An APC Analytic Approach to Analyzing and Predicting National Trends in Diabetes Incidence over Time

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http://BendixCarstensen.com

Emory University, Rollins School of Public Health, June 2019

An overview of APC models

- Data in a Lexis diagram — and where they come from.

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- Practical use in forecasting

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Models for tabulated data

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Conceptual set-up

Follow-up of the entire (male) population from 1943–2006 w.r.t. occurrence of testis cancer:

- Split follow-up time for all about 4 mil. men in 1-year classes by age and calendar time (y).
- Allocate testis cancer event $(d = 0, 1)$ to each.
- Analyze all $200,000,000$ records by a Poisson model.

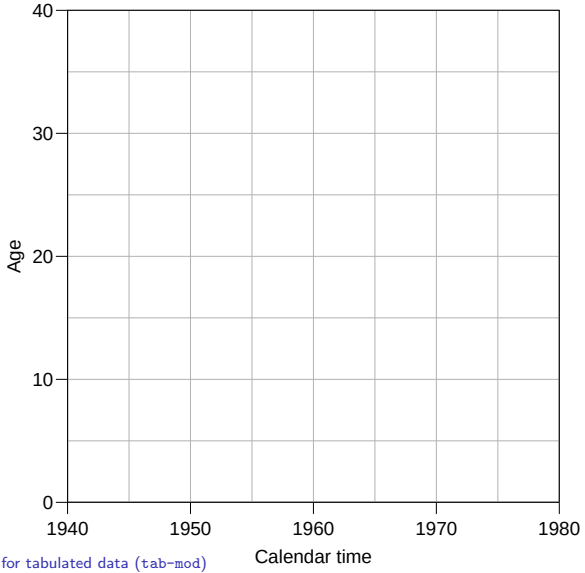
Realistic set-up

- Tabulate the follow-up time and events by age and period.
- 100 age-classes.
- 65 periods (single calendar years).
- 6500 aggregate records of (D, Y).
- Analyze by a Poisson model
- . . . note: I have not specified how the model looks

Practical set-up

- Tabulate only events (as obtained from the cancer registry) by age and period.
- 100 age-classes.
- 65 periods (single calendar years).
- 6500 aggregate records of D.
- Estimate the population follow-up based on census data from Statistics Denmark (Y_{pop}).
  ...or get it from the human mortality database.
- If disease is common: tabulate follow-up **after** diagnosis (Y_{dis}), and subtract from population follow-up.
- Analyze (D, Y) by Poisson model.

Lexis diagram [1]



Disease registers record events.

Official statistics collect population data.

[1] Named after the German statistician and economist **William Lexis** (1837–1914), who devised this diagram in the book "Einleitung in die Theorie der Bevölkerungsstatistik" (Karl J. Trübner, Strassburg, 1875).

EINLEITUNG

IN DIE

THEORIE

DER

BEVÖLKERUNGSSTATISTIK

VON

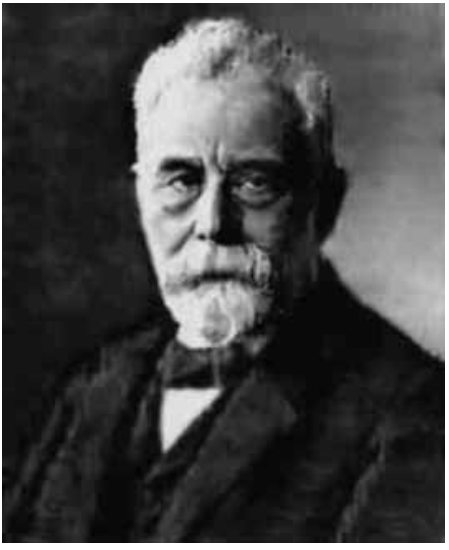
W. LEXIS

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

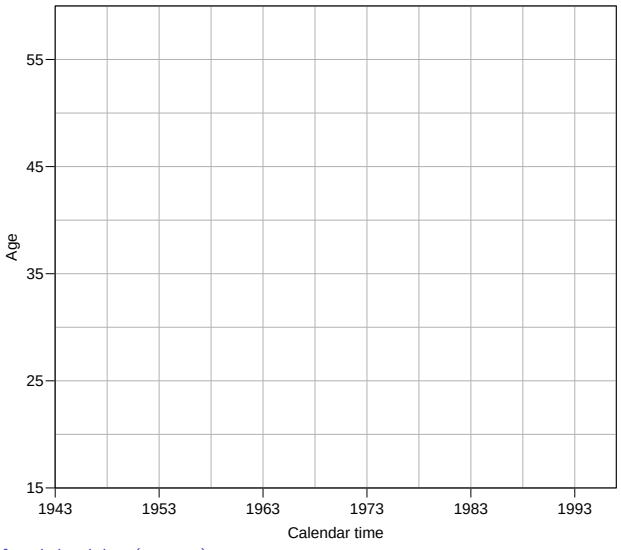
STRASSBURG

KARL J. TRÜBNER

1875.



Lexis diagram



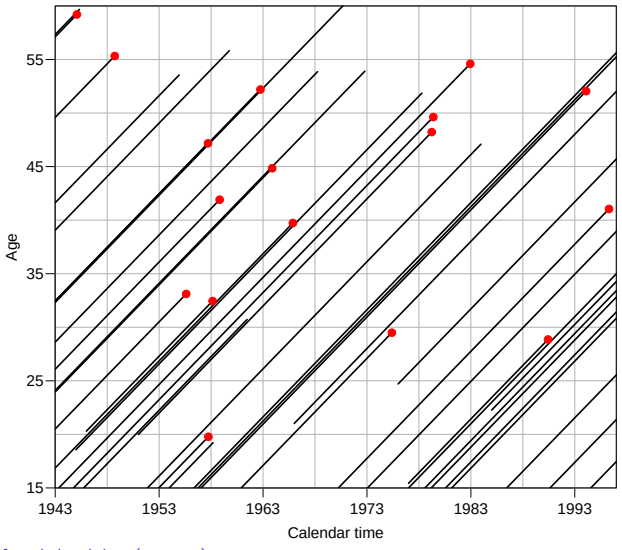
Registration of:

cases (D)

risk time,
person-years (Y)

in subsets of the Lexis diagram.

Lexis diagram



Registration of:

cases (D)

risk time,
person-years (Y)

in subsets of the Lexis diagram.

Rates available in each subset.

Register data

Classification of **cases** (D_{ap}) by age at diagnosis and date of diagnosis, and **population** (Y_{ap}) by age at risk and date at risk, in compartments of the Lexis diagram, e.g.:

```
> fCtable( xtabs( cbind(D,Y) ~ A + P, data=ts ), col.vars=3:2, w=8 )
```

	D				Y			
P	1943	1948	1953	1958	1943	1948	1953	1958
A								
15	2	3	4	1	773,812	744,217	794,123	972,853
20	7	7	17	8	813,022	744,706	721,810	770,859
25	28	23	26	35	790,501	781,827	722,968	698,612
30	28	43	49	51	799,293	774,542	769,298	711,596
35	36	42	39	44	769,356	782,893	760,213	760,452
40	24	32	46	53	694,073	754,322	768,471	749,912

In analysis format:

```
> ts

    A    P  D      Y
1  15 1943  2 773812
2  20 1943  7 813022
3  25 1943 28 790501
4  30 1943 28 799293
5  35 1943 36 769356
6  40 1943 24 694073
7  15 1948  3 744217
8  20 1948  7 744706
9  25 1948 23 781827
10 30 1948 43 774542
11 35 1948 42 782893
12 40 1948 32 754322
13 15 1953  4 794123
14 20 1953 17 721810
15 25 1953 26 722968
16 30 1953 49 769298
17 35 1953 39 760213
18 40 1953 46 768471
19 15 1958  1 972853
```

Tabulated data

Once data are in tabular form, models are restricted:

- Rates must be assumed constant in each cell of the table / subset of the Lexis diagram.
- With large cells (5×5 years) it is customary to put a separate parameter on each cell or on each levels of classifying factors.
- Output from the model will be rates and rate-ratios.
- Since we use multiplicative Poisson, usually the log rates and the log-RR are reported

Age-Period and Age-Cohort models

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Register data — rates

Rates in “tiles” of the Lexis diagram:

$$\lambda(a, p) = D_{ap} / Y_{ap}$$

Descriptive epidemiology based on disease registers:
How do the rates vary by age and time:

- Age-specific rates across periods.

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- Age-specific rates across cohorts.

Register data — rates

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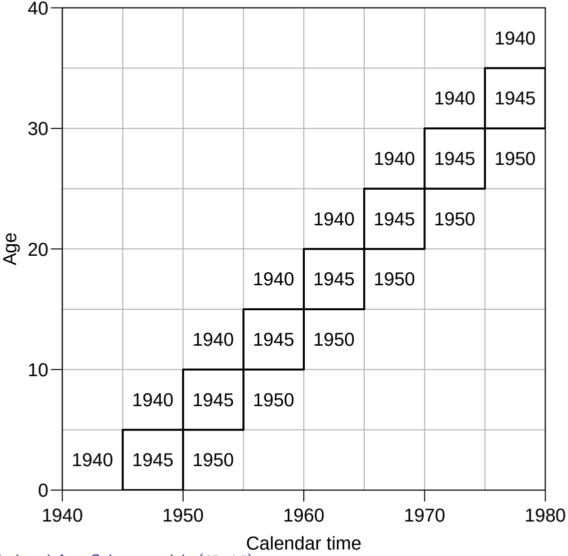
Descriptive epidemiology based on disease registers:
How do the rates vary by age and time:

- Age-specific rates across periods.
- Age-specific rates across cohorts.
- Age-standardized rates as a function of calendar time.
  (Weighted averages of the age-specific rates).

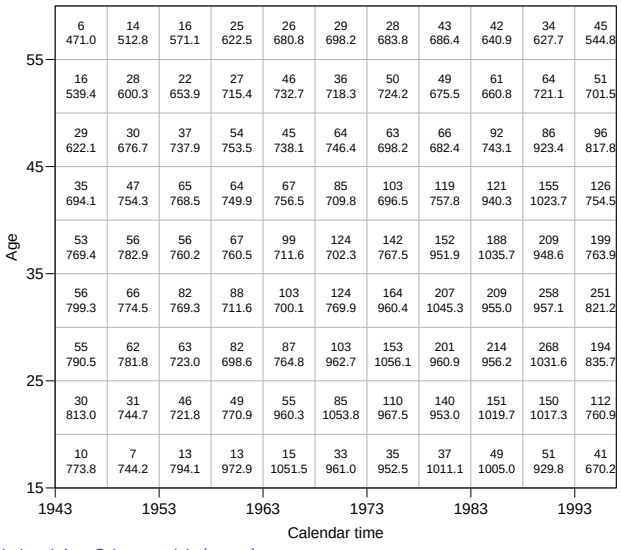
“Synthetic” cohorts



Events and risk time in cells along the diagonals are among persons with roughly same date of birth.

Successively overlapping 10-year periods.

