

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

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Emory University, Rollins School of Public Health,
CDC, Atlanta,

17 June 2019
18 June 2019

An overview of APC models

- ▶ Data in a Lexis diagram — and where they come from.
- ▶ Simple graphs of rates
- ▶ Simple AP and AC models
- ▶ APC models as they usually are
- ▶ APC models as they should be
- ▶ Parameters vs. fitted values
- ▶ Practical use in forecasting

Slides with code in **R** only briefly covered

Population occurrence rates

- ▶ Population rates occur in calendar time
- ▶ ... depend very strongly on age
- ▶ describe how rates have evolved
- ▶ predict how they will evolve in the future
- ▶ Rates as a function of age and calendar time:
 - ▶ data representation
 - ▶ modeling

Models for tabulated data

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<http://BendixCarstensen/APC>

tab-mod

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.

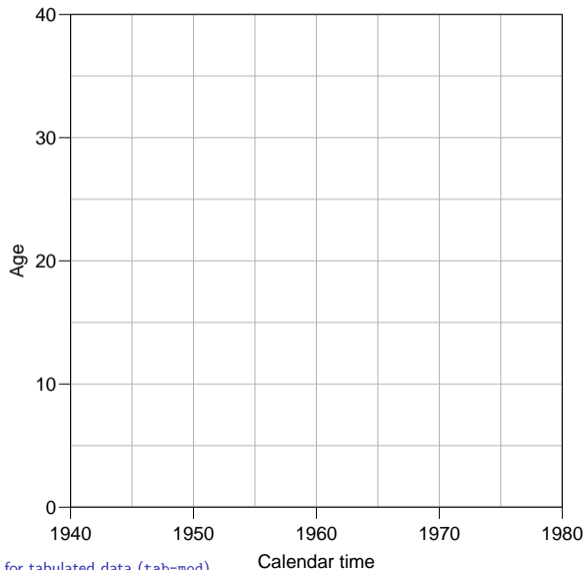
Realistic set-up

- ▶ 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.

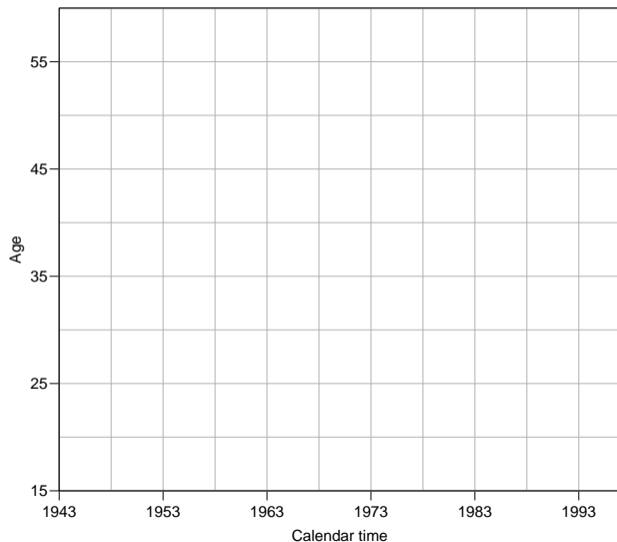
STRASSBURG

KARL J. TRÜBNER

1875.



Lexis diagram



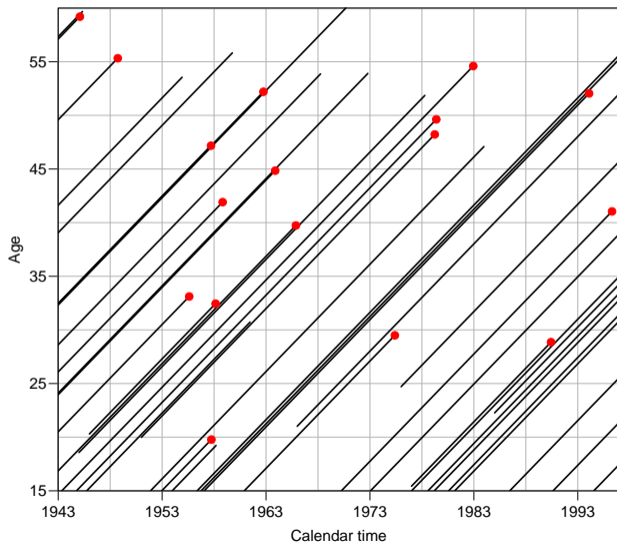
Registration of:

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 072852
```

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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AP-AC

Register data — rates

Rates in “tiles” of the Lexis diagram:

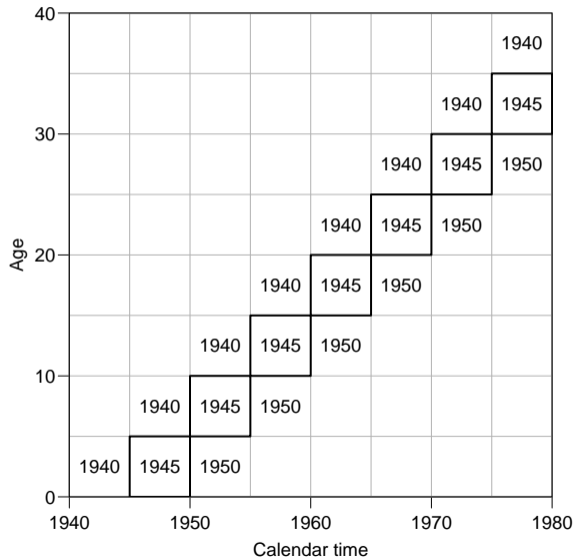
$$\lambda(a, p) = D_{ap} / Y_{ap}$$

Descriptive epidemiology based on disease registers:

How do the rates vary by age and time:

- ▶ Age-specific rates across periods.
- ▶ 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

55	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
45	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
35	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
25	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
15	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
	1943	1953	1963	1973	1983	1993					

Age-Period and Age-Cohort models (AP-AC)

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]
```

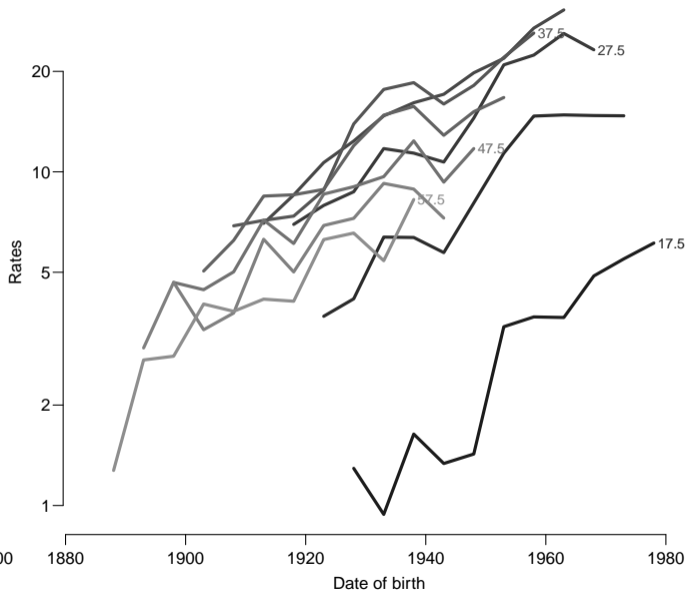
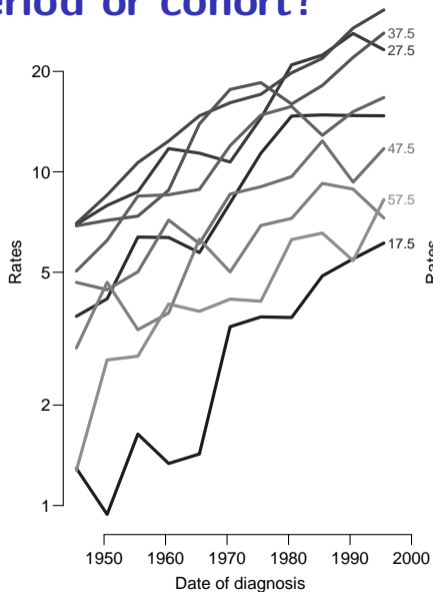
```
      P
A      1945.5      1950.5      1955.5      1960.5      1965.5      1970.5
17.5  1.2923036  0.9405857  1.6370257  1.3362759  1.4264867  3.4340862
```

