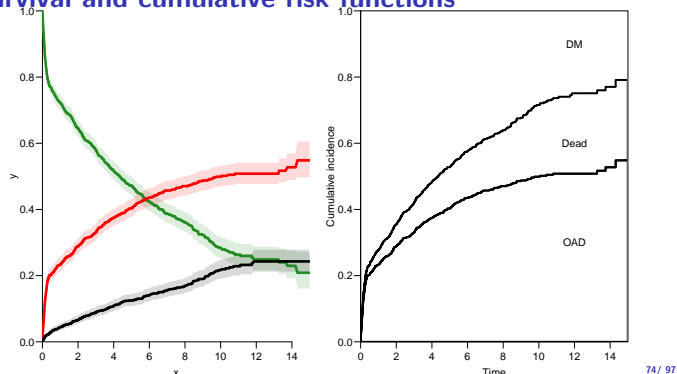
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## Cause-specific rates

- ▶ There is nothing wrong with modeling the cause-specific event-rates, the problem lies in how you transform them into probabilities.
- ▶ The relevant model for a competing risks situation normally consists of separate models for each of the cause-specific rates.
- ▶ ... not for technical or statistical reasons, but for **substantial** reasons:  
it is unlikely that rates of different types of event (OAD initiation and death, say) depend on time in the same way.

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## Survival and cumulative risk functions



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## Cause-specific rates

```
> Sdm <- splitMulti(Adm, tfd = seq(0, 20, 0.1))
> summary(Adm)

Transitions:
To
From DM OAD Dead Records: Events: Risk time: Persons:
DM 685 634 226 1545 860 5414.3 1545

> summary(Sdm)

Transitions:
To
From DM OAD Dead Records: Events: Risk time: Persons:
DM 54064 634 226 54924 860 5414.3 1545
```

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## Survival function and cumulative risks—don't

$$S(t) = \exp\left(-\int_0^t \lambda(u) + \mu(u) du\right)$$

$$R_{\text{Dead}}(t) = \int_0^t \mu(u) S(u) du$$

$$R_{\text{OAD}}(t) = \int_0^t \lambda(u) S(u) du$$

$$= \int_0^t \lambda(u) \exp\left(-\int_0^u \lambda(s) + \mu(s) ds\right) du$$

$$\neq \int_0^t \lambda(u) \exp\left(-\int_0^u \lambda(s) ds\right) du$$

$$= 1 - \exp\left(-\int_0^t \lambda(s) ds\right) \text{ --- nice formula, but wrong!}$$

Probability of OAD **assuming** Dead does not exist **and** rate of OAD unchanged!

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## Cause-specific rates

```
> round(cbind(
+ with(subset(Sdm, lex.Xst == "OAD" ), quantile(tfd + lex.dur, 0:5/5)),
+ with(subset(Sdm, lex.Xst == "Dead"), quantile(tfd + lex.dur, 0:5/5))), 2)

      [,1] [,2]
0%    0.00 0.01
20%   0.09 0.51
40%   0.24 1.73
60%   1.27 3.58
80%   3.37 6.20
100% 14.31 11.86

> okn <- c(0, 0.5, 3, 10)
> dkn <- c(0, 2.0, 5, 9)
> OAD.glm <- glm.Lexis(Sdm, ~ Ns(tfd, knots = okn), to = "OAD" )

stats::glm Poisson analysis of Lexis object Sdm with log link:
Rates for the transition: DM->OAD

> Dead.glm <- glm.Lexis(Sdm, ~ Ns(tfd, knots = dkn), to = "Dead")

stats::glm Poisson analysis of Lexis object Sdm with log link:
Rates for the transition: DM->Dead
```

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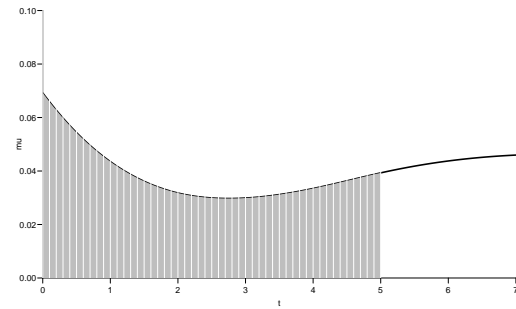


## Cause-specific rates

```
> int <- 0.01
> nd <- data.frame(tfd = seq(0, 15, int))
> l.glm <- ci.pred(DAD.glm, nd)
> m.glm <- ci.pred(Dead.glm, nd)
> matshade(nd$tfd,
+         cbind(l.glm, m.glm) * 100,
+         plot = TRUE,
+         yaxs="i", ylim = c(0, 20),
+         # log = "y", ylim = c(2, 20),
+         col = rep(c("red", "black"), 2), lwd = 3)
```