Lexis diagram: data



6 471.0	14 512.8	16 571.1	25 622.5	26 680.8	29 698.2	28 683.8	43 686.4	42 640.9	34 627.7	45 544.8
16 539.4	28 600.3	22 653.9	27 715.4	46 732.7	36 718.3	50 724.2	49 675.5	61 660.8	64 721.1	51 701.5
29 622.1	30 676.7	37 737.9	54 753.5	45 738.1	64 746.4	63 698.2	66 682.4	92 743.1	86 923.4	96 817.8
35 694.1	47 754.3	65 768.5	64 749.9	67 756.5	85 709.8	103 696.5	119 757.8	121 940.3	155 1023.7	126 754.5
53 769.4	56 782.9	56 760.2	67 760.5	99 711.6	124 702.3	142 767.5	152 951.9	188 1035.7	209 948.6	199 763.9
56 799.3	66 774.5	82 769.3	88 711.6	103 700.1	124 769.9	164 960.4	207 1045.3	209 955.0	258 957.1	251 821.2
55 790.5	62 781.8	63 723.0	82 698.6	87 764.8	103 962.7	153 1056.1	201 960.9	214 956.2	268 1031.6	194 835.7
30 813.0	31 744.7	46 721.8	49 770.9	55 960.3	85 1053.8	110 967.5	140 953.0	151 1019.7	150 1017.3	112 760.9
10 773.8	7 744.2	13 794.1	13 972.9	15 1051.5	33 961.0	35 952.5	37 1011.1	49 1005.0	51 929.8	41 670.2

Testis cancer cases in Denmark.

Male person-years in Denmark.

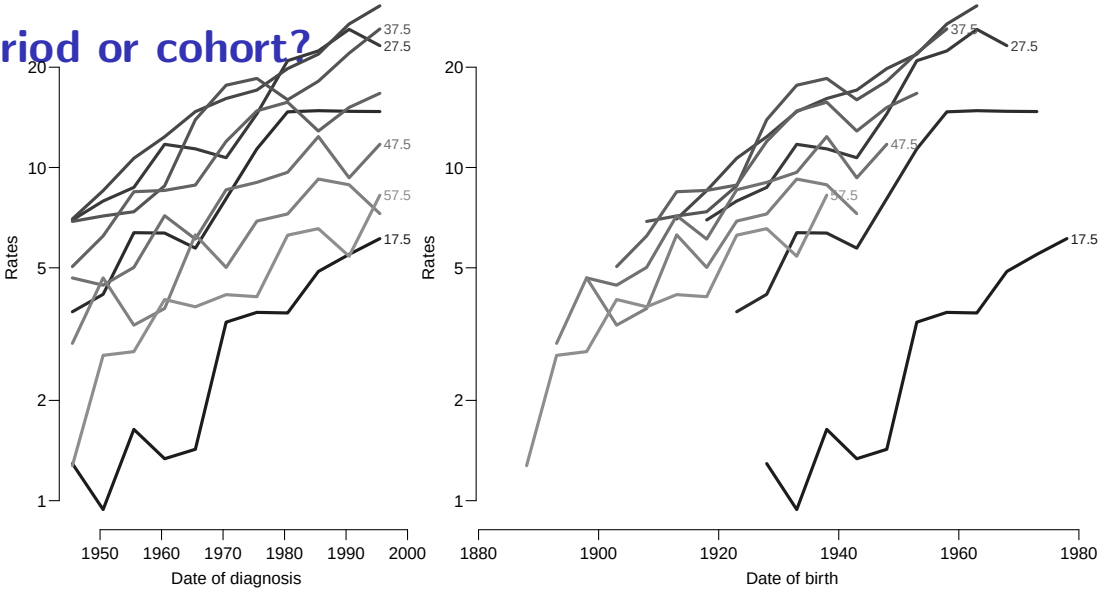
```
> library( Epi )
> data( testisDK )
> head( testisDK )

  A    P D        Y
1 0 1943 1 39649.50
2 1 1943 1 36942.83
3 2 1943 0 34588.33
4 3 1943 1 33267.00
5 4 1943 0 32614.00
6 5 1943 0 32020.33

> ts <- transform( subset( testisDK, A>14 & A<60 ),
+                  A = floor( A      /5)*5     +2.5,
+                  P = floor((P-1943)/5)*5+1943+2.5 )
> ts$C <- ts$P - ts$A
> trate <- xtabs( D ~ A + P, data = ts ) /
+          xtabs( Y ~ A + P, data = ts ) * 100000
> trate[1:5,1:6]

      P
A          1945.5     1950.5     1955.5     1960.5     1965.5     1970.5
  17.5  1.2923036  0.9405857  1.6370257  1.3362759  1.4264867  3.4340862
```

```
  22.5  3.6899378  4.1627194  6.3728682  6.3565492  5.7274822  8.0657826
  27.5  6.9576174  7.9301414  8.7140826 11.7375624 11.3753792 10.6996275
  32.5  7.0061961  8.5211703 10.6590661 12.3665762 14.7122260 16.1068525
  37.5  6.8888785  7.1529555  7.3663549  8.8105514 13.9126492 17.6571019
```

```
> par( mfrow=c(2,2) )
> rateplot( trate, col=gray(2:15/18), lwd=3, ann=TRUE )
>  wh = c("ap","ac","pa","ca")
> for( ptp in wh ) {
+    pdf( paste("./graph/AP-AC-",ptp,".pdf",sep=""), height=6, width=8 )
+    par( mar=c(3,3,1,1, mgp=c(3,1,0)/1.6, bty="n", las=1 ))
+    rateplot( trate, which=ptp,
+              col=gray(2:15/18), lwd=3, ann=TRUE, a.lim=c(15,60) )
+    dev.off()
+    }
>
```

```
> library( Epi )
> par( mar=c(3,3,.1,.1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> layout( mat=cbind(1,2),width=c(6,10) )
> for( ptp in c("pa","ca") )
+    rateplot( trate, which=ptp,
+              col=gray(2:15/18), lwd=3, ann=TRUE, a.lim=c(15,60) )
```

Period or cohort?



Age-Period model

Rates are proportional between periods:

$$\lambda(a,p) = a_a \times b_p \qquad \text{or} \qquad \log[\lambda(a,p)] = \alpha_a + \beta_p$$

Choose p_0 as reference period, where $\beta_{p_0} = 0$

$$\log[\lambda(a,p_0)] = \alpha_a + \beta_{p_0} = \alpha_a$$

Fitting the A-P model in R I

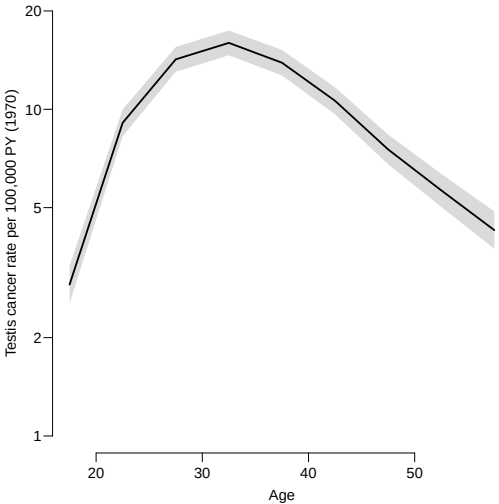
Reference period is the 5th period (1970.5 $\sim$ 1968–72):

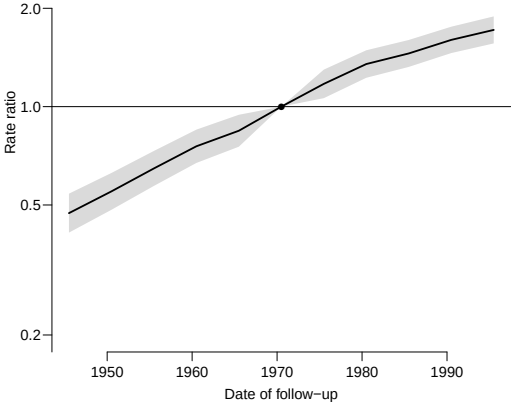
```
> ap <- glm( D ~ factor(A) - 1 + relevel( factor(P), "1970.5" ) +
+                  offset( log(Y/10^5) ),
+              family=poisson, data=ts )
> # summary( ap )
```

Estimates with confidence intervals

```
> par( mfrow=c(1,2), mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> matshade( seq(17.5,57.5,5), ci.exp(ap,subset="A"), plot=TRUE,
+           log="y", lwd=2, ylim=c(1,20), xlab="Age",
+           ylab="Testis cancer rate per 100,000 PY (1970)" )
> matshade( seq(1945.5,1995.5,5),
+           rbind( ci.exp(ap,subset="P")[1:5 ,], 1,
+                  ci.exp(ap,subset="P")[6:10,] ), plot=TRUE,
+           log="y", lwd=2, ylim=c(1,20)/5,
+           xlab="Date of follow-up", ylab="Rate ratio" )
> abline( h = 1)
> points( 1970.5, 1, pch=16 )
```

Estimates from Age-Period model





Age-cohort model

Rates are proportional between cohorts:

$$\lambda(a, c) = a_a \times c_c \qquad \text{or} \qquad \log[\lambda(a, p)] = \alpha_a + \gamma_c$$

Choose c_0 as reference cohort, where $\gamma_{c_0} = 0$

$$\log[\lambda(a, c_0)] = \alpha_a + \gamma_{c_0} = \alpha_a$$

Fitting the A-C model in R I

Reference cohort is the 1933 cohort:

```
> ac <- glm( D ~ factor(A) - 1 + relevel( factor(C), "1933" ) +
+                  offset( log(Y/10^5) ),
+             family=poisson, data=ts )
> summary( ac )

Call:
glm(formula = D ~ factor(A) - 1 + relevel(factor(C), "1933") +
    offset(log(Y/10^5)), family = poisson, data = ts)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.0796  -0.9538  -0.1620   0.5767   3.9525

Coefficients:
                              Estimate Std. Error z value Pr(>|z|)
factor(A)17.5                  0.61513    0.07534   8.165 3.23e-16
```

Fitting the A-C model in R II

```
factor(A)22.5                    1.89965    0.05342  35.558  < 2e-16
factor(A)27.5                    2.46911    0.04842  50.990  < 2e-16
factor(A)32.5                    2.70635    0.04695  57.639  < 2e-16
factor(A)37.5                    2.71211    0.04758  57.006  < 2e-16
factor(A)42.5                    2.58676    0.04993  51.803  < 2e-16
factor(A)47.5                    2.36542    0.05459  43.327  < 2e-16
factor(A)52.5                    2.18192    0.06098  35.782  < 2e-16
factor(A)57.5                    2.01519    0.06939  29.041  < 2e-16
relevel(factor(C), "1933")1888 -1.77316    0.41400  -4.283 1.84e-05
relevel(factor(C), "1933")1893 -1.05641    0.19017  -5.555 2.77e-08
relevel(factor(C), "1933")1898 -0.79897    0.12600  -6.341 2.28e-10
relevel(factor(C), "1933")1903 -0.87599    0.10389  -8.432  < 2e-16
relevel(factor(C), "1933")1908 -0.76707    0.08352  -9.184  < 2e-16
relevel(factor(C), "1933")1913 -0.56290    0.07006  -8.035 9.36e-16
relevel(factor(C), "1933")1918 -0.56702    0.06683  -8.484  < 2e-16
relevel(factor(C), "1933")1923 -0.36836    0.06124  -6.015 1.79e-09
relevel(factor(C), "1933")1928 -0.18832    0.05903  -3.190 0.001421
relevel(factor(C), "1933")1938  0.08958    0.05439   1.647 0.099585
relevel(factor(C), "1933")1943 -0.03107    0.05443  -0.571 0.568091
```