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:

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

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

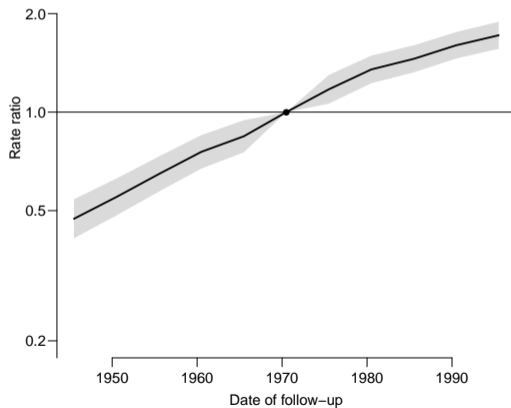
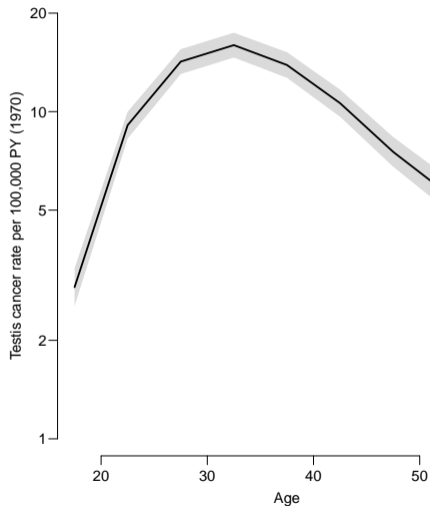
Reference period is the 5th period (1970.5 ~ 1968–72):

```
> 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:

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

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)

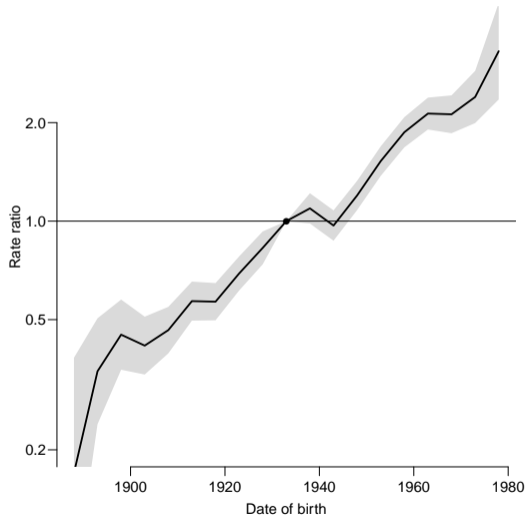
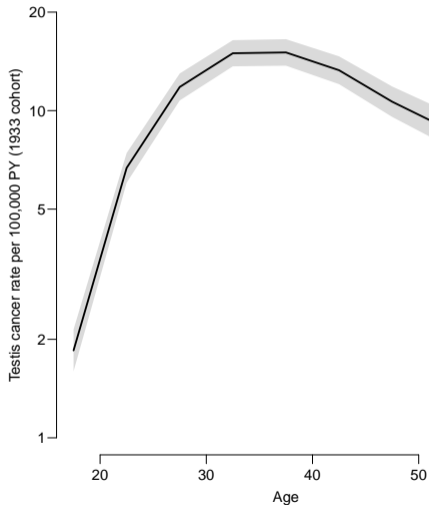
```
Null deviance: 29193.6 on 2430 degrees of freedom
Residual deviance: 2767.8 on 2403 degrees of freedom
AIC: 8972.2
```

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



Hang on:

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 exchange 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

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

Parametric models

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

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

- ▶ **Data** is discrete (1-year, 5-year) intervals
- ▶ **Models** are continuous, prediction at **any** value for a , p or c
- ▶ 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	0.1895
Ns(A, knots = seq(15, 50, , 4))1	1.2480	0.0475	26.2816	0.0000	1.1549	1.3411
Ns(A, knots = seq(15, 50, , 4))2	3.5475	0.1394	25.4553	0.0000	3.2743	3.8207
Ns(A, knots = seq(15, 50, , 4))3	-0.1530	0.0322	-4.7525	0.0000	-0.2161	-0.0899
Ns(P, knots = seq(1950, 1990, , 5))1	0.5795	0.0616	9.4032	0.0000	0.4587	0.7003
Ns(P, knots = seq(1950, 1990, , 5))2	0.8348	0.0409	20.4259	0.0000	0.7547	0.9149
Ns(P, knots = seq(1950, 1990, , 5))3	1.2830	0.0744	17.2465	0.0000	1.1372	1.4288
Ns(P, knots = seq(1950, 1990, , 5))4	0.8935	0.0359	24.8785	0.0000	0.8231	0.9639

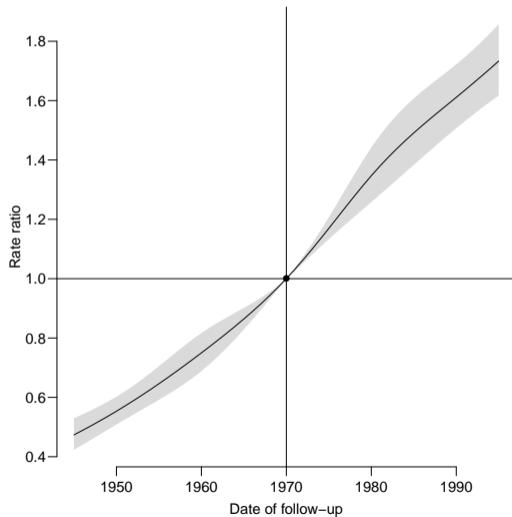
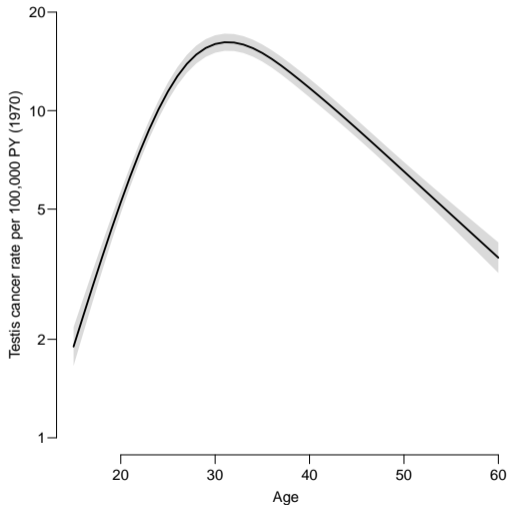
Quantitative, natural splines II

