

Representation of follow-up

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IARC, Lyon,
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Bendix Carstensen

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time-split

Follow-up and rates

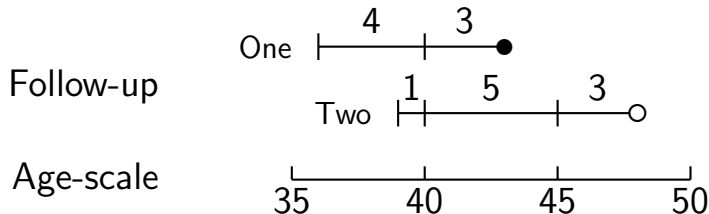
- ▶ In follow-up studies we estimate rates from:
 - ▶ D — events, deaths
 - ▶ Y — person-years
 - ▶ $\hat{\lambda} = D/Y$ rates
 - ▶ ... empirical counterpart of intensity — **estimate**
- ▶ Rates differ between persons.
- ▶ Rates differ **within** persons:
 - ▶ By age
 - ▶ By calendar time
 - ▶ By disease duration
 - ▶ ...
- ▶ Multiple timescales.
- ▶ Multiple states (little boxes — later)

Examples: stratification by age

If follow-up is rather short, age at entry is OK for age-stratification.

If follow-up is long, use stratification by categories of **current age**, both for:

No. of events, D , and Risk time, Y .



— assuming a constant rate λ throughout.

Representation of follow-up data

A cohort or follow-up study records:

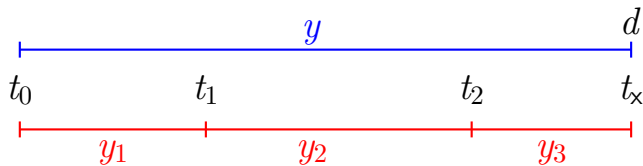
Events and **Risk time**.

The outcome is thus **bivariate**: (d, y)

Follow-up **data** for each individual must therefore have (at least) three variables:

Date of entry	entry	date variable
Date of exit	exit	date variable
Status at exit	fail	indicator (0/1)

Specific for each **type** of outcome.



Probability

$$P(d \text{ at } t_x | \text{entry } t_0)$$

$$= P(\text{surv } t_0 \rightarrow t_1 | \text{entry } t_0)$$

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

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

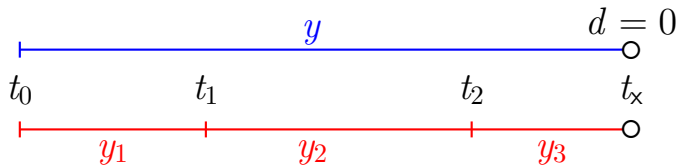
log-Likelihood

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

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

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

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



Probability

$$P(\text{surv } t_0 \rightarrow t_x | \text{entry } t_0)$$

$$= P(\text{surv } t_0 \rightarrow t_1 | \text{entry } t_0)$$

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

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

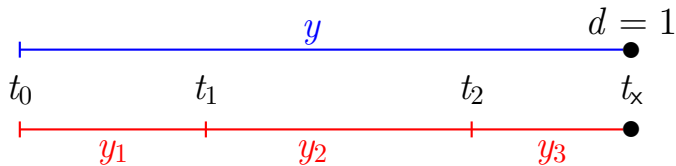
log-Likelihood

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

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

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

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



Probability

$P(\text{event at } t_x | \text{entry } t_0)$

$= P(\text{surv } t_0 \rightarrow t_1 | \text{entry } t_0)$

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

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

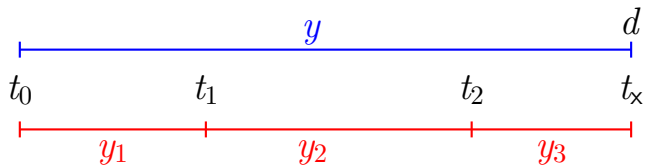
log-Likelihood

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

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

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

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



Probability

$$P(d \text{ at } t_x | \text{entry } t_0)$$

$$= P(\text{surv } t_0 \rightarrow t_1 | \text{entry } t_0)$$

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

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

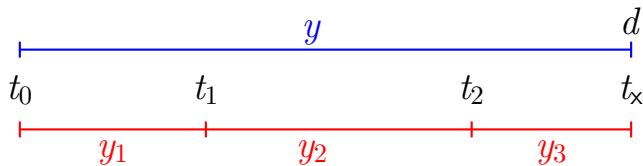
log-Likelihood

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

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

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

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



Probability

$$P(d \text{ at } t_x | \text{entry } t_0)$$

$$= P(\text{surv } t_0 \rightarrow t_1 | \text{entry } t_0)$$

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

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

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 (λ_i) in each interval

Dividing time into bands:

If we want to compute D and Y in intervals on some timescale we must decide on:

Origin: The date where the time scale is 0:

- ▶ Age — 0 at date of birth
- ▶ Disease duration — 0 at date of diagnosis
- ▶ Occupation exposure — 0 at date of hire

Intervals: How should it be subdivided:

- ▶ 1-year classes? 5-year classes?
- ▶ Equal length?

Aim: Separate rate in each interval

Example: cohort with 3 persons:

Id	Bdate	Entry	Exit	St
1	14/07/1952	04/08/1965	27/06/1997	1
2	01/04/1954	08/09/1972	23/05/1995	0
3	10/06/1987	23/12/1991	24/07/1998	1

- ▶ Age bands: 10-years intervals of current age.
- ▶ Split Y for every subject accordingly
- ▶ Treat each segment as a separate unit of observation.
- ▶ Keep track of exit status in each interval.

Splitting the follow up

	subj. 1	subj. 2	subj. 3
Age at E ntry:	13.06	18.44	4.54
Age at e X it:	44.95	41.14	11.12
S tatus at exit:	Dead	Alive	Dead
<hr/>			
<i>Y</i>	31.89	22.70	6.58
<i>D</i>	1	0	1

Age	subj. 1		subj. 2		subj. 3		Σ	
	<i>Y</i>	<i>D</i>	<i>Y</i>	<i>D</i>	<i>Y</i>	<i>D</i>	<i>Y</i>	<i>D</i>
0–	0.00	0	0.00	0	5.46	0	5.46	0
10–	6.94	0	1.56	0	1.12	1	8.62	1
20–	10.00	0	10.00	0	0.00	0	20.00	0
30–	10.00	0	10.00	0	0.00	0	20.00	0
40–	4.95	1	1.14	0	0.00	0	6.09	1
Σ	31.89	1	22.70	0	6.58	1	60.17	2

Splitting the follow-up

id	Bdate	Entry	Exit	St	risk	int
1	14/07/1952	03/08/1965	14/07/1972	0	6.9432	10
1	14/07/1952	14/07/1972	14/07/1982	0	10.0000	20
1	14/07/1952	14/07/1982	14/07/1992	0	10.0000	30
1	14/07/1952	14/07/1992	27/06/1997	1	4.9528	40
2	01/04/1954	08/09/1972	01/04/1974	0	1.5606	10
2	01/04/1954	01/04/1974	31/03/1984	0	10.0000	20
2	01/04/1954	31/03/1984	01/04/1994	0	10.0000	30
2	01/04/1954	01/04/1994	23/05/1995	0	1.1417	40
3	10/06/1987	23/12/1991	09/06/1997	0	5.4634	0
3	10/06/1987	09/06/1997	24/07/1998	1	1.1211	10

Keeping track of calendar time too?

Timescales

- ▶ A timescale is a variable that varies **deterministically** *within* each person during follow-up:
 - ▶ Age
 - ▶ Calendar time
 - ▶ Time since treatment
 - ▶ Time since relapse
- ▶ All timescales advance at the same pace (1 year per year . . .)
- ▶ Note: Cumulative exposure is **not** a timescale.

Follow-up on several timescales

- ▶ The risk-time is the same on all timescales
- ▶ Only need the entry point on each time scale:
 - ▶ Age at entry.
 - ▶ Date of entry.
 - ▶ Time since treatment at entry.
 - if time of treatment is the entry, this is 0 for all.

- ▶ **Response variable** in analysis of rates:

(d, y) (**event, duration**)

- ▶ **Covariates** in analysis of rates:
 - ▶ **timescales**
 - ▶ other (fixed) measurements
- ▶ ... do not confuse **duration** and **timescale** !