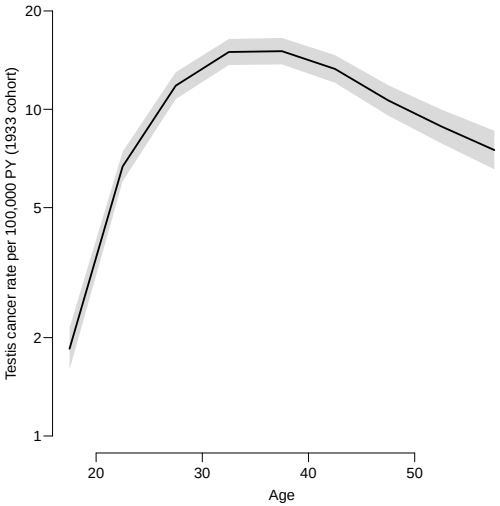
Fitting the A-C model in R III

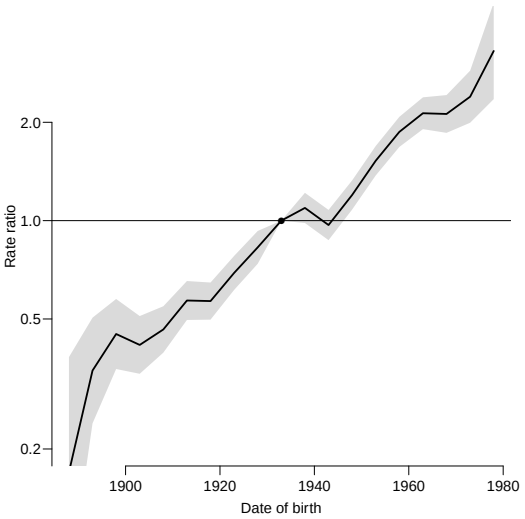
```
relevel(factor(C), "1933")1948  0.18088    0.05256   3.441 0.000579
relevel(factor(C), "1933")1953  0.42239    0.05309   7.956 1.77e-15
relevel(factor(C), "1933")1958  0.62544    0.05421  11.537  < 2e-16
relevel(factor(C), "1933")1963  0.75687    0.05727  13.215  < 2e-16
relevel(factor(C), "1933")1968  0.75183    0.06799  11.057  < 2e-16
relevel(factor(C), "1933")1973  0.87343    0.09373   9.318  < 2e-16
relevel(factor(C), "1933")1978  1.19601    0.17340   6.898 5.29e-12

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 29193.6  on 2430  degrees of freedom
Residual deviance:  2767.8  on 2403  degrees of freedom
AIC: 8972.2

Number of Fisher Scoring iterations: 5
```

Estimates with confidence intervals

```
> par( mfrow=c(1,2), mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> matshade( seq(17.5,57.5,5), ci.exp(ac,subset="A"), plot=TRUE,
+           log="y", lwd=2, ylim=c(1,20), xlab="Age",
+           ylab="Testis cancer rate per 100,000 PY (1933 cohort)" )
> matshade( seq(1888,1978,5),
+           rbind( ci.exp(ac,subset="C")[1:9 ,], 1,
+                  ci.exp(ac,subset="C")[10:18,] ), plot=TRUE,
+           log="y", lwd=2, ylim=c(1,20)/5,
+           xlab="Date of birth", ylab="Rate ratio" )
> abline( h = 1)
> points( 1933, 1, pch=16 )
```

Estimates from Age-Cohort model





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- models do not use the fact that $50 < 55 < 60$.

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Age, period and cohort are **quantitative** variables

- but the models we fitted does not use this feature
- they are **exchangeable** models for the A, P and C effects
- meaning that you can exhange the names of two age-classes and still get the same fit
- models do not use the fact that $50 < 55 < 60$.
- we need parametric models for the A, P and C effects

$$\log\big(\lambda(a,p)\big) = f(a) + g(p) \qquad \log\big(\lambda(a,p)\big) = f(a) + h(p-a)$$

Parametric models

- f, g and h are **smooth**, **continuous** functions:

$$\log\big(\lambda(a,p)\big) = f(a) + g(p) \qquad \log\big(\lambda(a,p)\big) = f(a) + h(p-a)$$

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- **Data** is discrete (1-year, 5-year) intervals

Parametric models

- f, g and h are **smooth**, **continuous** functions:

$$\log\big(\lambda(a,p)\big) = f(a) + g(p) \qquad \log\big(\lambda(a,p)\big) = f(a) + h(p-a)$$

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- Reference is now to a **specific** age or data — not an age-**band** or **period**
- **Results** are functions to be shown as **curves**
- in the form of **predictions** and
- **contrasts** between predictions (RR between p and p_{ref})

Quantitative, natural splines I

```
> library(splines)
> ap <- glm( D ~ Ns(A,knots=seq(15,50,,4)) +
+                Ns(P,knots=seq(1950,1990,,5)),
+            offset = log(Y/10^5),
+            family = poisson, data=ts )
> round( ci.lin(ap), 4 )

                                      Estimate StdErr       z      P    2.5%   97.5
(Intercept)                             0.0499 0.0712  0.7011 0.4833 -0.0896  0.189
Ns(A, knots = seq(15, 50, , 4))1        1.2480 0.0475 26.2816 0.0000  1.1549  1.341
Ns(A, knots = seq(15, 50, , 4))2        3.5475 0.1394 25.4553 0.0000  3.2743  3.820
Ns(A, knots = seq(15, 50, , 4))3       -0.1530 0.0322 -4.7525 0.0000 -0.2161 -0.089
Ns(P, knots = seq(1950, 1990, , 5))1    0.5795 0.0616  9.4032 0.0000  0.4587  0.700
Ns(P, knots = seq(1950, 1990, , 5))2    0.8348 0.0409 20.4259 0.0000  0.7547  0.914
Ns(P, knots = seq(1950, 1990, , 5))3    1.2830 0.0744 17.2465 0.0000  1.1372  1.428
Ns(P, knots = seq(1950, 1990, , 5))4    0.8935 0.0359 24.8785 0.0000  0.8231  0.963
```

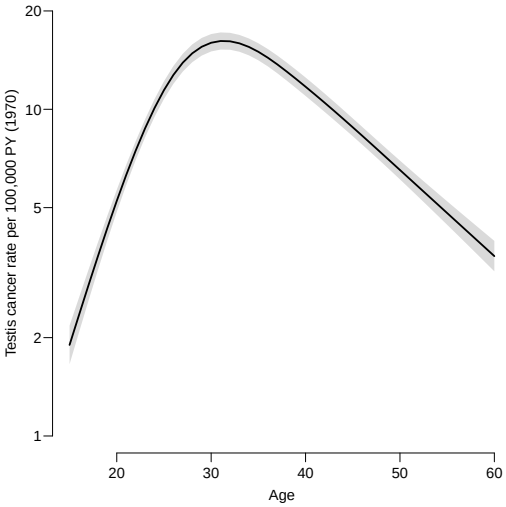
Quantitative, natural splines II

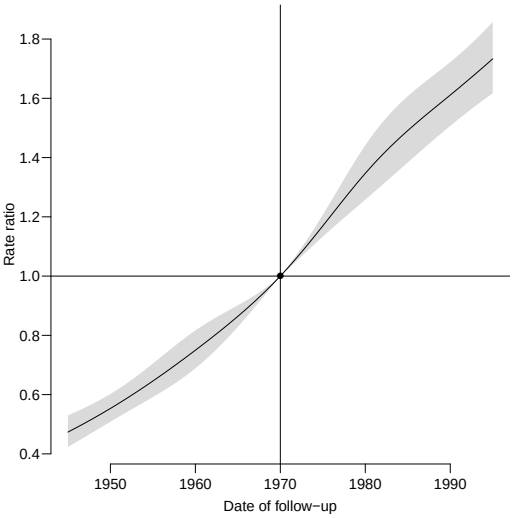
```
> ac <- glm( D ~ Ns(A,knots=seq(15,50,,4)) +
+                Ns(C,knots=seq(1910,1965,,9)),
+            offset = log(Y/10^5),
+            family = poisson, data=ts )
```

Period model predicions I

```
> ndA  <- data.frame( A=15:60, P=1970     , Y=1 )
> ndP  <- data.frame( A=30   , P=1945:1995, Y=1 )
> ndRp <- data.frame( A=30   , P=1970     , Y=1 )
> par( mfrow=c(1,2), mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> matshade( ndA$A,
+           ci.pred(ap,ndA)*10^5, # <- predicted rates using ndA
+           plot=TRUE, log="y", lwd=2, ylim=c(1,20), xlab="Age",
+           ylab="Testis cancer rate per 100,000 PY (1970)" )
> matshade( ndP$P,
+           ci.exp(ap,list(ndP,ndRp)),  # <- RR comparing ndP vs. ndRp
+           plot=TRUE, xlab="Date of follow-up", ylab="Rate ratio" )
> abline( h = 1, v=1970 )
> points( 1970, 1, pch=16 )
```

Estimates from Age-Period model



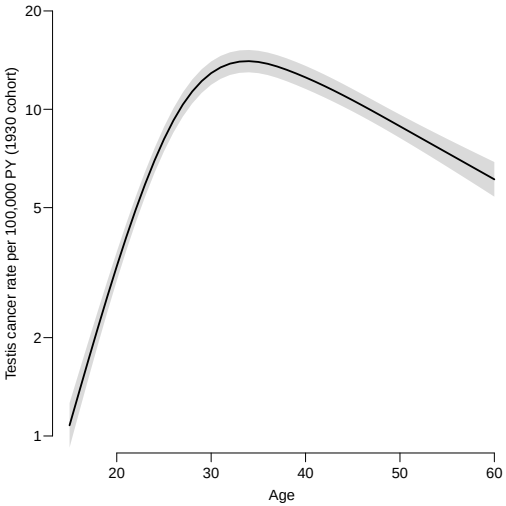


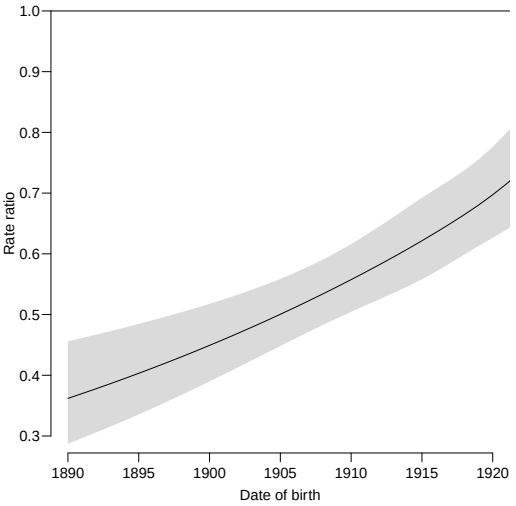
Cohort model I

```
> ndA  <- data.frame( A=15:60, C=1930     , Y=1 )
> ndC  <- data.frame( A=30   , C=1890:1975, Y=1 )
> ndRc <- data.frame( A=30   , C=1930     , Y=1 )
> par( mfrow=c(1,2), mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> matshade( ndA$A, ci.pred(ac,ndA)*10^5, plot=TRUE,
+           log="y", lwd=2, ylim=c(1,20), xlab="Age",
+           ylab="Testis cancer rate per 100,000 PY (1930 cohort)" )
> matshade( ndC$C, ci.exp(ac,list(ndC,ndRc)), plot=TRUE,
+           xlab="Date of birth", ylab="Rate ratio", xlim=c(1890,1920), ylim=c(0.3
> abline( h = 1, v=1930 )
> abline( v=c(1940,1945), col=gray(0.7) )
> points( 1930, 1, pch=16 )
```