```
> 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 predictions 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

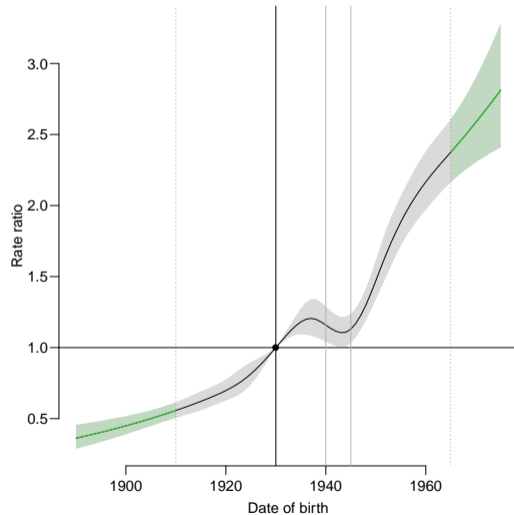
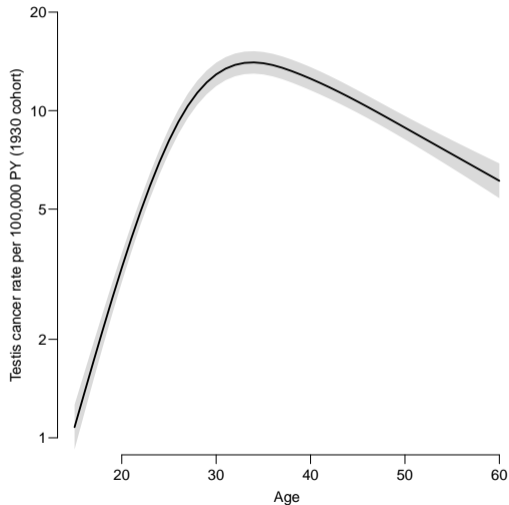
```
> ndA <- data.frame( A=15:60, C=1930      , Y=1 )
> ndC <- data.frame( A=30      , C=1890:1975, Y=1 )
> ndRc <- data.frame( A=30      , C=1930      , Y=1 )
> par( mfrow=c(1,2), mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> matshade( ndA$A, ci.pred(ac,ndA)*10^5, plot=TRUE,
+           log="y",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



Age-drift model

Bendix Carstensen

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Diabetes Incidence over Time

Emory University, Rollins School of Public Health,
CDC, Atlanta,

17 June 2019

18 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?

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

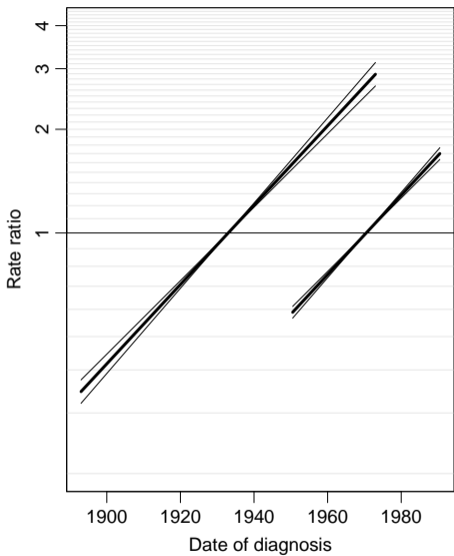
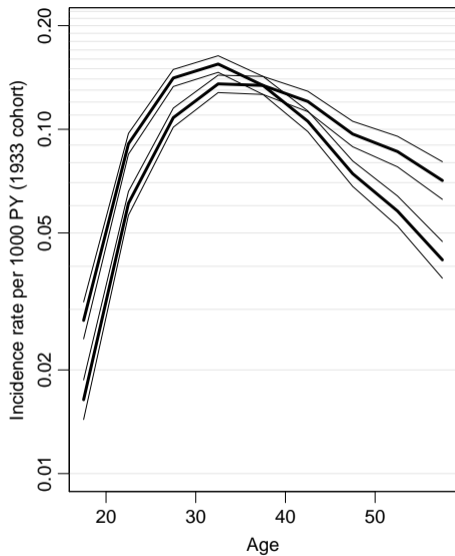
$$\begin{aligned} \alpha_a + \beta(p - p_0) &= \alpha_a + \beta(a + c - (a_0 + c_0)) \\ &= \underbrace{\alpha_a + \beta(a - a_0)}_{\text{cohort age-effect}} + \beta(c - c_0) \end{aligned}$$

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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APC-cat

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
```

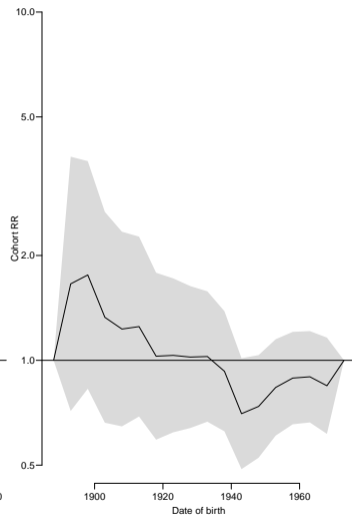
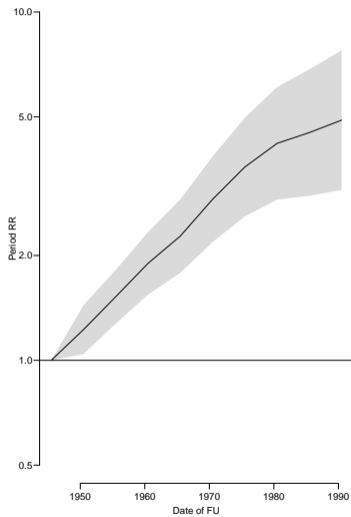
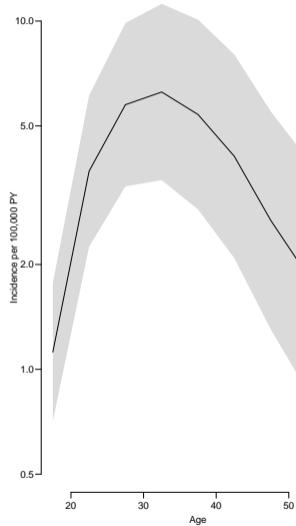
```
[1] 34
```