Follow-up data in Epi — Lexis objects

```
> thoro[1:6,1:8]
```

	id	sex	birthdat	contrast	injecdat	volume	exitdat	exitstat
1	1	2	1916.609	1	1938.791	22	1976.787	1
2	2	2	1927.843	1	1943.906	80	1966.030	1
3	3	1	1902.778	1	1935.629	10	1959.719	1
4	4	1	1918.359	1	1936.396	10	1977.307	1
5	5	1	1902.931	1	1937.387	10	1945.387	1
6	6	2	1903.714	1	1937.316	20	1944.738	1

Timescales of interest:

- ▶ Age
- ▶ Calendar time
- ▶ Time since injection

Definition of Lexis object

```
thL <- Lexis( entry = list( age = injecdat-birthdat,  
                           per = injecdat,  
                           tfi = 0 ),  
             exit = list( per = exitdat ),  
             exit.status = as.numeric(exitstat==1),  
             data = thoro )
```

entry is defined on **three** timescales,

but **exit** is only needed on **one** timescale:

Follow-up time is the same on all timescales:

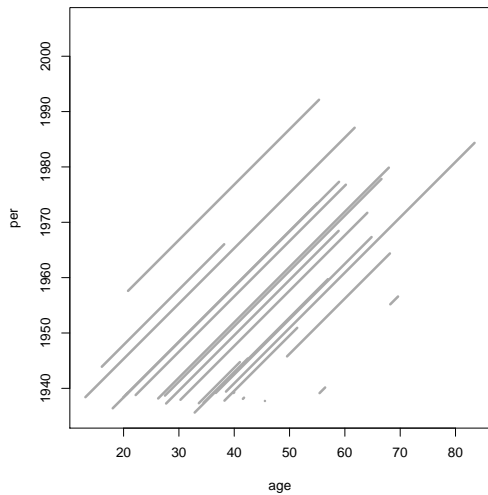
`exitdat - injecdat`

One element of **entry** and **exit** must have same name (**per**).

The looks of a Lexis object

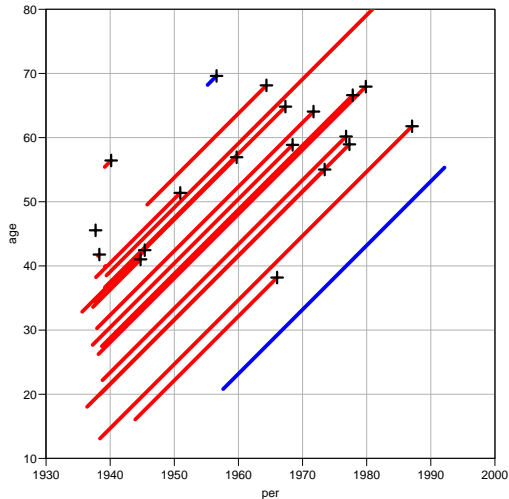
```
> thL[1:4,1:9]
  age      per tfi lex.dur lex.Cst lex.Xst lex.id
1 22.18 1938.79  0  37.99      0      1      1
2 49.54 1945.77  0  18.59      0      1      2
3 68.20 1955.18  0   1.40      0      1      3
4 20.80 1957.61  0  34.52      0      0      4
...

> summary( thL )
Transitions:
      To
From   0    1 Records:  Events:  Risk time:  Persons:
      0 504 1964      2468      1964      51934.08      2468
```



```
> plot( thL, lwd=3 )
```

Representation of follow-up (time-split)



```

> plot( thL, 2:1, lwd=5, col=c("red","blue")[thL$contrast],
+       grid=TRUE, lty.grid=1, col.grid=gray(0.7),
+       xlim=1930+c(0,70), xaxs="i", ylim= 10+c(0,70), yaxs="i", las=1 )
> points( thL, 2:1, pch=c(NA,3)[thL$lex.Xst+1],lwd=3, cex=1.5 )

```

EINLEITUNG
IN DIE
THEORIE
DER
BEVÖLKERUNGSSTATISTIK

VON
W. LEXIS
DR. DER STAATSWISSENSCHAFTEN UND DER PHILOSOPHIE,
O. PROFESSOR DER STATISTIK IN DORPAT.