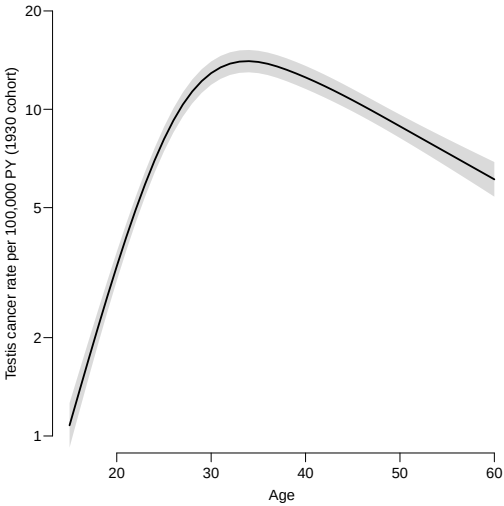
```
> par( mfrow=c(1,2), mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> matshade( ndA$A, ci.pred(ac,ndA)*10^5, plot=TRUE,
+           log="y", lwd=2, ylim=c(1,20), xlab="Age",
+           ylab="Testis cancer rate per 100,000 PY (1930 cohort)" )
> matshade( ndC$C, ci.exp(ac,list(ndC,ndRc)), plot=TRUE,
+           xlab="Date of birth", ylab="Rate ratio" )
> lo <- ndC$C<=1910
> hi <- ndC$C>=1965
> matshade( ndC$C[lo], ci.exp(ac,list(ndC,ndRc))[lo,], col="limegreen" )
> matshade( ndC$C[hi], ci.exp(ac,list(ndC,ndRc))[hi,], col="limegreen" )
> abline(v=c(1910,1965),lty=3,col=gray(0.5))
> abline( h = 1, v=1930 )
> abline( v=c(1940,1945), col=gray(0.7) )
> points( 1930, 1, pch=16 )
```

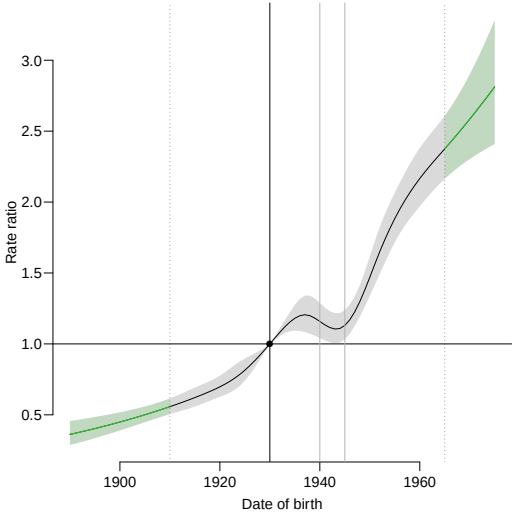
Estimates from Age-Cohort model





Estimates from Age-Cohort model





Age-drift model

Bendix Carstensen

An APC Analytic Approach to Analyzing and Predicting National Trends in Diabetes Incidence over Time
Emory University, Rollins School of Public Health,June 2019

`http://BendixCarstensen/APC`

Ad

Linear effect of period:

$$\log[\lambda(a,p)] = \alpha_a + \beta_p = \alpha_a + \beta(p - p_0)$$

that is, $\beta_p = \beta(p - p_0)$.

Linear effect of cohort:

$$\log[\lambda(a,p)] = \tilde{\alpha}_a + \gamma_c = \tilde{\alpha}_a + \gamma(c - c_0)$$

that is, $\gamma_c = \gamma(c - c_0)$

Age and linear effect of period:

```
> apd <- glm( D ~ factor( A ) - 1 + I(P-1970.5) +
+             offset( log( Y ) ),
+             family=poisson )
> summary( apd )

Call:
glm(formula = D ~ factor(A) - 1 + I(P - 1970.5) + offset(log(Y)), family = poisson

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-2.97593  -0.77091   0.02809   0.95914   2.93076

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
factor(A)17.5 -3.58065    0.06306  -56.79   <2e-16
...
factor(A)57.5 -3.17579    0.06256  -50.77   <2e-16
I(P - 1970.5)  0.02653    0.00100   26.52   <2e-16

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 89358.53  on 81  degrees of freedom
Residual deviance:   126.07  on 71  degrees of freedom
```

Age and linear effect of cohort:

```
> acd <- glm( D ~ factor( A ) - 1 + I(C-1933) +
+             offset( log( Y ) ),
+             family=poisson )
> summary( acd )

Call:
glm(formula = D ~ factor(A) - 1 + I(C - 1933) + offset(log(Y)), family = poisson)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-2.97593  -0.77091   0.02809   0.95914   2.93076

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
factor(A)17.5 -4.11117    0.06760  -60.82   <2e-16
...
factor(A)57.5 -2.64527    0.06423  -41.19   <2e-16
I(C - 1933)    0.02653    0.00100   26.52   <2e-16

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 89358.53  on 81  degrees of freedom
Residual deviance:   126.07  on 71  degrees of freedom
```

What goes on?

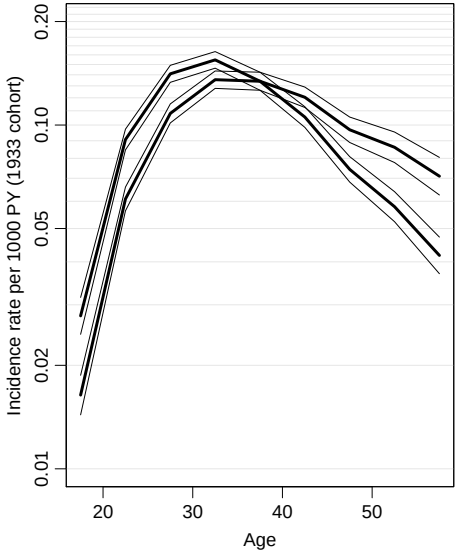
$$p = a + c \qquad p_0 = a_0 + c_0$$

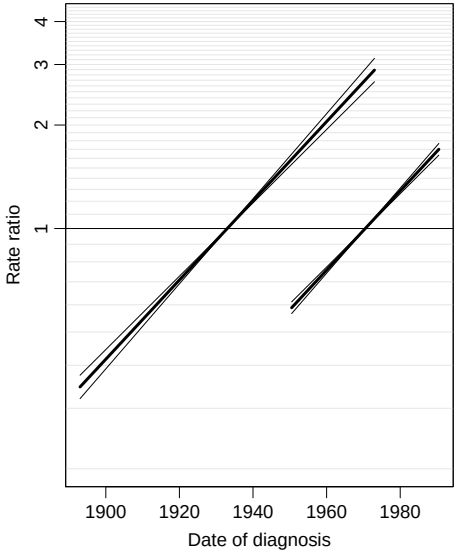
$$\begin{aligned} \alpha_a + \beta(p - p_0) &= \alpha_a + \beta\big(a + c - (a_0 + c_0)\big) \\ &= \underbrace{\alpha_a + \beta(a - a_0)}_{\text{cohort age-effect}} + \beta(c - c_0) \end{aligned}$$

The two **models** are the same.
The **parametrization** is different.

The age-curve refers either

- to a period (cross-sectional rates) or
- to a cohort (longitudinal rates).





Which age-curve is period and which is cohort?

Age-Period-Cohort model

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The age-period-cohort model

$$\log[\lambda(a, p)] = \alpha_a + \beta_p + \gamma_c$$

- Three effects:

The age-period-cohort model

$$\log[\lambda(a, p)] = \alpha_a + \beta_p + \gamma_c$$

- Three effects:
  - a — Age (at diagnosis)

The age-period-cohort model

$$\log[\lambda(a, p)] = \alpha_a + \beta_p + \gamma_c$$

- Three effects:
  - a — Age (at diagnosis)
  - p — Period (of diagnosis)

The age-period-cohort model

$$\log[\lambda(a, p)] = \alpha_a + \beta_p + \gamma_c$$

- Three effects:
  - a — Age (at diagnosis)
  - p — Period (of diagnosis)
  - c — Cohort (of birth)

The age-period-cohort model

$$\log[\lambda(a, p)] = \alpha_a + \beta_p + \gamma_c$$

- Three effects:
  - a — Age (at diagnosis)
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  - c — Cohort (of birth)
- No assumptions about the **shape** of effects.

The age-period-cohort model

$$\log[\lambda(a, p)] = \alpha_a + \beta_p + \gamma_c$$

- Three effects:
  - a — `Age` (at diagnosis)
  - p — `Period` (of diagnosis)
  - c — `Cohort` (of birth)
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- Levels of `A`, `P` and `C` are assumed **exchangeable**

The age-period-cohort model

$$\log[\lambda(a, p)] = \alpha_a + \beta_p + \gamma_c$$

- Three effects:
  - a — `Age` (at diagnosis)
  - p — Period (of diagnosis)
  - c — `Cohort` (of birth)
- No assumptions about the **shape** of effects.
- Levels of `A`, `P` and `C` are assumed **exchangeable**
- *i.e.* no assumptions about the relationship between parameter estimates and the **scaled values** of `A`, `P` and `C`

Fitting the model in R I

```
> m.apc <- glm( D ~ 0 + factor(A) + factor(P) + factor(C),
+               offset = log(Y), family = poisson, data = tc )
> round( ci.lin( m.apc ), 4 )

                Estimate StdErr        z      P     2.5%    97.5%
factor(A)17.5   -11.3989 0.2332 -48.8886 0.0000 -11.8559 -10.9419
factor(A)22.5   -10.2022 0.2552 -39.9849 0.0000 -10.7023  -9.7021
factor(A)27.5    -9.7634 0.2755 -35.4328 0.0000 -10.3035  -9.2233
factor(A)32.5    -9.6795 0.2974 -32.5482 0.0000 -10.2624  -9.0966
factor(A)37.5    -9.8283 0.3201 -30.7015 0.0000 -10.4557  -9.2009
factor(A)42.5   -10.1047 0.3435 -29.4182 0.0000 -10.7779  -9.4315
factor(A)47.5   -10.5268 0.3676 -28.6390 0.0000 -11.2472  -9.8064
factor(A)52.5   -10.8863 0.3921 -27.7650 0.0000 -11.6548 -10.1179
factor(A)57.5   -11.2709 0.4082 -27.6079 0.0000 -12.0710 -10.4707
factor(P)1950.5   0.2029 0.0825   2.4598 0.0139   0.0412   0.3645
factor(P)1955.5   0.4204 0.0908   4.6297 0.0000   0.2424   0.5984
factor(P)1960.5   0.6410 0.1055   6.0769 0.0000   0.4343   0.8477
```