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 )
```

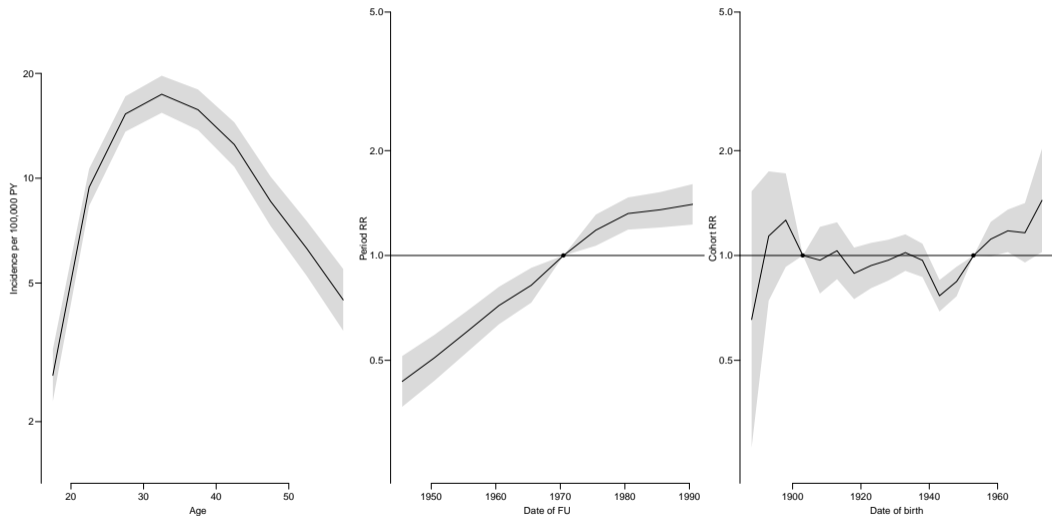
A, P, C effects



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



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

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<http://BendixCarstensen/APC>

Lexis-tab

Tabulation of register data

55	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
45	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
35	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
25	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
15	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
	1943	1953	1963	1973	1983	1993					

Testis cancer cases
in Denmark.

Male person-years
in Denmark.

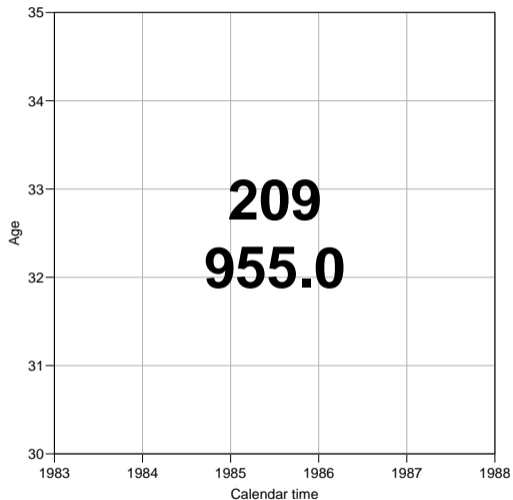
Tabulation of register data

	6	14	16	25	26	29	28	43	42	34	45
55	471.0	512.8	571.1	622.5	680.8	698.2	683.8	686.4	640.9	627.7	544.8
	16	28	22	27	46	36	50	49	61	64	51
	539.4	600.3	653.9	715.4	732.7	718.3	724.2	675.5	660.8	721.1	701.5
45	29	30	37	54	45	64	63	66	92	86	96
	622.1	676.7	737.9	753.5	738.1	746.4	698.2	682.4	743.1	923.4	817.8
	35	47	65	64	67	85	103	119	121	155	126
	694.1	754.3	768.5	749.9	756.5	709.8	696.5	757.8	940.3	1023.7	754.5
35	53	56	56	67	99	124	142	152	188	209	199
	769.4	782.9	760.2	760.5	711.6	702.3	767.5	951.9	1035.7	948.6	763.9
	56	66	82	88	103	124	164	207	209	258	251
	799.3	774.5	769.3	711.6	700.1	769.9	960.4	1045.3	955.0	957.1	821.2
25	55	62	63	82	87	103	153	201	214	268	194
	790.5	781.8	723.0	698.6	764.8	962.7	1056.1	960.9	956.2	1031.6	835.7
	30	31	46	49	55	85	110	140	151	150	112
	813.0	744.7	721.8	770.9	960.3	1053.8	967.5	953.0	1019.7	1017.3	760.9
15	10	7	13	13	15	33	35	37	49	51	41
	773.8	744.2	794.1	972.9	1051.5	961.0	952.5	1011.1	1005.0	929.8	670.2
	1943	1953	1963	1973	1983	1993					

Testis cancer cases
in Denmark.

Male person-years
in Denmark.

Tabulation of register data



Testis cancer cases in Denmark.

Male person-years in Denmark.

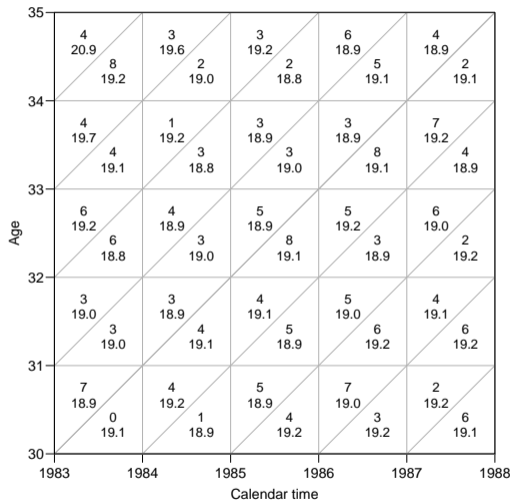
Tabulation of register data

Age	1983	1984	1985	1986	1987	1988
35	12 40.2	5 38.7	5 38.0	11 37.9	6 38.0	
34	8 38.7	4 38.0	6 37.9	11 38.0	11 38.1	
33	12 38.1	7 37.9	13 38.0	8 38.1	8 38.2	
32	6 38.0	7 38.0	9 38.1	11 38.2	10 38.3	
31	7 38.0	5 38.0	9 38.1	10 38.2	8 38.3	
30						

Testis cancer cases in Denmark.

Male person-years in Denmark.

Tabulation of register data




Testis cancer cases in Denmark.


Male person-years in Denmark.

Subdivision by year of birth (cohort).

Major sets in the Lexis diagram

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

B-sets: Classification by age and cohort. ()

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

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 $a = p - c$.

Lexis triangles

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

We may classify cases and risk time by all three factors

Lexis triangles:

Upper triangles: age and period, earliest born cohort. (∇)

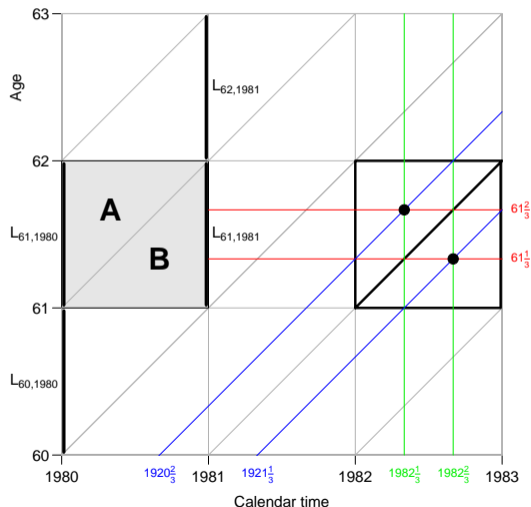
Lower triangles: age and period, latest born cohort. (\triangleleft)

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.
- ▶ mean date at risk.
- ▶ mean cohort at risk.

Tabulation by age, period and cohort



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

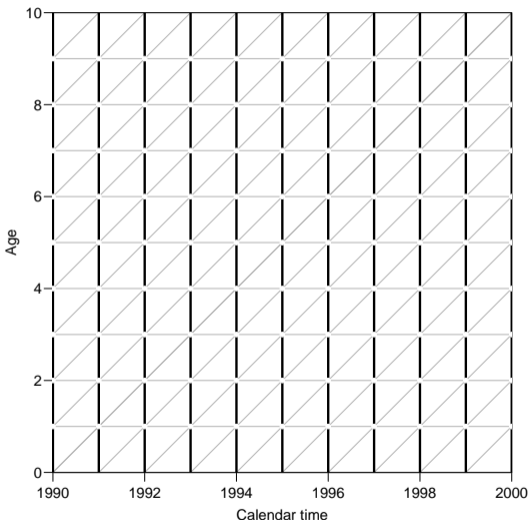
These are correct midpoints for age, period and cohort must be used in modeling.

