

Demography and epidemiology: Age-Period-Cohort models in the computer age

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Abstract

Analysis of rates from disease registers are often reported inadequately because of too coarse tabulation of data and because of confusion about the mechanics of the age-period-model used for analysis. Rates must be considered as observations in a Lexis diagram, and tabulation a necessary reduction of data, which should be as small as possible.

This paper gives a guide to analysis of rates from a Lexis diagram by the age-period-cohort model. Three aspects need to be considered separately: 1) Tabulation of cases and person-years, 2) Modelling of age, period and cohort effects and 3) Parametrization and reporting of the estimated effects. It is argued that most of the confusion in the literature comes from failure to make a clear distinction between these three aspects. A set of recommendations for the practitioner is given and a package for **R** that implements the recommendations is introduced.

KEYWORDS: Age-period-cohort model, Lexis diagram, follow-up studies, Poisson model, parametrization, epidemiology, demography.

1 Introduction

Disease registries collect information on disease occurrence in populations by recording new cases by diagnosis, sex, age and date of diagnosis etc. Description of disease rates by age and time is best conceptualised by regarding the observations in a Lexis-diagram.

The age-period-cohort-model is a *descriptive* tool for observations from a Lexis diagram, typically from cancer registries or other disease registers. The model describes rates as a product of an age-effect, a period effect and a cohort effect. The aim is to give an overview of 1) the magnitude of the rates, 2) the variation by age and 3) time trends in the rates.

The database used as basis for the descriptive analysis is a tabulation of events (deaths, diagnoses of disease) and population size over a certain time period and age span, possibly restricted to certain birth cohorts.

The classical age-period-cohort models has been formulated as a model for this table where the effect of age, period and cohort are modelled as factors, i.e. with one parameter per level in the tabulation. In order to keep the number of parameters at a manageable level and to obtain reasonably smooth curves for the effects, the tabulation has usually been by 5-year age and period intervals.

Since the date of diagnosis is the sum of the date of birth and the age at diagnosis, there will be a constraint in any model which includes these three variables on a linear scale. The literature is abundant with attempts to overcome this so called identifiability problem. It is of course futile to overcome the problem of having two variables as well as their sum in the same linear model. The identifiability problem is not much different from any other problem that arises from convenience formulation of models by over-parametrization as is for example often the case in the two-way ANOVA model. As such it cannot be solved properly without a view to the subject matter.

In this paper I formulate the age-period-cohort model as a general model for observation in the Lexis diagram. The main point is that the tabulation of data should

not be taken for granted, but be part of the data analysis and as little information as possible should be thrown away by tabulation. This requires a formulation that allows any kind of tabulation of data, not only by age and date of event, but also by date of birth, and not necessarily in intervals of the same length. I will separate the issues of the *tabulation* of the data, the *model* for the age, period and cohort effects and the *parametrization* of these. These three issues are mixed up in many papers discussing the models, mainly because the tabulation of data has been taken for granted, and the default model has been a factor model.

Section 2 gives a brief overview of the initial steps of an analysis of observations in a Lexis diagram, section 3 discusses tabulation of cases and person-years by age, period and cohort, and the implications for analysis. In section 4 the Poisson model for rates is briefly reviewed and the options for modelling the *underlying* rates from the Lexis diagram discussed. The core of the paper is in sections 5 and 6, where the parametrization of the age-period-cohort model is discussed *without* reference to tabulation of data and the particular parametric form chosen for the three effects. Finally I give a few remarks about graphical display of results in section 8 and in section 9 I use data on testis cancer incidence in Denmark to illustrate the options given. In the discussion in section 10, a set of recommendations are given for practical analysis and reporting of rates observed in a Lexis diagram.

2 Description of rates.

Initial plots

Prior to analysis by age-period-cohort models one should always plot the observed rates. This will of course require that cases and person years be tabulated in classes that are sufficiently large to produce fairly stable rates. There are four classical plots that should be made:

1. Rates versus age, observations within each period connected, i.e. cross-sectional age-specific rates.
2. Rates versus age, observations within each birth cohort connected, i.e. longitudinal age-specific rates.
3. Rates versus period, observations within each age-class connected.
4. Rates versus cohort, observations within each age-class connected.

These four plots are initial explorations of whether rates are proportional between periods or cohorts; the first and third will exhibit parallel lines if age-specific rates are proportional between periods (i.e. follow an age-period model), the second and fourth if they are proportional between cohorts (i.e. follow an age-cohort model).

These plots require a reasonably coarse tabulation to be informative. But the tabulation used for a first simple overview of data need not be the basis for the entire analysis.

An example of these four plots are given for rates of testis cancer in Denmark. An important feature of these plots is the recognition of the *absolute* level of the rates.

The figures used as basis for the plots are in table 1.