Fitting the model in R II

factor(P)1965.5	0.8214	0.1241	6.6199	0.0000	0.5782	1.0645
factor(P)1970.5	1.0644	0.1444	7.3689	0.0000	0.7813	1.3474
factor(P)1975.5	1.2780	0.1665	7.6738	0.0000	0.9516	1.6044
factor(P)1980.5	1.4344	0.1896	7.5651	0.0000	1.0628	1.8060
factor(P)1985.5	1.5058	0.2134	7.0565	0.0000	1.0875	1.9240
factor(P)1990.5	1.5880	0.2356	6.7396	0.0000	1.1262	2.0498
factor(C)1893	0.5056	0.4289	1.1786	0.2385	-0.3351	1.3463
factor(C)1898	0.5644	0.3840	1.4699	0.1416	-0.1882	1.3170
factor(C)1903	0.2843	0.3556	0.7995	0.4240	-0.4126	0.9812
factor(C)1908	0.2068	0.3284	0.6299	0.5288	-0.4367	0.8504
factor(C)1913	0.2230	0.3034	0.7350	0.4624	-0.3717	0.8177
factor(C)1918	0.0271	0.2815	0.0964	0.9232	-0.5246	0.5789
factor(C)1923	0.0328	0.2597	0.1263	0.8995	-0.4762	0.5418
factor(C)1928	0.0215	0.2394	0.0900	0.9283	-0.4478	0.4909
factor(C)1933	0.0252	0.2199	0.1145	0.9088	-0.4058	0.4561
factor(C)1938	-0.0724	0.2027	-0.3572	0.7209	-0.4696	0.3248
factor(C)1943	-0.3528	0.1871	-1.8862	0.0593	-0.7195	0.0138
factor(C)1948	-0.3047	0.1731	-1.7606	0.0783	-0.6440	0.0345
factor(C)1953	-0.1792	0.1626	-1.1020	0.2705	-0.4978	0.1395

Fitting the model in R III

```
factor(C)1958    -0.1174 0.1558  -0.7532 0.4513  -0.4228   0.1881
factor(C)1963    -0.1088 0.1541  -0.7062 0.4801  -0.4108   0.1932
factor(C)1968    -0.1681 0.1623  -1.0353 0.3005  -0.4863   0.1501
factor(C)1973     0.0000 0.0000      NaN    NaN   0.0000   0.0000
```

No. of parameters

`A` has $9(A)$ levels
`P` has $10(P)$ levels
`C=P-A` has $18(C = A + P - 1)$ levels
Age-drift model has $A + 1 = 10$ parameters
Age-period model has $A + P - 1 = 18$ parameters
Age-cohort model has $A + C - 1 = 26$ parameters
Age-period-cohort model has $A + P + C - 3 = 34$ parameters:

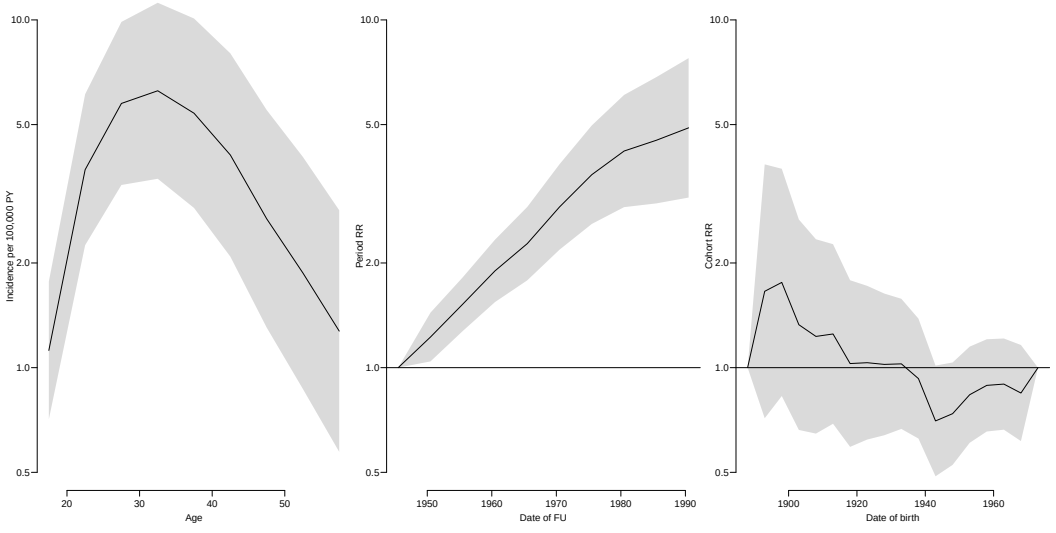
```
> length( coef(m.apc) ) ; sum( !is.na(coef(m.apc)) )
[1] 35
[1] 34
```

The missing parameter is because of the **identifiability problem**.

A, P, C effects

```
> par( mfrow=c(1,3), mar=c(3,3,0.1,0.1), mgp=c(3,1,0)/1.6 )
> m.apc <- glm( D ~ 0 + factor(A) + factor(P) + factor(C),
+               offset = log(Y), family = poisson, data = tc )
> #
> matshade( seq(17.5,57.5,5), ci.exp(m.apc,subset="A")*10^5, plot=TRUE,
+           log="y", ylab="Incidence per 100,000 PY", xlab="Age", ylim=c(0.5,10) )
> #
> matshade( seq(1945.5,1990.5,5), rbind(1,ci.exp(m.apc,subset="P")), plot=TRUE,
+           log="y", ylab="Period RR", xlab="Date of FU", ylim=c(0.5,10) )
> abline( h=1 )
> #
> matshade( seq(1888,1973,5), rbind(1,ci.exp(m.apc,subset="C")), plot=TRUE,
+           log="y", ylab="Cohort RR", xlab="Date of birth", ylim=c(0.5,10) )
> abline( h=1 )
```

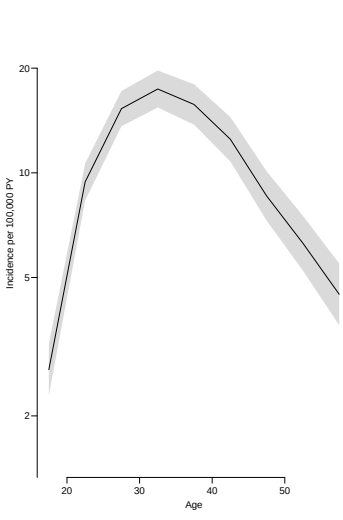
A, P, C effects

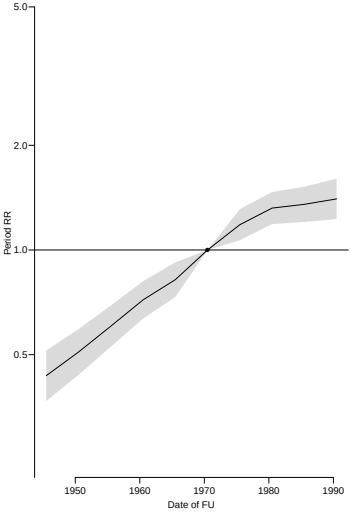

10.0
5.0
2.0
1.0
0.5
Incidence per 100,000 PY
20
30
40
50
Age
Period RR
1950
1960
1970
1980
1990
Date of FU
Cohort RR
1900
1920
1940
1960
Date of birth

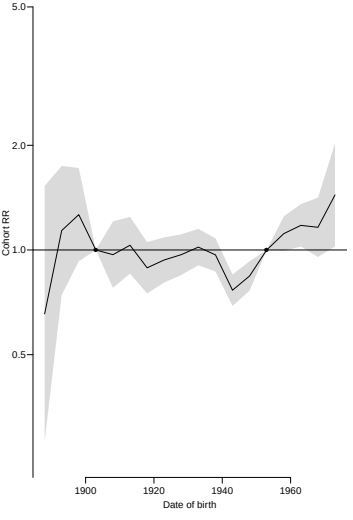
A, P, C effects, different reference

```
> m.apc <- glm( D ~ 0 + factor(A) + relevel(factor(P),6) +
+                                   Relevel(factor(C),c(4,1:3,5:13,15:18,14)),
+               offset = log(Y), family = poisson, data = tc )
> #
> par( mfrow=c(1,3), mar=c(3,3,0.1,0.1), mgp=c(3,1,0)/1.6 )
> matshade( seq(17.5,57.5,5), ci.exp(m.apc,subset="A")*10^5, plot=TRUE,
+           log="y", ylab="Incidence per 100,000 PY", xlab="Age", ylim=c(0.5,10)*3
> #
> matshade( seq(1945.5,1990.5,5), rbind(1,ci.exp(m.apc,subset="P"))[c(2:6,1,7:10),
+           log="y", ylab="Period RR", xlab="Date of FU", ylim=c(0.5,10)/2 )
> abline( h=1 ) ; points( 1970.5, 1, pch=16 )
> #
> matshade( seq(1888,1973,5), rbind(1,ci.exp(m.apc,subset="C"))[c(2:4,1,5:13,18,14
+           log="y", ylab="Cohort RR", xlab="Date of birth", ylim=c(0.5,10)/2 )
> abline( h=1 ); points( c(1903,1953), c(1,1), pch=16 )
```

A, P, C effects


20
10
5
2
Incidence per 100,000 PY
20
30
40
50
Age


5.0
2.0
1.0
0.5
Period RR
1950
1960
1970
1980
1990
Date of FU


5.0
2.0
1.0
0.5
Cohort RR
1900
1920
1940
1960
Date of birth

Test for effects

```
> tc.acp <- apc.fit( tc, model="factor", ref.c=1943, print.AOV=FALSE )
```

```
> print( tc.acp$Anova, digits=4 )
```

	Model	Mod.df.	Mod.dev.	df.	dev.	Pr(>Chi)	dev/df	H0
1	Age	81	1114.65	NA	NA	NA	NA	
2	Age-drift	80	131.77	1	982.879	9.458e-216	982.879	zero drift
3	Age-Cohort	64	70.20	16	61.570	2.840e-07	3.848	Coh eff|dr.
4	Age-Period-Cohort	56	38.78	8	31.418	1.183e-04	3.927	Per eff|Coh
5	Age-Period	72	122.23	16	83.451	3.950e-11	5.216	Coh eff|Per
6	Age-drift	80	131.77	8	9.538	2.990e-01	1.192	Per eff|dr.

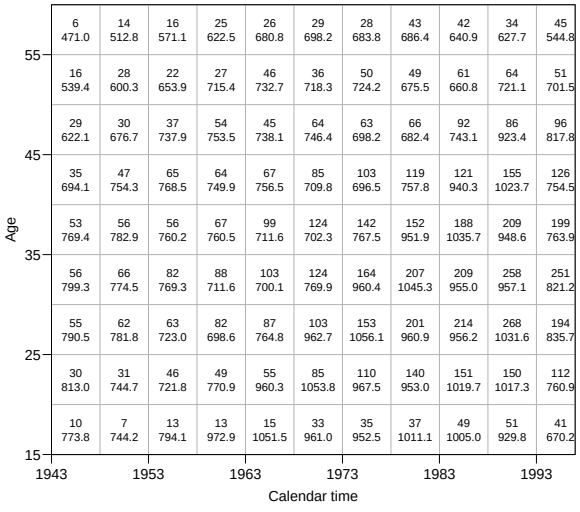
Tabulation in the Lexis diagram

Bendix Carstensen

An APC Analytic Approach to Analyzing and Predicting National Trends in Diabetes Incidence over Time
Emory University, Rollins School of Public Health,June 2019

`http://BendixCarstensen/APC`

Tabulation of register data



Testis cancer cases in Denmark.

Male person-years in Denmark.