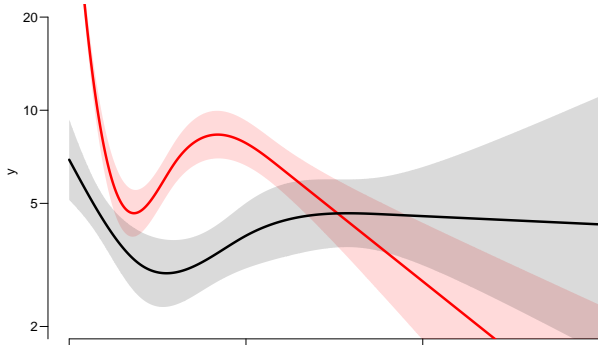
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## Integrals with R



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## Survival and cumulative risk functions



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## Numerical integration with R

```
> mid <- function(x) x[-1] - diff(x) / 2
> (x <- c(1:5, 7, 10))
[1] 1 2 3 4 5 7 10
> mid(x)
[1] 1.5 2.5 3.5 4.5 6.0 8.5
```

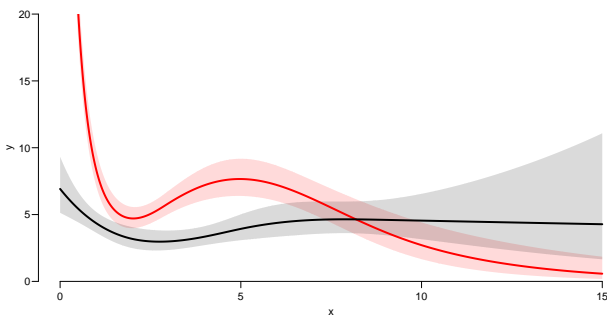
`mid(x)` is a vector that is 1 shorter than the vector `x`, just as `diff(x)` is.

So if we want the integral over the period 0 to 5 years, we want the sum over the first 500 intervals, corresponding to the first 501 interval endpoints:

```
> cbind(diff(t), mid(mu))[1:5,]
      [,1]      [,2]
2 0.01 0.069022
3 0.01 0.068685
4 0.01 0.068350
5 0.01 0.068017
6 0.01 0.067686
```

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## Survival and cumulative risk functions



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## Numerical integration with R

In practice we will want the integral **function** of  $\mu$ , so for every  $t$  we want  $M(t) = \int_0^t \mu(s) ds$ . This is easily accomplished by the function `cumsum`:

```
> Mu <- c(0, cumsum(diff(t) * mid(mu)))
> head(cbind(t, Mu))
      t      Mu
2 0.01 0.00069022
3 0.02 0.00137707
4 0.03 0.00206057
5 0.04 0.00274074
6 0.05 0.00341760
```

Note the first value which is the integral from 0 to 0, so by definition 0.

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## Integrals with R

- Integrals look scary to many people, but they are really just areas under curves.
- The key is to understand how a curve is represented in R.
- A curve of the function  $\mu(t)$  is a set of two vectors: one vector of  $t$ s and one vector  $y = \mu(t)$ s.
- When we have a model such as the `glm` above that estimates the mortality as a function of time (`tfd`), we can get the mortality as a function of time by first choosing the timepoints, say from 0 to 15 years in steps of 0.01 year ( $\approx 4$  days), using `ci.pred`
- Then use the formulae with all the integrals to get the state probabilities.

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## Cumulative risks from parametric models

If we have estimates of  $\lambda$  and  $\mu$  as functions of time, we can derive the cumulative risks.

In practice this will be by numerical integration; compute the rates at closely spaced intervals and evaluate the integrals as sums. This is easy.

but what is not so easy is to come up with confidence intervals for the cumulative risks.

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## Integrals with R

```
> t <- seq(0, 15, 0.01)
> nd <- data.frame(tfd = t)
> mu <- ci.pred(Dead.glm, nd)[,1]
> head(cbind(t, mu))
      t      mu
1 0.00 0.069190
2 0.01 0.068853
3 0.02 0.068517
4 0.03 0.068183
5 0.04 0.067851
6 0.05 0.067520

> plot(t, mu, type="l", lwd = 3,
+      xlim = c(0, 7), xaxs = "i",
+      ylim = c(0, 0.1), yaxs = "i")
> polygon(t[c(1:501, 501:1)], c(mu[1:501], rep(0, 501)),
+        col = "gray", border = "transparent")
> abline(v=0.50/10, col="white")
```

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## Simulation of cumulative risks: `ci.Crisk`

- generate a random vector from the multivariate normal distribution with mean equal to the parameters of the model, and variance-covariance equal to the estimated variance-covariance of the parameter estimates
- use this to generate a simulated set of rates  $(\lambda(t), \mu(t))$ , evaluated at a closely spaced times
- use these in numerical integration to derive state probabilities at these times
- repeat 1000 times, say, to obtain 1000 sets of state probabilities at these times
- use these to derive confidence intervals for the state probabilities as the 2.5 and 97.5 percentiles of the state probabilities at each time