STRASSBURG
KARL J. TRÜBNER
1875.



Splitting follow-up time

```
> spl1 <- splitLexis( thL, breaks=seq(0,100,20),  
>                               time.scale="age" )  
> round(spl1,1)
```

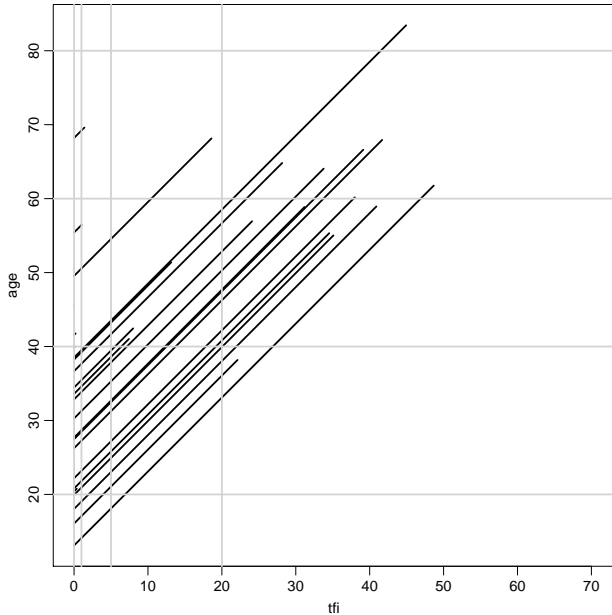
	age	per	tfi	lex.dur	lex.Cst	lex.Xst	id	sex	birthdat	contrast	injecdat	vol
1	22.2	1938.8	0.0	17.8	0	0	1	2	1916.6	1	1938.8	
2	40.0	1956.6	17.8	20.0	0	0	1	2	1916.6	1	1938.8	
3	60.0	1976.6	37.8	0.2	0	1	1	2	1916.6	1	1938.8	
4	49.5	1945.8	0.0	10.5	0	0	640	2	1896.2	1	1945.8	
5	60.0	1956.2	10.5	8.1	0	1	640	2	1896.2	1	1945.8	
6	68.2	1955.2	0.0	1.4	0	1	3425	1	1887.0	2	1955.2	
7	20.8	1957.6	0.0	19.2	0	0	4017	2	1936.8	2	1957.6	
8	40.0	1976.8	19.2	15.3	0	0	4017	2	1936.8	2	1957.6	
...												

Split on another timescale

```
> spl2 <- splitLexis( spl1, time.scale="tfi",  
                      breaks=c(0,1,5,20,100) )
```

```
> round( spl2, 1 )
```

	lex.id	age	per	tfi	lex.dur	lex.Cst	lex.Xst	id	sex	birthdat	contrast	inje
1	1	22.2	1938.8	0.0	1.0	0	0	1	2	1916.6	1	19
2	1	23.2	1939.8	1.0	4.0	0	0	1	2	1916.6	1	19
3	1	27.2	1943.8	5.0	12.8	0	0	1	2	1916.6	1	19
4	1	40.0	1956.6	17.8	2.2	0	0	1	2	1916.6	1	19
5	1	42.2	1958.8	20.0	17.8	0	0	1	2	1916.6	1	19
6	1	60.0	1976.6	37.8	0.2	0	1	1	2	1916.6	1	19
7	2	49.5	1945.8	0.0	1.0	0	0	640	2	1896.2	1	19
8	2	50.5	1946.8	1.0	4.0	0	0	640	2	1896.2	1	19
9	2	54.5	1950.8	5.0	5.5	0	0	640	2	1896.2	1	19
10	2	60.0	1956.2	10.5	8.1	0	1	640	2	1896.2	1	19
11	3	68.2	1955.2	0.0	1.0	0	0	3425	1	1887.0	2	19
12	3	69.2	1956.2	1.0	0.4	0	1	3425	1	1887.0	2	19
13	4	20.8	1957.6	0.0	1.0	0	0	4017	2	1936.8	2	19
14	4	21.8	1958.6	1.0	4.0	0	0	4017	2	1936.8	2	19
15	4	25.8	1962.6	5.0	14.2	0	0	4017	2	1936.8	2	19
16	4	40.0	1976.8	19.2	0.8	0	0	4017	2	1936.8	2	19
17	4	40.8	1977.6	20.0	14.5	0	0	4017	2	1936.8	2	19



age	tfi	lex.dur	lex.Cst	lex.Xst
22.2	0.0	1.0	0	0
23.2	1.0	4.0	0	0
27.2	5.0	12.8	0	0
40.0	17.8	2.2	0	0
42.2	20.0	17.8	0	0
60.0	37.8	0.2	0	1