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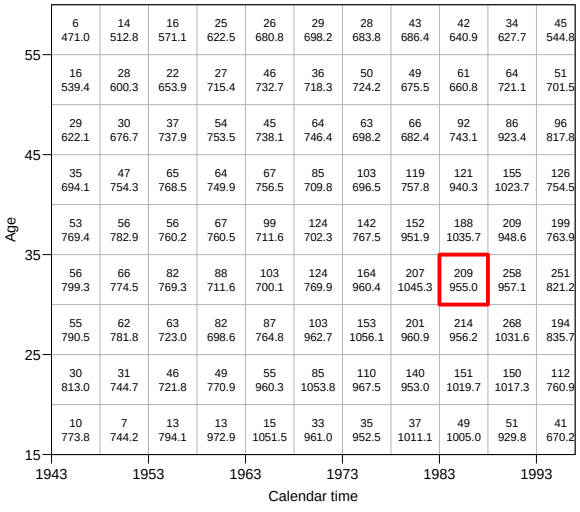

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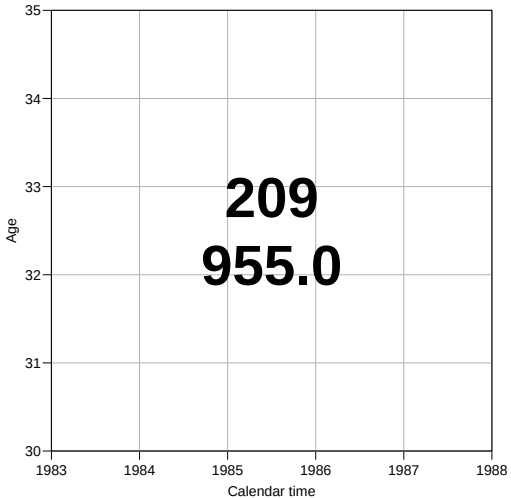

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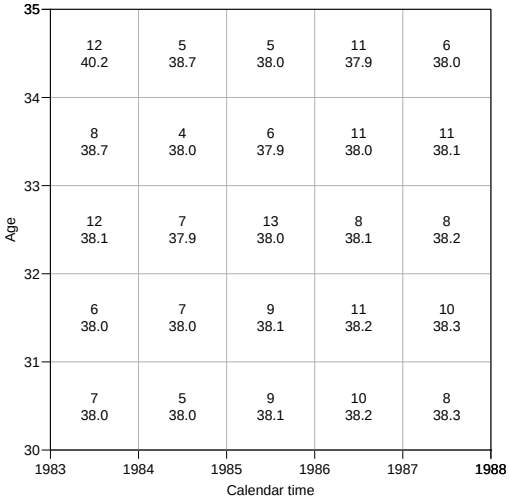

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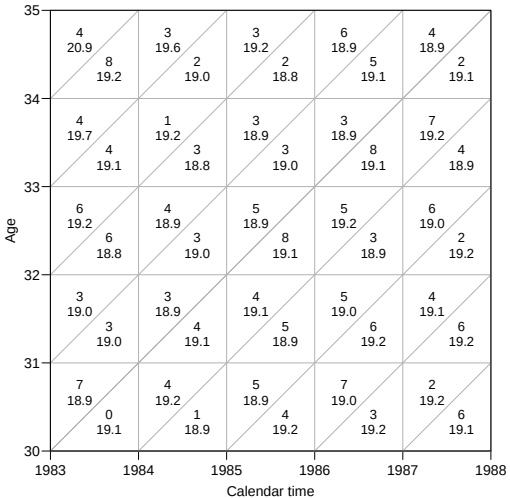

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Subdivision by year of birth (cohort).

Major sets in the Lexis diagram

A-sets: Classification by age and period. (□)

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C-sets: Classification by cohort and period. ()

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The mean age, period and cohort for these sets is just the mean of the tabulation interval.

The mean of the third variable is found by using $a = p - c$.

Analysis of rates from a complete observation in a Lexis diagram need not be restricted to these classical sets classified by two factors.

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Lower triangles: age and period, latest born cohort. ($\triangle$)

Mean a, p and c during FU in triangles

Modeling requires that each set (=observation in the dataset) be assigned a value of age, period and cohort. So for each triangle we need:

- mean age at risk.

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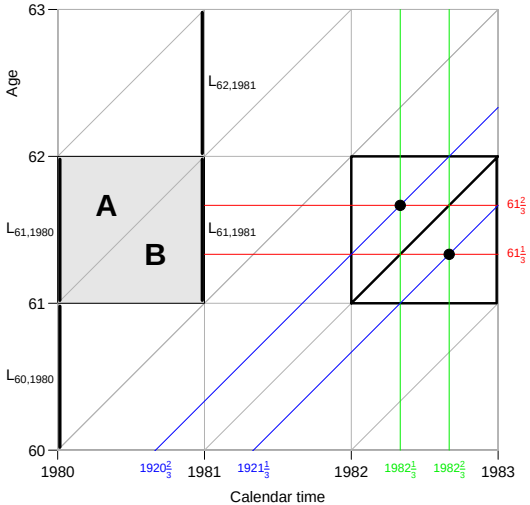
Tabulation by age, period and cohort

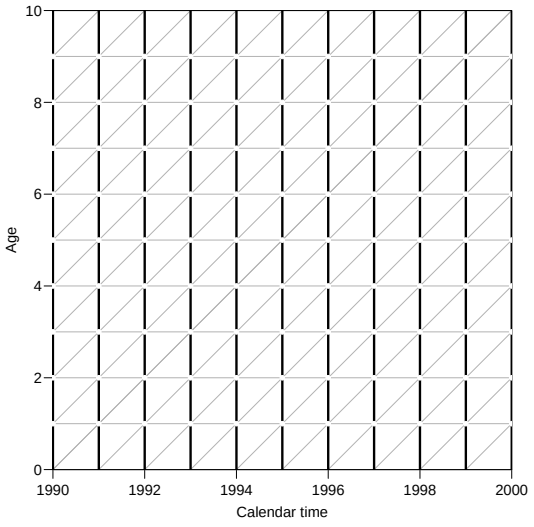


Gives triangular sets with differing mean age, period and cohort:

These are correct midpoints for age, period and cohort must be used in modeling.

From population figures to risk time

Population figures in the form of size of the population at certain date are available from most statistical bureaus.



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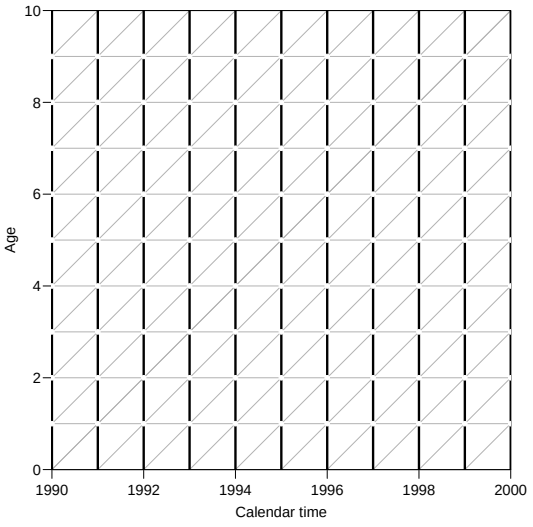

From population figures to risk time

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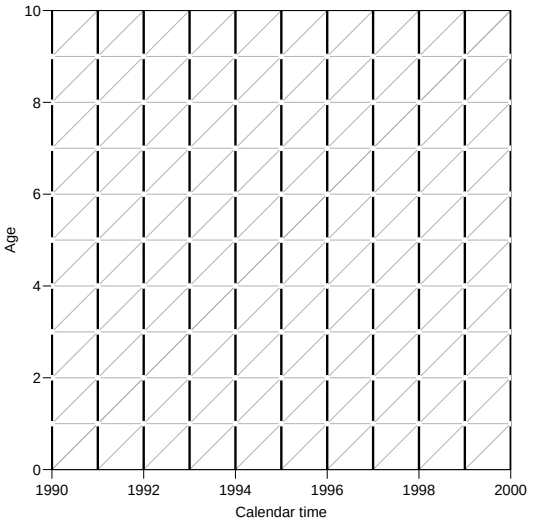
We want risk time figures for the population in the squares and triangles in the diagram.



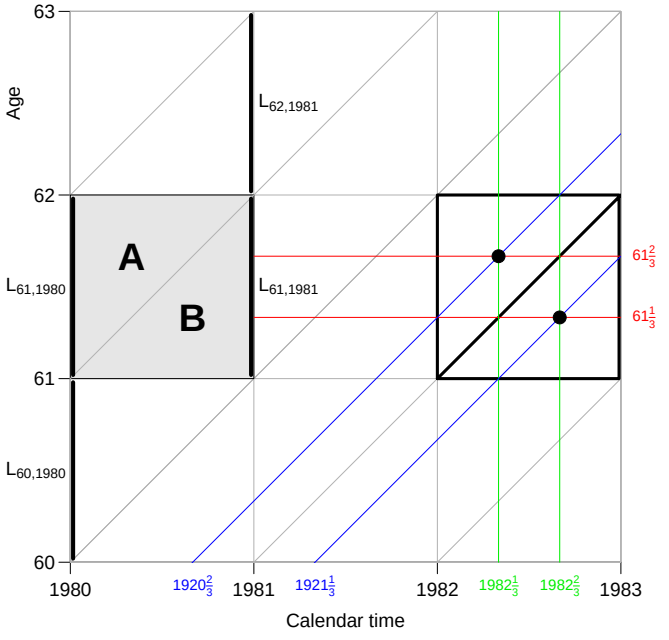
Summary:

Population risk time (N2Y):

A: $(\frac{1}{3}\mathsf{L}_{a,p} + \frac{1}{6}\mathsf{L}_{a+1,p+1}) \times 1\text{y}$

B: $(\frac{1}{6}\mathsf{L}_{a-1,p} + \frac{1}{3}\mathsf{L}_{a,p+1}) \times 1\text{y}$

Mean age, period and cohort:
$\frac{1}{3}$ into the interval.



APC-model: Parametrization

Bendix Carstensen

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Age-Period-Cohort model

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. . . it must be **external** to the **model**.

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Biologically interpretable: what happens in the lifespan of a cohort?

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Bureaucratically interpretable: what was seen at a given date?

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4. Use the functions:
$$\begin{aligned}
\tilde{f}(a) &= \hat{f}(a) + \mu + \beta a + \hat{h}(c_0) + \beta c_0 \\
\tilde{g}(p) &= \hat{g}(p) - \mu - \beta p \\
\tilde{h}(c) &= \hat{h}(c) \qquad + \beta c - \hat{h}(c_0) - \beta c_0
\end{aligned}$$

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- A better founded solution is needed...