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.

This corresponds to population sizes along the vertical lines in the diagram.

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



Summary:

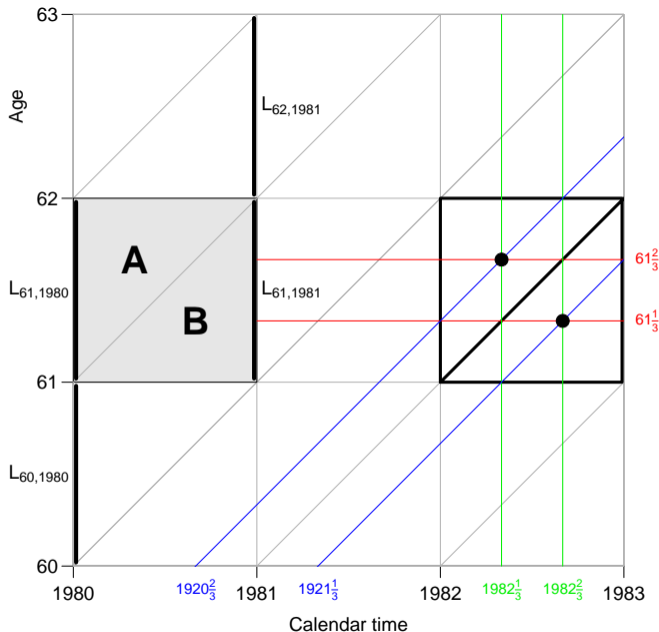
Population risk time
(N2Y):

$$\mathbf{A:} \left(\frac{1}{3}L_{a,p} + \frac{1}{6}L_{a+1,p+1} \right) \times 1y$$

$$\mathbf{B:} \left(\frac{1}{6}L_{a-1,p} + \frac{1}{3}L_{a,p+1} \right) \times 1y$$

Mean age, period and cohort:

$\frac{1}{3}$ into the interval.



APC-model: Parametrization

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APC-par

Age-Period-Cohort model

$$\log(\lambda_{ap}) = \alpha_a + \beta_p + \gamma_c = f(a) + g(p) + h(c)$$

... but $c = p - q \Leftrightarrow p - a - c = 0$

$$\begin{aligned}\log(\lambda_{ap}) &= f(a) + g(p) + h(c) + \gamma(p - a - c) \\ &= f(a) - \mu_p + \mu_c - \gamma a + \\ &\quad g(p) + \mu_p \qquad \qquad \qquad + \gamma p + \\ &\quad h(c) \qquad \qquad \qquad - \mu_c - \gamma c\end{aligned}$$

A decision on parametrization is needed.

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

Parametrization principle

The problem is to choose μ_a , μ_c and γ according to some (**external!**) criterion for the functions.

1. The age-function should be interpretable as log age-specific rates in a cohort c_0 after adjustment for the period effect.
2. The cohort function is 0 at a **reference cohort** c_0 , interpretable as log-RR relative to cohort c_0 .
3. The **period** function is **0 on average** with **0 slope**, interpretable as log-RR relative to the age-cohort prediction. (residual log-RR).

This will yield cohort age-effects a.k.a. **longitudinal** age effects.

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

Period-major parametrization

- ▶ Alternatively, the period function could be constrained to be 0 at a reference date, p_0 .
- ▶ Age-effects would refer to age specific rates at p_0
- ▶ Cohort effects constrained to be 0 on average with 0 slope.
- ▶ Gives period or **cross-sectional** age-effects

Bureaucratically interpretable: what was seen at a given date?

Implementation:

1. Obtain any set of parameters $f(a)$, $g(p)$, $h(c)$.
2. Extract the trend from the period effect (find μ and β):

$$\tilde{g}(p) = \hat{g}(p) - (\mu + \beta p)$$

(regression of $\hat{g}(p)$ on p)

3. Decide on a reference cohort c_0 .
4. Use the functions:

$$\tilde{f}(a) = \hat{f}(a) + \mu + \beta a + \hat{h}(c_0) + \beta c_0$$

$$\tilde{g}(p) = \hat{g}(p) - \mu - \beta p$$

$$\tilde{h}(c) = \hat{h}(c) + \beta c - \hat{h}(c_0) - \beta c_0$$

“Extract the trend”

- ▶ **Not** a well-defined concept:
 - ▶ Regress $\hat{g}(p)$ on p for all units in the dataset.
 - ▶ Regress $\hat{g}(p)$ on p for all different values of p .
 - ▶ Weighted regression — what weights?
- ▶ A better founded solution is needed. . .

“Extract the trend”

- ▶ A solution from linear algebra:
 - ▶ Take the columns from the parametric period effect,
 - ▶ projection on the orthogonal to $(1, p)$
 - ▶ requires an inner product in the observation space
 - ▶ should be an inner product using person-years as weights
- ▶ Stepwise process:
 - ▶ Fit Age-Cohort model
 - ▶ compute the predicted values for the observed data
 - ▶ use the log of these as offset in a model with only Period
 - ▶ 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 )
```