Likelihood for a constant rate

- ▶ This setup is for a situation where it is assumed that rates are constant in each of the intervals.
- ▶ Each observation in the dataset contributes a term to the likelihood.
- ▶ Each term looks like a contribution from a Poisson variate (albeit with values only 0 or 1)
- ▶ Rates can vary along several timescales simultaneously.
- ▶ Models can include fixed covariates, as well as the timescales (the left end-points of the intervals) as continuous variables.
- ▶ The latter is where we will need splines.

The Poisson likelihood for split data

- ▶ Split records (one per **person-interval** (p, i)):

$$\sum_{p,i} (d_{pi} \log(\lambda) - \lambda y_{pi}) = D \log(\lambda) - \lambda Y$$

- ▶ Assuming that the death indicator ($d_{pi} \in \{0, 1\}$) is Poisson, a model with with offset $\log(y_{pi})$ will give the same result.
- ▶ If we assume that rates are constant we get the simple expression with (D, Y)
- ▶ ... but the split data allows models that assume different rates for different (d_{pi}, y_{pi}) , so rates can vary **within** a person's follow-up.

Where is (d_{pi}, y_{pi}) in the split data?

```
> spl1 <- splitLexis( thL , breaks=seq(0,100,20) , time.scale="age" )
> spl2 <- splitLexis( spl1, breaks=c(0,1,5,20,100), time.scale="tfi" )
> options( digits=5 )
> spl2[1:10,1:11]
```

	lex.id	age	per	tfi	lex.dur	lex.Cst	lex.Xst	id	sex	birthdat	contrast
1	1	22.182	1938.8	0.000	1.00000	0	0	1	2	1916.6	1
2	1	23.182	1939.8	1.000	4.00000	0	0	1	2	1916.6	1
3	1	27.182	1943.8	5.000	12.81793	0	0	1	2	1916.6	1
4	1	40.000	1956.6	17.818	2.18207	0	0	1	2	1916.6	1
5	1	42.182	1958.8	20.000	17.81793	0	0	1	2	1916.6	1
6	1	60.000	1976.6	37.818	0.17796	0	1	1	2	1916.6	1
7	2	16.063	1943.9	0.000	1.00000	0	0	2	2	1927.8	1
8	2	17.063	1944.9	1.000	2.93703	0	0	2	2	1927.8	1
9	2	20.000	1947.8	3.937	1.06297	0	0	2	2	1927.8	1
10	2	21.063	1948.9	5.000	15.00000	0	0	2	2	1927.8	1

— and what are covariates for the rates?

Analysis of results

- ▶ d_{pi} — events in the variable: `lex.Xst`:
In the model as response: `lex.Xst==1`
- ▶ y_{pi} — risk time: `lex.dur` (duration):
In the model as offset `log(y)`, `log(lex.dur)`.
- ▶ Covariates are:
 - ▶ timescales (age, period, time in study)
 - ▶ other variables for this person (constant or *assumed* constant in each interval).
- ▶ Model rates using the covariates in `glm`:
— no difference between time-scales and other covariates.

Fitting a simple model

```
> stat.table( contrast,  
+             list( D = sum( lex.Xst ),  
+                 Y = sum( lex.dur ),  
+                 Rate = ratio( lex.Xst, lex.dur, 100 ) ),  
+             margin = TRUE,  
+             data = spl2 )
```

contrast	D	Y	Rate
1	928.00	20094.74	4.62
2	1036.00	31839.35	3.25
Total	1964.00	51934.08	3.78

Fitting a simple model

contrast	D	Y	Rate
1	928.00	20094.74	4.62
2	1036.00	31839.35	3.25

```
> m0 <- glm( (lex.Xst==1) ~ factor(contrast) - 1,  
+           offset = log(lex.dur/100),  
+           family = poisson,  
+           data = spl2 )  
> round( ci.exp( m0 ), 2 )
```

```
                exp(Est.) 2.5% 97.5%  
factor(contrast)1      4.62 4.33  4.93  
factor(contrast)2      3.25 3.06  3.46
```