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  - longitudinal age-effects, cohort with a reference and period as residuals
- Both implemented in `apc.fit`

ML and residual modeling

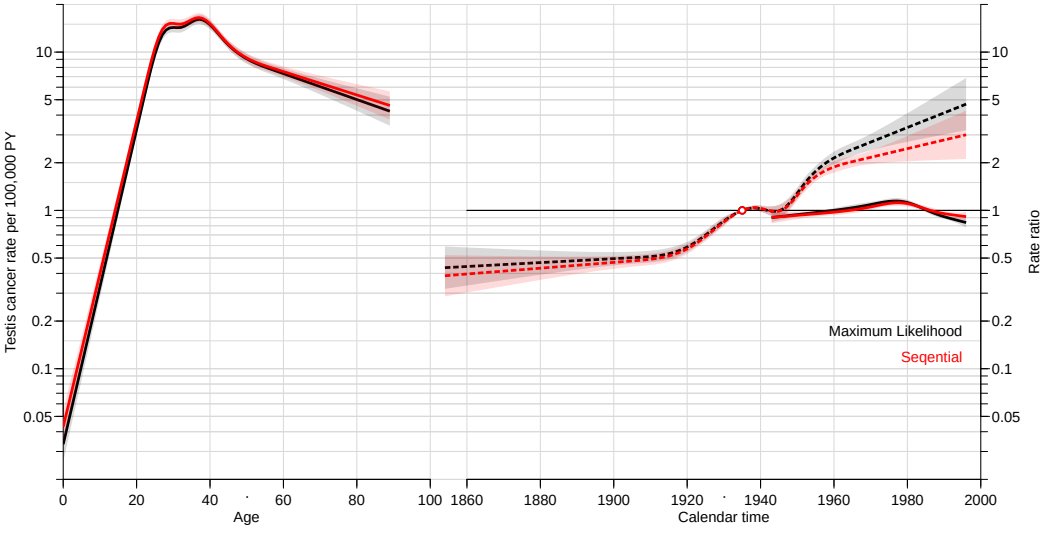
```
> library( Epi )
> data( testisDK )
> head( testisDK )

  A    P D        Y
1 0 1943 1 39649.50
2 1 1943 1 36942.83
3 2 1943 0 34588.33
4 3 1943 1 33267.00
5 4 1943 0 32614.00
6 5 1943 0 32020.33

> mm <- apc.fit( data=testisDK, ref.c=1935, parm="ACP" , npar=c(6,5,8), scale=10^5

[1] "ML of APC-model Poisson with log(Y) offset : ( ACP ):\n"
              Model Mod. df. Mod. dev. Test df.  Test dev.      Pr(>Chi) Test dev/
1               Age     4854  6008.406       NA         NA            NA
2         Age-drift     4853  4864.393        1 1144.01295 8.976155e-251 1144.0129
3       Age-Cohort     4847  4758.975        6  105.41779  1.853664e-20   17.5696
4 Age-Period-Cohort     4844  4704.333        3   54.64241  8.184605e-12   18.2141
5       Age-Period     4850  4846.349        6  142.01605  3.762037e-28   23.6693
6         Age-drift     4853  4864.393        3   18.04415  4.307234e-04    6.0147
```

Two ways of fixing parameters



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- . . . or sequential fitting of models (different model)
- There is no magical fix that allows you to escape this, it comes from using variables a, p and $p - a$

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- . . . but the **fitted values** are the same (except for the sequential method).

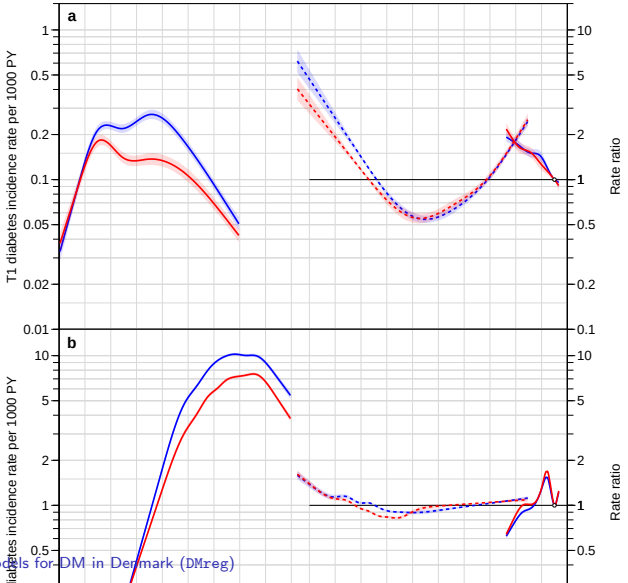
APC-models for DM in Denmark

Bendix Carstensen

An APC Analytic Approach to Analyzing and Predicting National Trends in Diabetes Incidence over Time
Emory University, Rollins School of Public Health,June 2019

`http://BendixCarstensen/APC` `DMreg`

Age-Period-Cohort analysis of DM in Denmark



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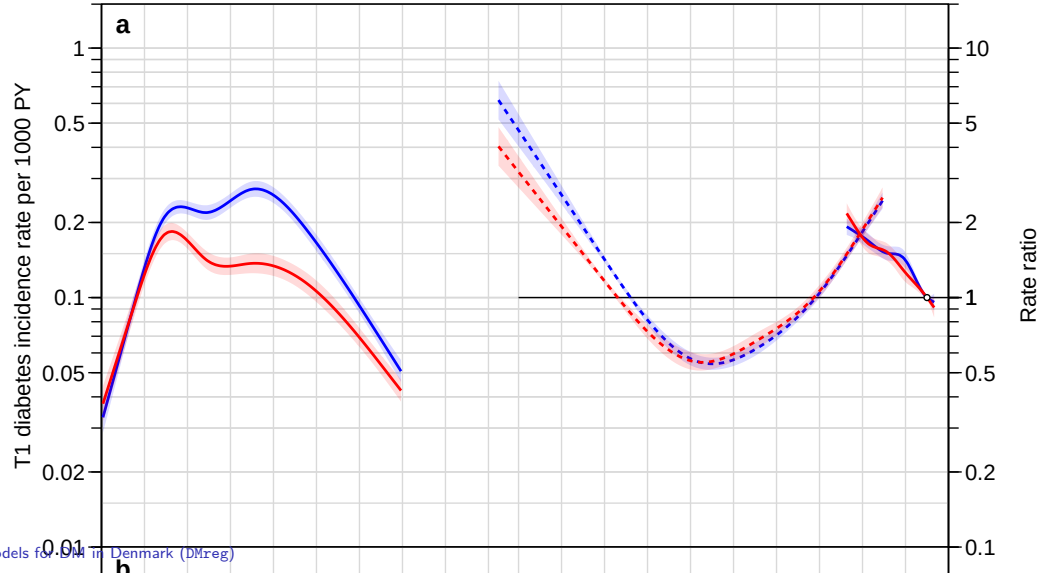

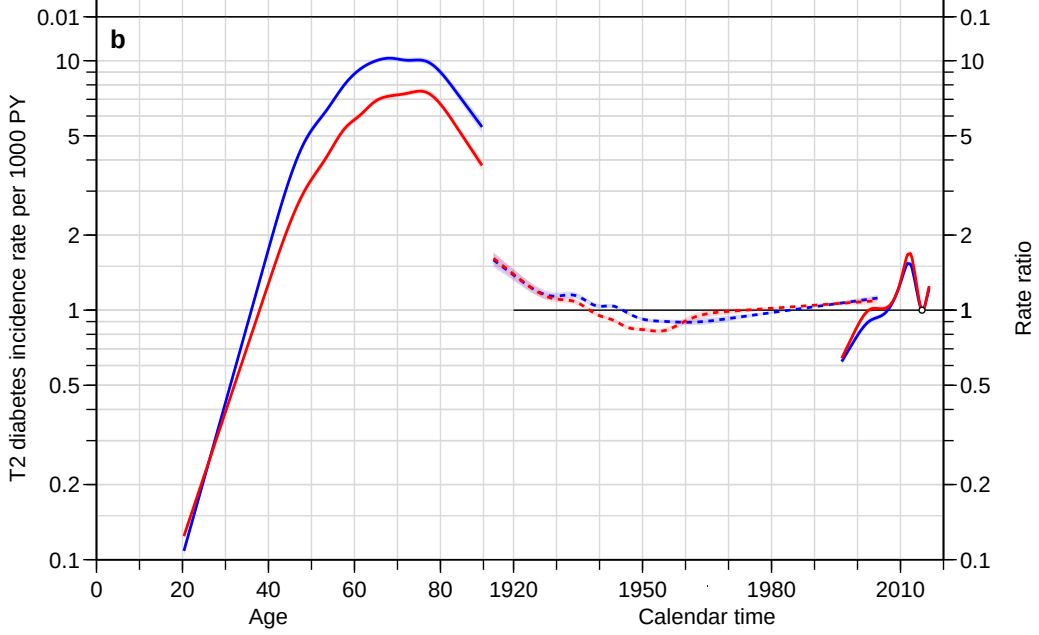
b
T2 diabetes incidence rate per 1000 PY
Rate ratio
0.01
0.1
10
5
2
1
0.5
0.2
0.1
0
20
40
60
80
1920
1950
1980
2010
Age
Calendar time

Incidence rates

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  - peaks ages 65–80
  - decrease after 80
  - peak rates at 7–10 cases per 1000 PY (2015)
  - change by calendar time: 3.3% /year
  - very irregular calendar time pattern

Age-Period-Cohort analysis of DM in Denmark

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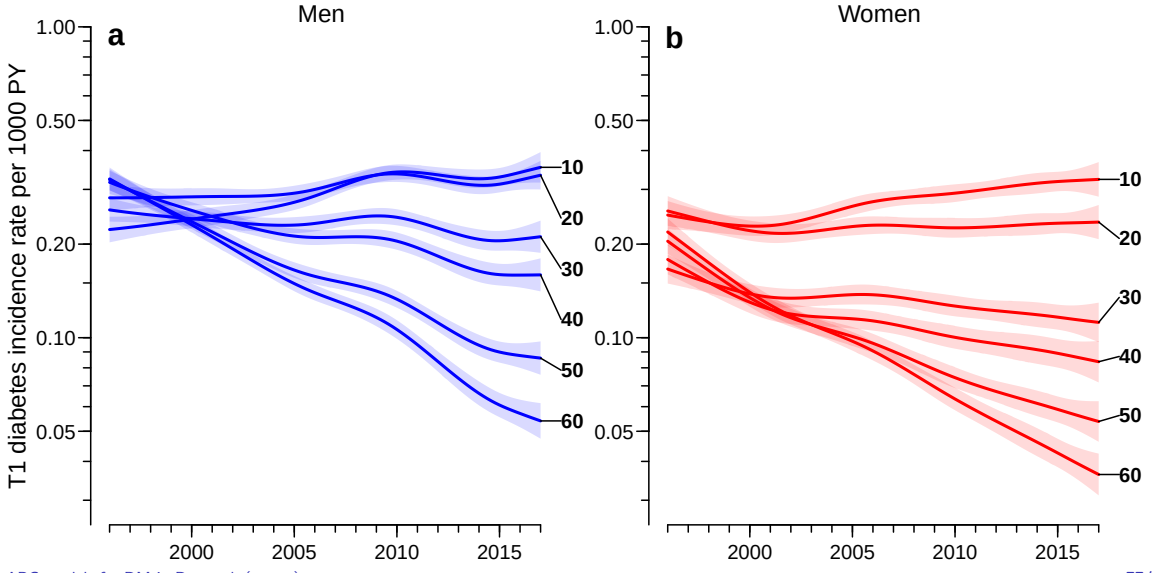
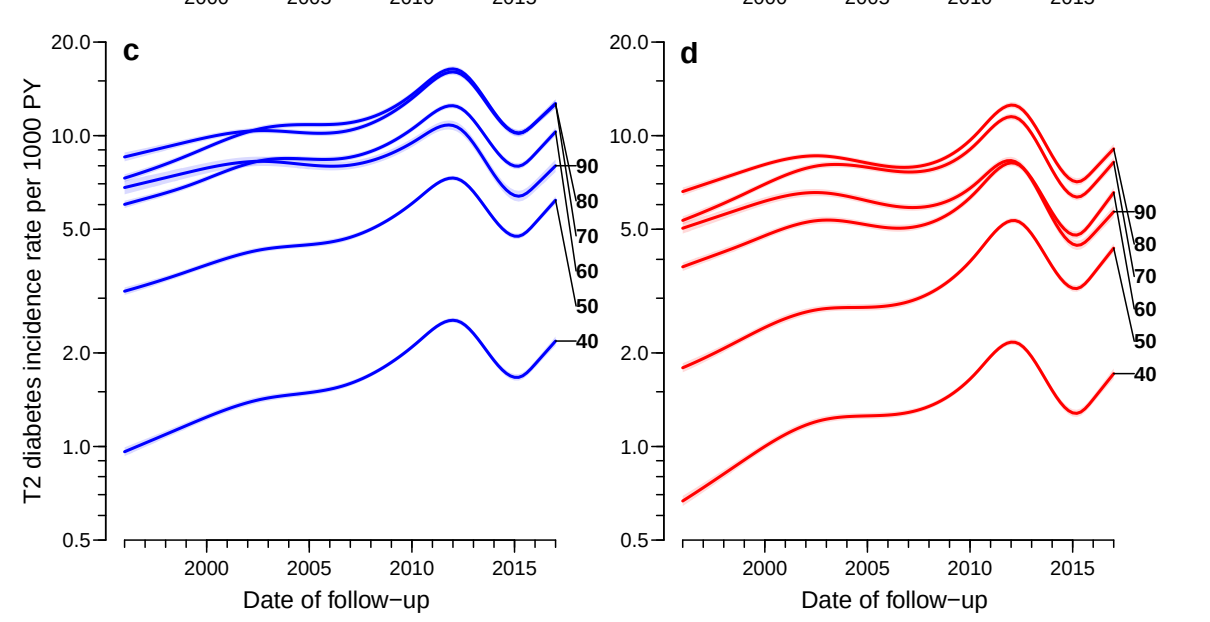
- . . . but may overshoot