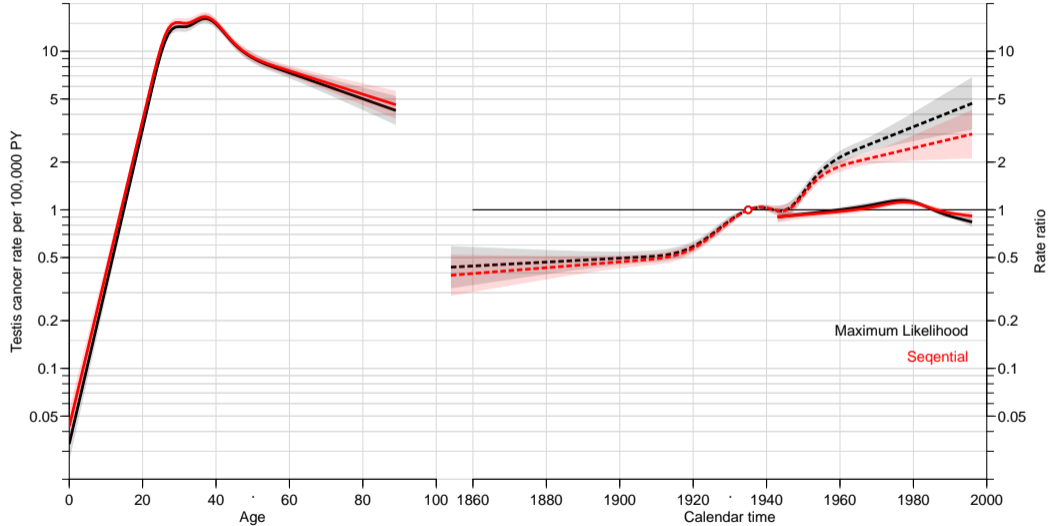
```
   A   P D   Y  
1 0 1943 1 39649.50  
2 1 1943 1 36942.83  
3 2 1943 0 34588.33  
4 3 1943 1 33267.00  
5 4 1943 0 32614.00  
6 5 1943 0 32020.33
```

```
> 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./Pr(>Chi)
1	Age	4854	6008.406	NA	NA	NA	
2	Age-drift	4853	4864.393	1	1144.01295	8.976155e-251	1144.01295
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



Parametrization of the APC model is arbitrary

- ▶ Separation of the three effects relies on arbitrary principles, e.g.:
 - ▶ Age is the primary effect
 - ▶ Cohort the secondary, reference c_0
 - ▶ Period is the residual
 - ▶ Inner product for trend extraction
- ▶ ... 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 $p - a$
- ▶ Any fix has some (hidden) assumption(s)
- ▶ ... 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,
CDC, Atlanta,

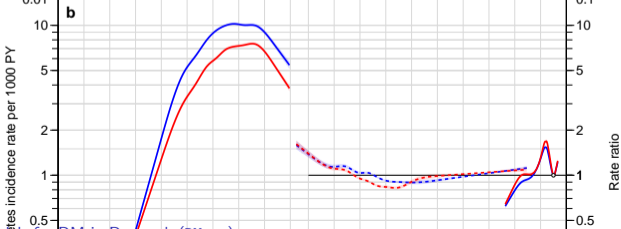
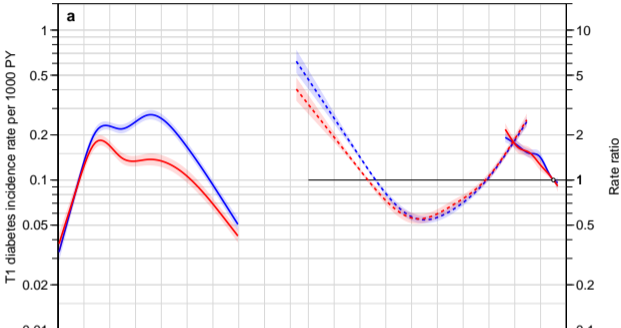
17 June 2019

18 June 2019

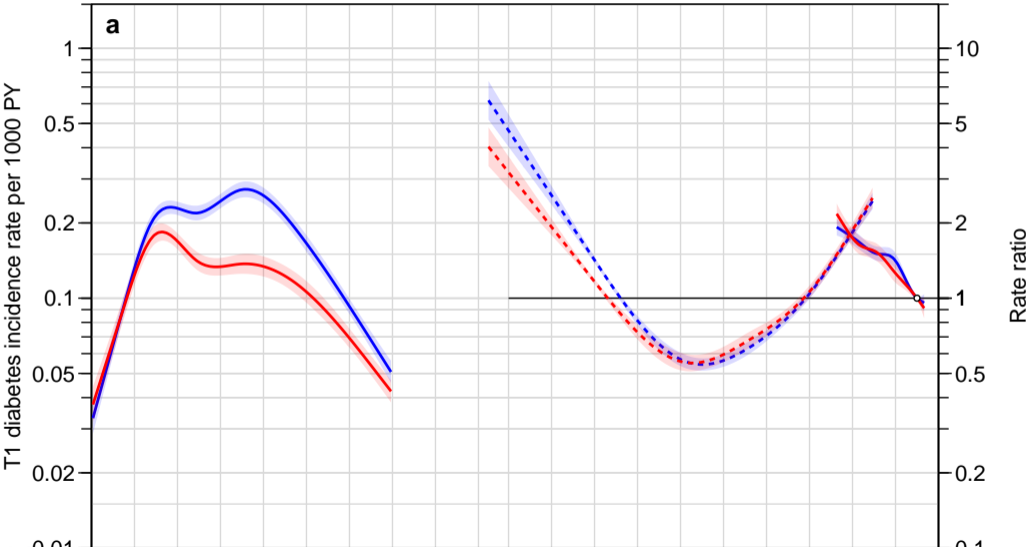
<http://BendixCarstensen/APC>

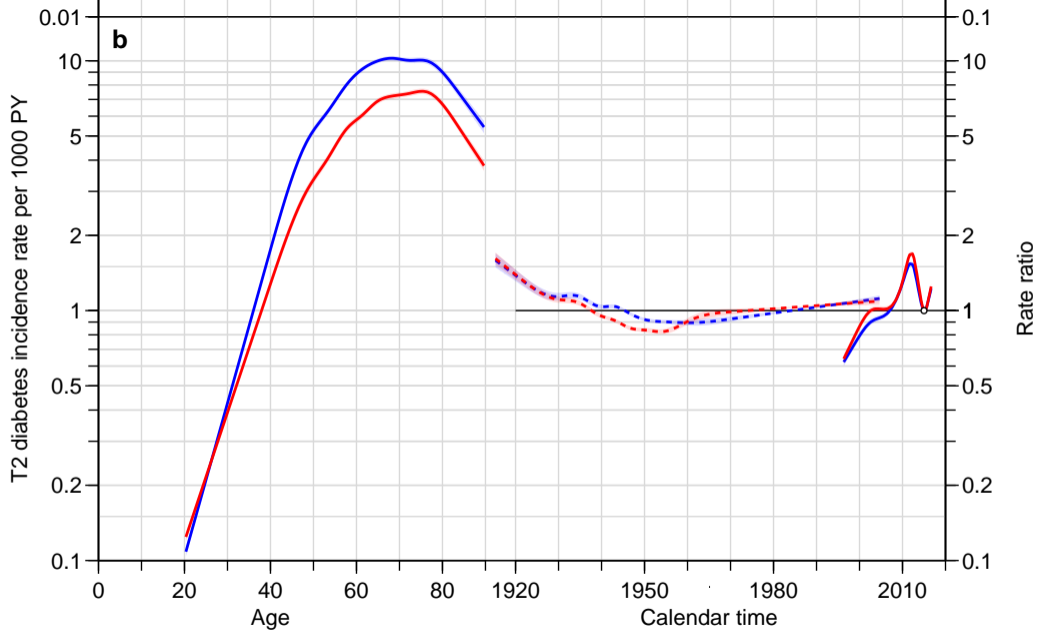
DMreg

Age-Period-Cohort analysis of DM in Denmark



Age-Period-Cohort analysis of DM in Denmark





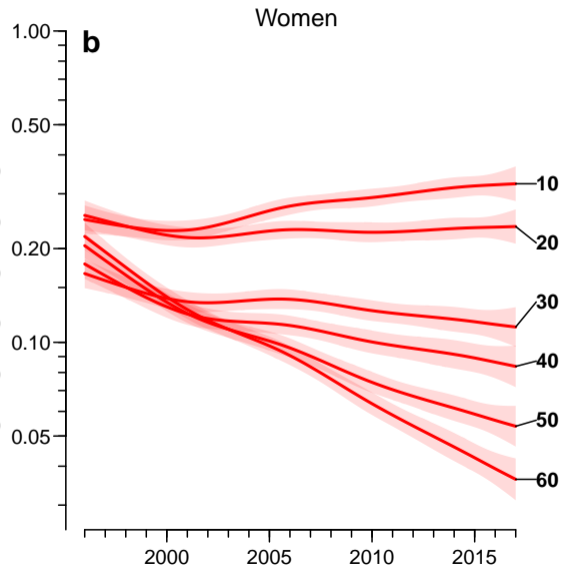
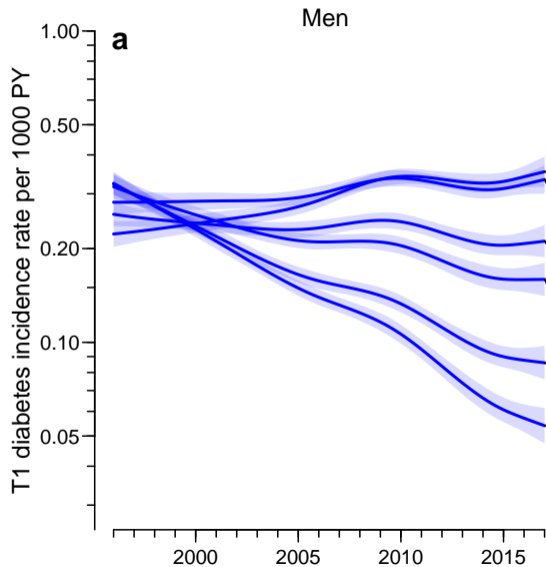
Incidence rates

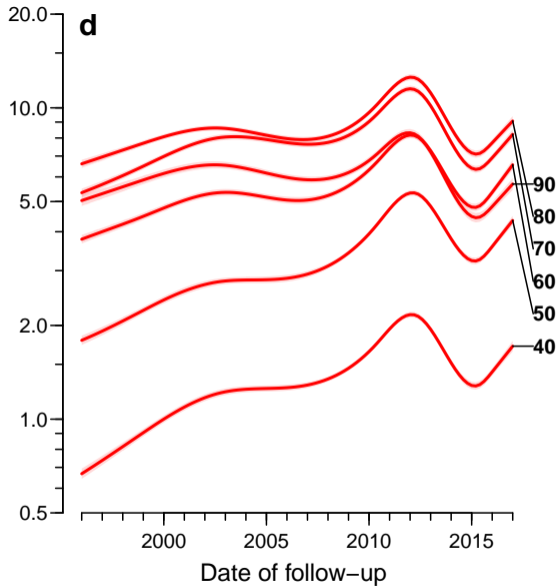
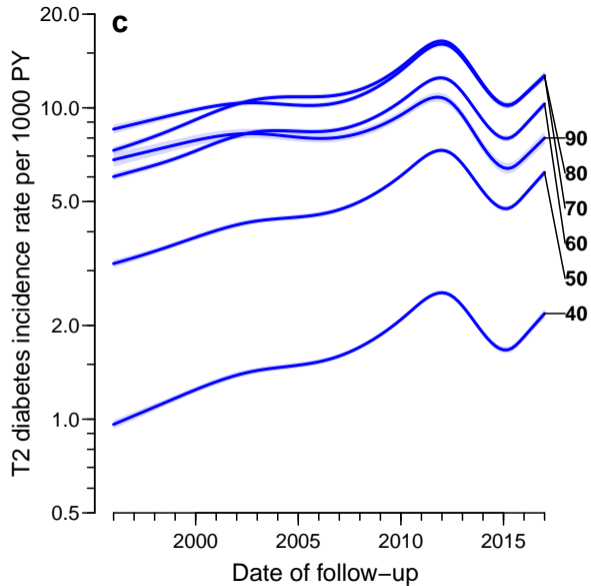
- ▶ T1D:
 - ▶ peaks ages 15–40, weak increase for men, weak decrease for women.
 - ▶ decrease after age 40
 - ▶ peak rates at 10–20 cases per 100,000 PY (2015)
 - ▶ change by calendar time: -3.5% /year
- ▶ T2D:
 - ▶ peaks ages 65–80
 - ▶ decrease after 80