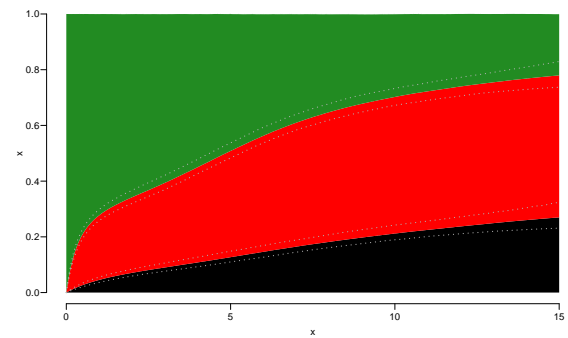
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## Cumulative risks from parametric models

```
> cR <- ci.Crisk(mods = list(OAD = OAD.glm,
+                           Dead = Dead.glm),
+               nd = nd)
NOTE: Times are assumed to be in the column tfd at equal distances of 0.01
> str(cR)
List of 4
 $ Crisk: num [1:1501, 1:3, 1:3] 1 0.992 0.984 0.976 0.969 ...
 .. attr(*, "dimnames")=List of 3
 .. ..$ tfd : chr [1:1501] "0" "0.01" "0.02" "0.03" ...
 .. ..$ cause: chr [1:3] "Surv" "OAD" "Dead"
 .. ..$ : chr [1:3] "50%" "2.5%" "97.5%"
 $ Srisk: num [1:1501, 1:2, 1:3] 0 0.000692 0.001375 0.002049 0.002715 ...
 .. attr(*, "dimnames")=List of 3
 .. ..$ tfd : chr [1:1501] "0" "0.01" "0.02" "0.03" ...
 .. ..$ cause: chr [1:2] "Dead" "Dead+OAD"
 .. ..$ : chr [1:3] "50%" "2.5%" "97.5%"
 $ Stime: num [1:1501, 1:3, 1:3] 0 0.00996 0.01984 0.02964 0.03937 ...
 .. attr(*, "dimnames")=List of 3
 .. ..$ tfd : chr [1:1501] "0" "0.01" "0.02" "0.03" ...
```

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## Survival and cumulative risk functions



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## Cumulative risks from parametric models

So now plot the cumulative *risks* of being in each of the states (the *Crisk* component):

```
> matshade(cR$Stime, cbind(cR$Crisk[,1,],
+                         cR$Crisk[,2,],
+                         cR$Crisk[,3,]), plot = TRUE,
+         lwd = 2, col = c("limegreen", "red", "black"))
```

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## Expected life time: using simulated objects

The areas between the lines (up to say 10 years) are **expected sojourn times**, that is:

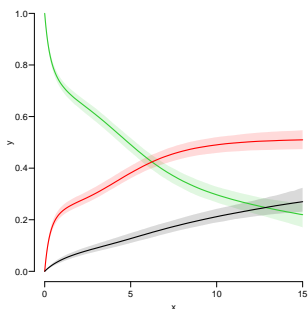
- ▶ expected years alive without OAD
- ▶ expected years lost to death without OAD
- ▶ expected years after OAD, including years dead after OAD

Not all of these are of direct relevance; actually only the first may be so.

They are available (with simulation-based confidence intervals) in the component of `cR`, `Stime` (*Sojourn time*).

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## Survival and cumulative risk functions



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## Expected life time: using simulated objects

A relevant quantity would be the expected time alive without OAD during the first 5, 10 and 15 years:

```
> str(cR$Stime)
num [1:1501, 1:3, 1:3] 0 0.00996 0.01984 0.02964 0.03937 ...
- attr(*, "dimnames")=List of 3
 ..$ tfd : chr [1:1501] "0" "0.01" "0.02" "0.03" ...
 ..$ cause: chr [1:3] "Surv" "OAD" "Dead"
 ..$ : chr [1:3] "50%" "2.5%" "97.5%"
> round(cR$Stime[c("5", "10", "15"), "Surv", ], 1)
tfd 50% 2.5% 97.5%
 5 3.2 3.1 3.3
10 5.1 4.9 5.3
15 6.4 6.0 6.7
```

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## Stacked probabilities: (matrix 2 polygons)

```
> mat2pol(cR$Crisk[,3:1,1], col = c("forestgreen", "red", "black")[3:1])
```

1st argument to `mat2pol` must be a 2-dimensional matrix, with rows representing the *x*-axis of the plot, and columns states.

The component `Srisk` has the confidence limits of the stacked probabilities:

```
> mat2pol(cR$Crisk[,3:1,1], col = c("forestgreen", "red", "black")[3:1])
> matlines(as.numeric(dimnames(cR$Srisk)[["tfd"]]),
+         cbind(cR$Srisk[, "Dead" , 2:3],
+             cR$Srisk[, "Dead+OAD", 2:3]),
+         lty = 3, lwd = 2, col = gray(0.7))
```

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