Age-Period-Cohort analysis of DM in Denmark




c
d
T2 diabetes incidence rate per 1000 PY
20.0
10.0
5.0
2.0
1.0
0.5
2000
2005
2010
2015
Date of follow−up
90
80
70
60
50
40

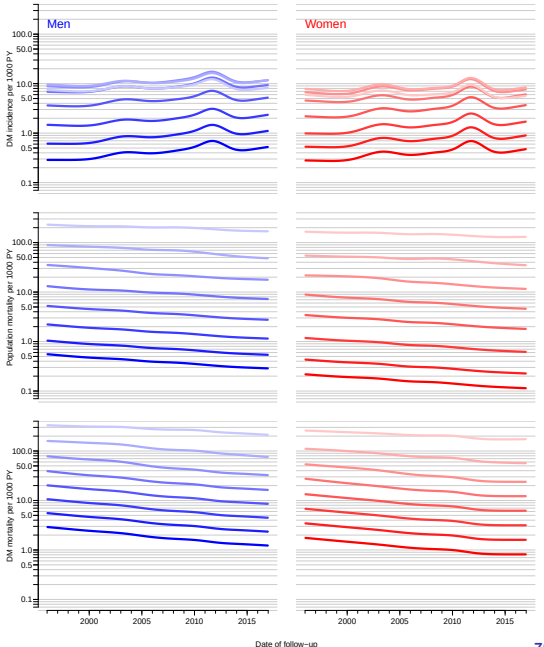
Predictions for total DM

Incidence of total DM

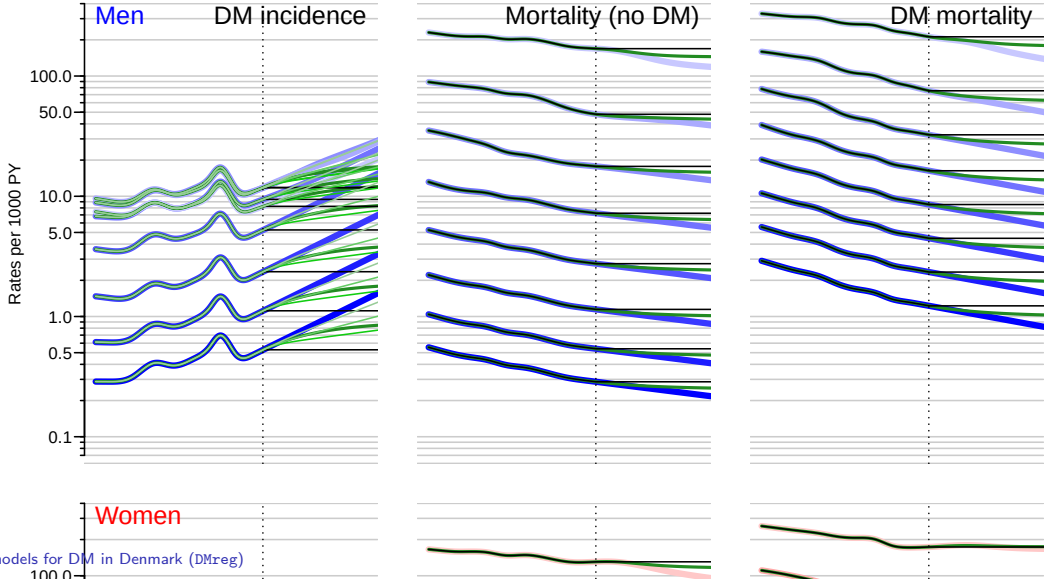
Mortality in total DM

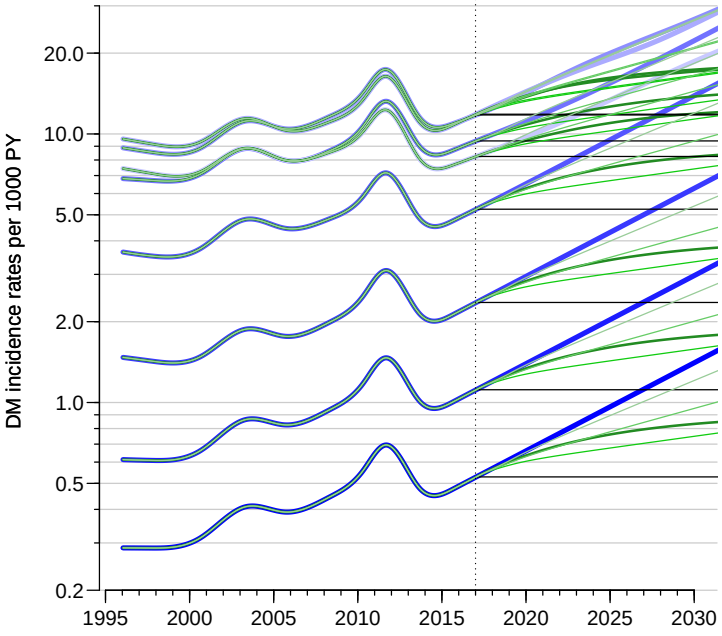
Mortality in no DM

Ages 20, 30,. . . ,90
(strong to weak color)



Future rates for total DM




DM incidence rates per 1000 PY
20.0
10.0
5.0
2.0
1.0
0.5
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1995
2000
2005
2010
2015
2020
2025
2030

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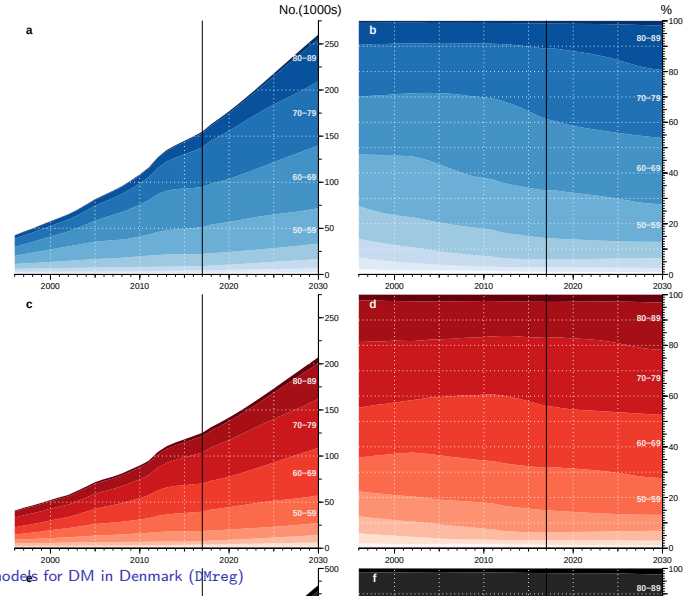
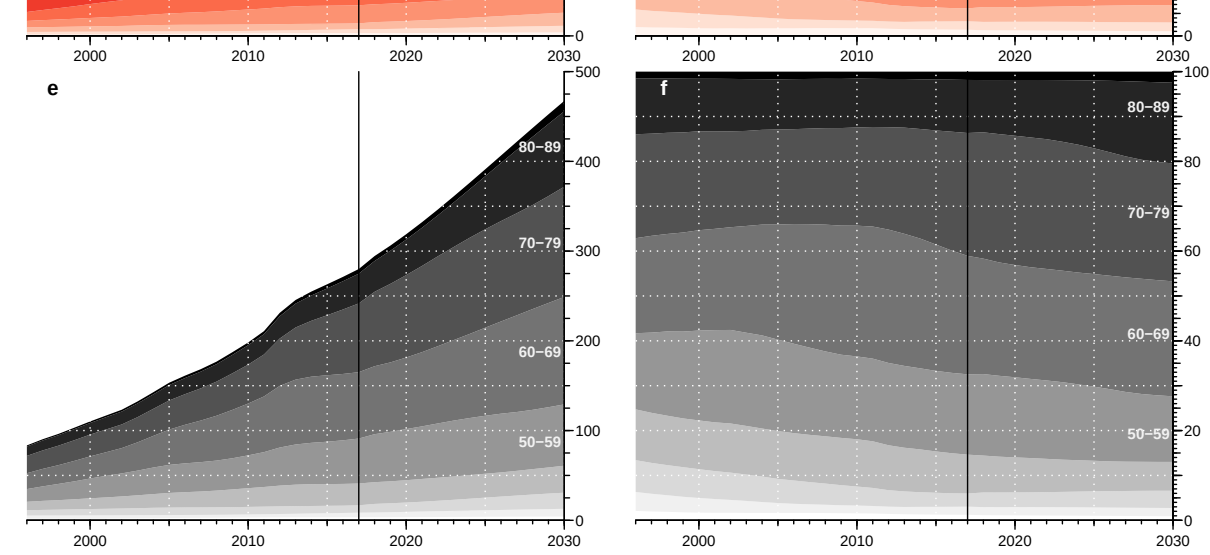
5. From this we know the prevalence of DM as of 2017-**02**-01, in one month older age
6. Multiply with population forecast from Statistics Denmark to get the **number** of prevalent cases at any future time

Future number of prevalent cases (M/W)




e
80–89
70–79
60–69
50–59
0
100
200
300
400
500
2000
2010
2020
2030
f
80–89
70–79
60–69
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0
20
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- The parametric compnent of age, period and cohort can only be derived using explicit constraints (3 of them to be precise)

More

A complete account of all analyses is in:
`http://bendixcarstensen.com/DMreg/NewAna.pdf`