 - ▶ peak rates at 7–10 cases per 1000 PY (2015)
 - ▶ change by calendar time: 3.3% /year
 - ▶ very irregular calendar time pattern

Age-Period-Cohort analysis of DM in Denmark

- ▶ Alternative to showing the (arbitrarily fixed) age-, period- and cohort-components, is to show the predicted rates
- ▶ ... for a fixed age (50 years, say) as a function of calendar time
- ▶ The natural splines constrain P and C components to be linear at the end, so easy to extrapolate rates at any desired age into the future
- ▶ ... but may overshoot

Age-Period-Cohort analysis of DM in Denmark





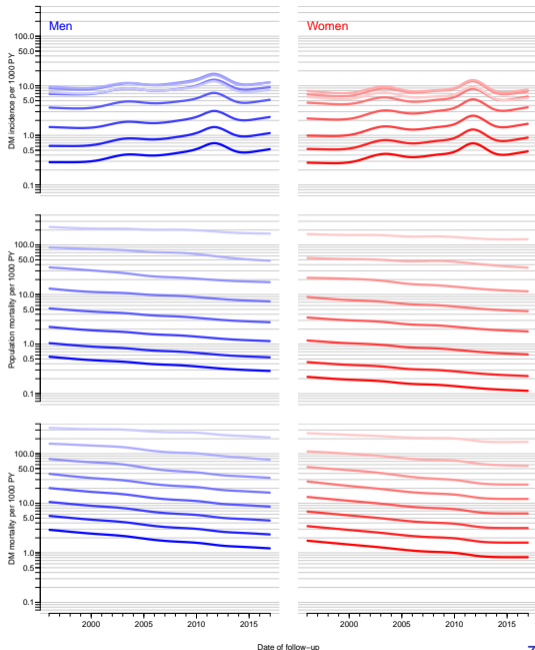
Predictions for total DM

Incidence of total DM

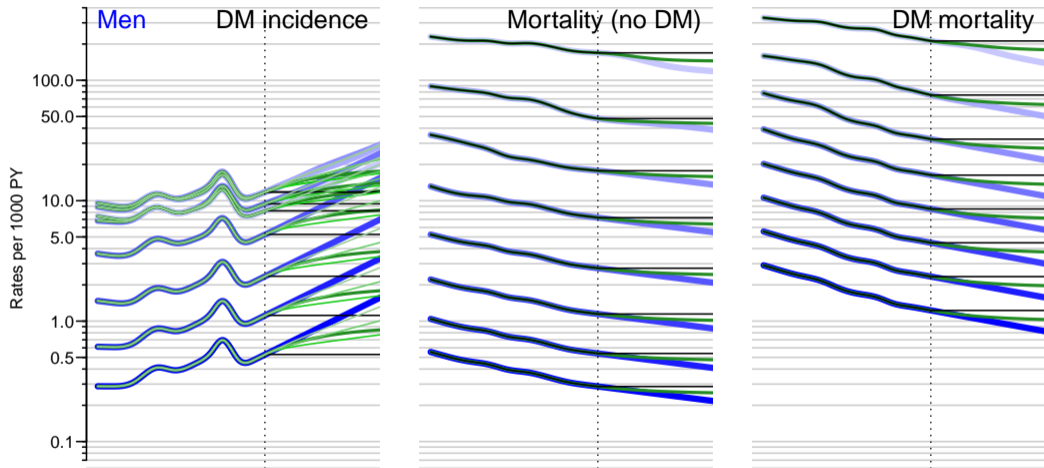
Mortality in total DM

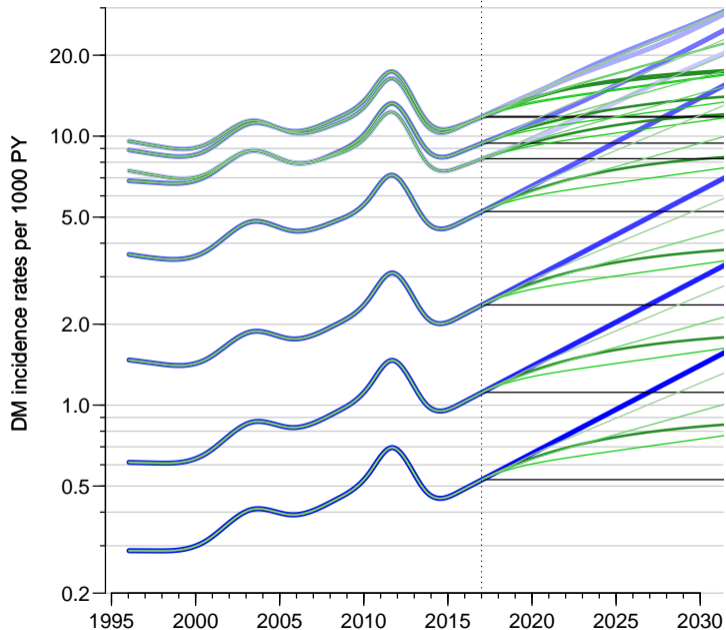
Mortality in no DM

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



Future rates for total DM





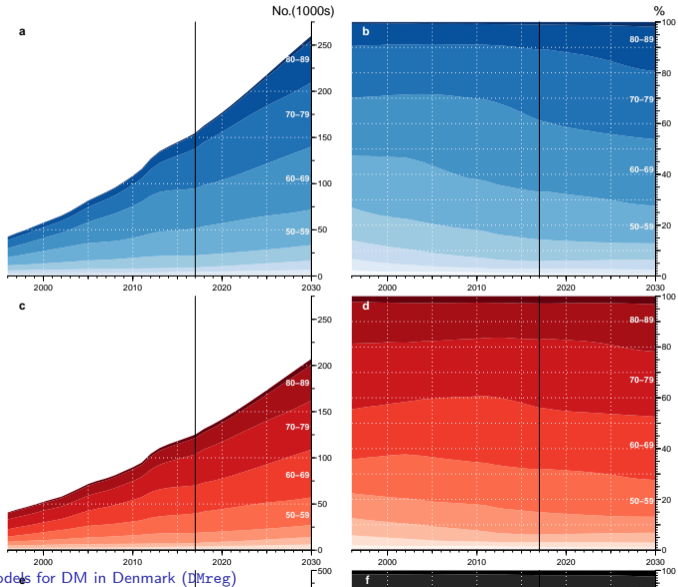
Projection scenarios for incidence rates

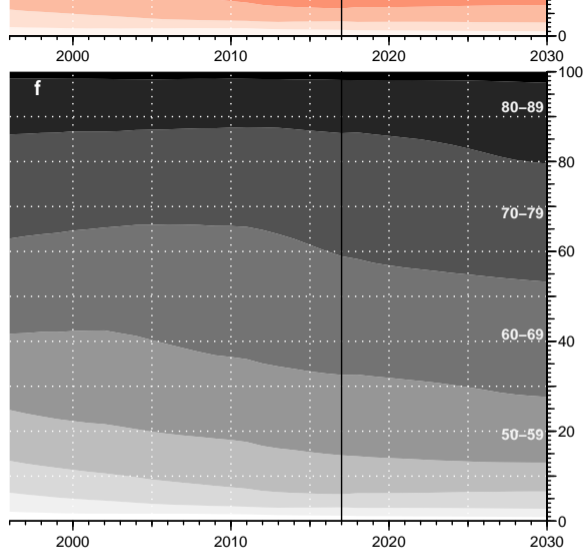
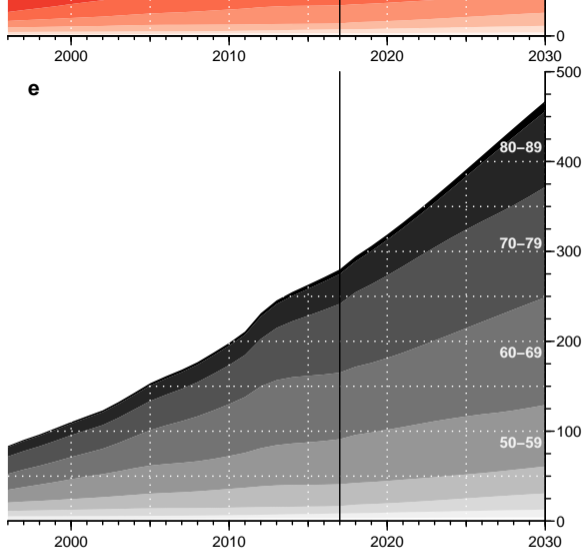
- ▶ Incidence rates (6 scenarios)
 - ▶ Simple linear projection of period and cohort effects
 - ▶ Attenuation of **slopes** of age-specific rates:
Every 5 years the slope is halved
 - ▶ Simple linear increase in incidence rates 2017–2030:
0%/year, 2%/year, 4%/year, 6%/year,
- ▶ Mortality rates (3 scenarios)
 - ▶ Simple linear projection of period and cohort effects
 - ▶ Attenuation of **slopes** of age-specific rates:
Every 5 years the slope is halved
 - ▶ Constant rates as of 2017

Future number of prevalent cases

1. Start with prevalence as of 2017-01-01:
The predicted prevalences for each month of age (1200 classes)