SMR

Bendix Carstensen

Representation of follow-up

IARC, Lyon,
June 2018

<http://BendixCarstensen.com/SPE>

Cohorts where all are exposed

When there is no comparison group we may ask:

Do mortality rates in cohort differ from those of an **external** population, for example:

Rates from:

- ▶ Occupational cohorts
- ▶ Patient cohorts

compared with reference rates obtained from:

- ▶ Population statistics (mortality rates)
- ▶ Hospital registers (disease rates)

Cohort rates vs. population rates: RSR

- ▶ **Additive:** $\lambda(a) = \delta(a) + \lambda_P(a)$
- ▶ Note that the survival (since $a = a_0$, say) is:

$$S(a) = \exp\left(-\int_{a_0}^a \delta(a) + \lambda_P(a) da\right)$$

$$= \exp\left(-\int_{a_0}^a \delta(a) da\right) \times S_P(a)$$

$$\Rightarrow r(a) = S(a)/S_P(a) = \exp\left(-\int_{a_0}^a \delta(a) da\right)$$

- ▶ Additive model for rates \Leftrightarrow Relative survival model.

Cohort rates vs. population rates: SMR

- ▶ **Multiplicative:** $\lambda(a) = \theta\lambda_P(a)$
- ▶ Cohort rates proportional to reference rates:
 $\lambda(a) = \theta \times \lambda_P(a)$ — θ the same in all age-bands.
- ▶ D_a deaths during Y_a person-years an age-band a gives the likelihood:

$$\begin{aligned} D_a \log(\lambda(a)) - \lambda(a) Y_a &= D_a \log(\theta \lambda_P(a)) - \theta \lambda_P(a) Y_a \\ &= D_a \log(\theta) + D_a \log(\lambda_P(a)) - \theta(\lambda_P(a) Y_a) \end{aligned}$$

- ▶ The constant $D_a \log(\lambda_P(a))$ does not involve θ , and so can be dropped.

- ▶ $\lambda_P(a) Y_a = E_a$ is the “expected” number of cases in age a , so the log-likelihood contribution from age a is:

$$D_a \log(\theta) - \theta(\lambda_P(a) Y_a) = D_a \log(\theta) - \theta(E_a)$$

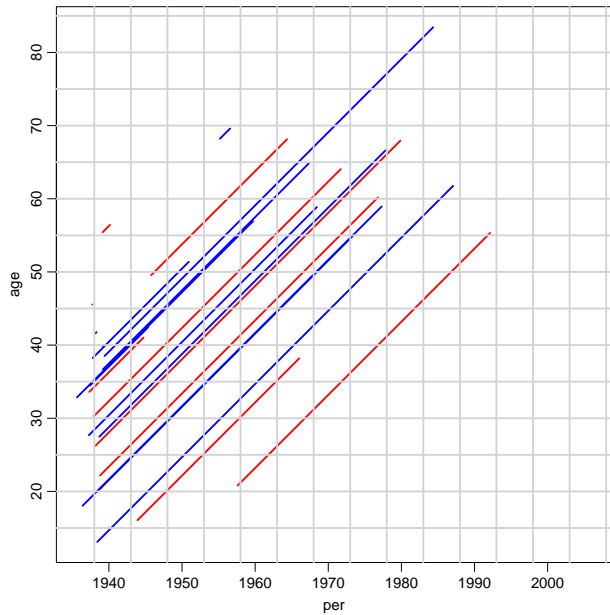
- ▶ **Note:** $\lambda_P(a)$ is known for all values of a .
- ▶ The log-likelihood is similar to the log-likelihood for a rate, except that person-years Y is replaced by expected numbers, E , so:

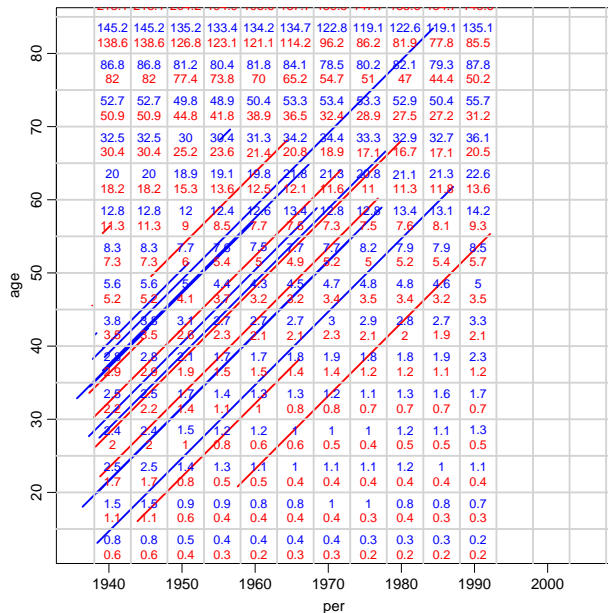
$$\hat{\theta} = \frac{D}{\lambda_P Y} = \frac{D}{E} = \frac{\text{Observed}}{\text{Expected}} = \text{SMR}$$

- ▶ SMR is the maximum likelihood estimator of the relative mortality in the cohort.

Modelling the SMR in practise

- ▶ As for the rates, the SMR can be modelled using individual data.
- ▶ Response is d_i , the event indicator (lex.Xst).
- ▶ log-offset is the expected value for each piece of follow-up,
 $e_i = y_i \times \lambda_P$ (lex.dur * rate)
- ▶ λ_P is the population rate corresponding to the age, period and sex of the follow-up period y_i .





Split the data to fit with population data

```
> tha <- splitLexis(thL, time.scale="age", breaks=seq(0,90,5) )  
> thap <- splitLexis(tha, time.scale="per", breaks=seq(1938,2038,5) )  
> dim( thap )
```

```
[1] 23094    21
```

Create variables to fit with the population data

```
> thap$agr <- timeBand( thap, "age", "left" )  
> thap$cal <- timeBand( thap, "per", "left" )  
> round( thap[1:5,c("lex.id","age","agr","per","cal","lex.dur","lex.Xst","sex")],
```

	lex.id	age	agr	per	cal	lex.dur	lex.Xst	sex
1	1	22.18	20	1938.79	1938	2.82	0	2
2	1	25.00	25	1941.61	1938	1.39	0	2
3	1	26.39	25	1943.00	1943	3.61	0	2
4	1	30.00	30	1946.61	1943	1.39	0	2
5	1	31.39	30	1948.00	1948	3.61	0	2

```

> data( gmortDK )
> gmortDK[1:6,1:6]

  agr per sex  risk  dt  rt
1   0  38   1 996019 14079 14.135
2   5  38   1 802334   726  0.905
3  10  38   1 753017   600  0.797
4  15  38   1 773393  1167  1.509
5  20  38   1 813882  2031  2.495
6  25  38   1 789990  1862  2.357

> gmortDK$cal <- gmortDK$per+1900
> #
> thapx <- merge( thap, gmortDK[,c("agr","cal","sex","rt")] )
> #
> thapx$E <- thapx$lex.dur * thapx$rt / 1000

```

```

> stat.table( contrast,
+             list( D = sum( lex.Xst ),
+                 Y = sum( lex.dur ),
+                 E = sum( E ),
+                 SMR = ratio( lex.Xst, E ) ),
+             margin = TRUE,
+             data = thapx )

```

contrast	D	Y	E	SMR
1	923.00	20072.53	222.01	4.16
2	1036.00	31839.35	473.88	2.19
Total	1959.00	51911.87	695.89	2.82

contrast	D	Y	E	SMR
1	923.00	20072.53	222.01	4.16
2	1036.00	31839.35	473.88	2.19
Total	1959.00	51911.87	695.89	2.82

```
> m.SMR <- glm( lex.Xst ~ factor(contrast) - 1,
+             offset = log(E),
+             family = poisson,
+             data = thapx )
> round( ci.exp( m.SMR ), 2 )
```

	exp(Est.)	2.5%	97.5%
factor(contrast)1	4.16	3.90	4.43
factor(contrast)2	2.19	2.06	2.32

- ▶ Analysis of SMR is like analysis of rates:
- ▶ Replace Y with E — that's all!