2. Use incidence rates to predict the fraction of non-DM that will be DM one month later (and one month older)
3. Use mortality for DM to predict the fraction of the prevalent cases that will survive one month (and be one month older)
4. Use mortality for non-DM to predict how many of the non-DM will survive one month (and be one month older)
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)





Future number of prevalent cases (M/W)

- ▶ Total no. prevalent cases increase from 287,000 in 2017 to 467,000 in 2030.
- ▶ The population of DM cases will be older — the over-80 will increase from 13 to 20%
- ▶ The incidence rates are erratic toward the end of the observation period, so prediction to 2040 is not feasible
- ▶ Scenarios with 2%, resp. 4% annual increase from 2017 level of incidence gives predictions of 445,000 and 482,000 prevalent cases.

Mehodological points

- ▶ Incidence and mortality in tables by age, period and cohort in 1-year classes (Lexis triangles)
- ▶ Score the correct mean age, period and cohort in each
- ▶ Model with smooth functions for age, period and cohort — a kind of parametric smoothing of the rates over the Lexis diagram
- ▶ Use the predicted rates in 1-month steps to project future prevalence
- ▶ Small steps important — we assume that DM and death cannot occur in the same interval. 1 year intervals rendes this too probable
- ▶ The parametric component 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>

A more complete account of APC-modeling can be found in the course material from the European Doctoral School of Demography:

<http://bendixcarstensen.com/APC/EDSD-2019/>