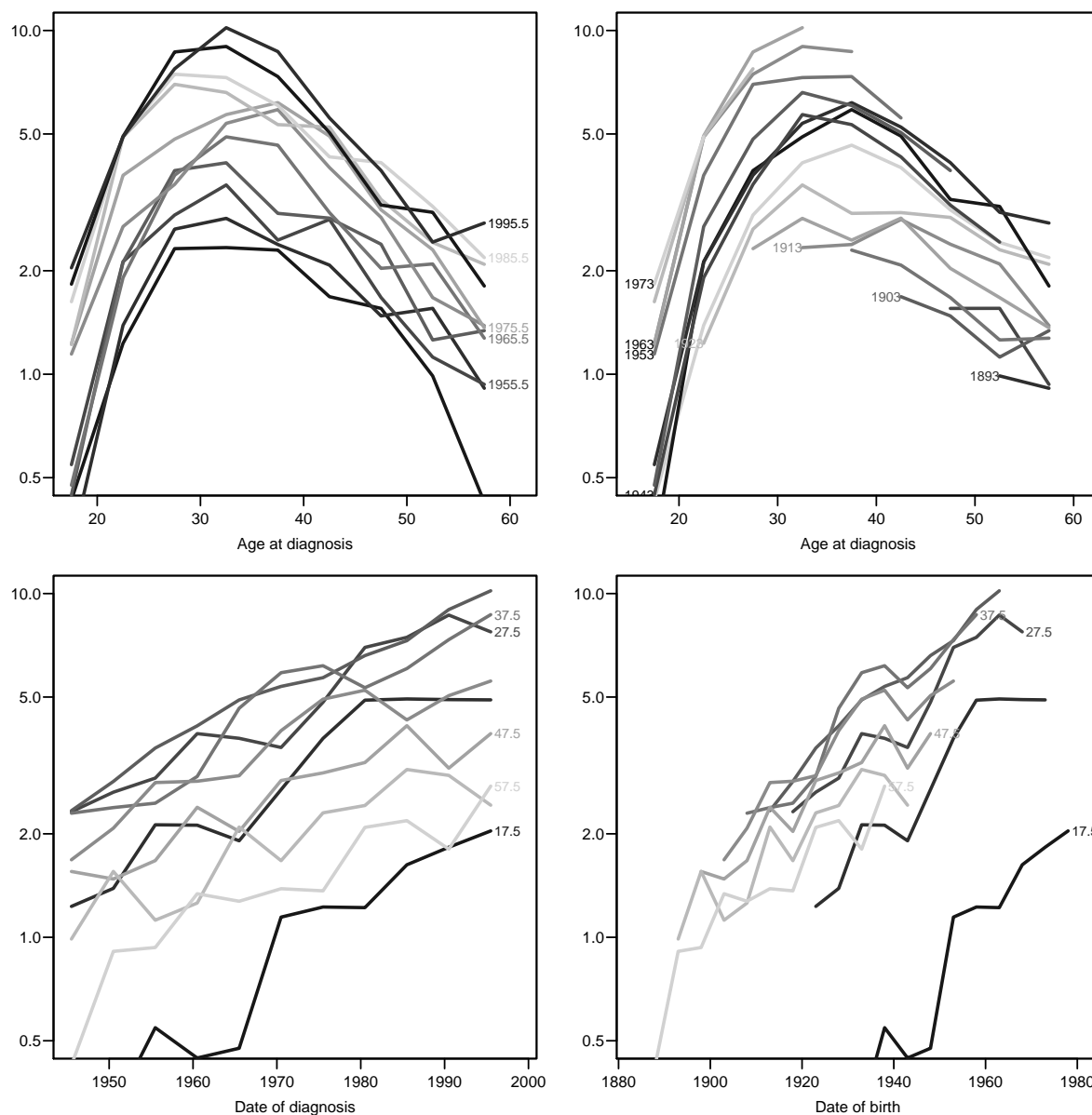


Figure 1: The classical four plots for rates observed in a Lexis diagram. Rates of testis cancer (per 100,000 person-years) in Denmark 1943–97 in ages 15–65 years.

Top left: Age-specific rates by period of diagnosis. Top right: Age-specific rates by date of birth. Bottom left: Period-specific rates by age. Bottom right: Cohort-specific rates by age.

Table 1: *Cases of testis cancer and male person-years in Denmark 1943–96 in 5-year classes. The mean date in the period 1943–47 is 1945.5, etc. The last period 1993–1996 is only 4 years, so the mean date is here 1995.0. The bold-face entry in the table is further subdivided in 50 subsets by one-year classes of age, period and cohort in figure 1.*

Mean	Mean period										
age	1945.5	1950.5	1955.5	1960.5	1965.5	1970.5	1975.5	1980.5	1985.5	1990.5	1995.0
Cases											
17.5	10	7	13	13	15	33	35	37	49	51	41
22.5	30	31	46	49	55	85	110	140	151	150	112
27.5	55	62	63	82	87	103	153	201	214	268	194
32.5	56	66	82	88	103	124	164	207	209	258	251
37.5	53	56	56	67	99	124	142	152	188	209	199
42.5	35	47	65	64	67	85	103	119	121	155	126
47.5	29	30	37	54	45	64	63	66	92	86	96
52.5	16	28	22	27	46	36	50	49	61	64	51
57.5	6	14	16	25	26	29	28	43	42	34	45
62.5	9	12	11	13	20	18	28	23	26	15	10
Person-years (in 1000s)											
17.5	2321	2233	2382	2919	3155	2883	2858	3033	3015	2789	2011
22.5	2439	2234	2165	2313	2881	3162	2902	2859	3059	3052	2283
27.5	2372	2345	2169	2096	2294	2888	3168	2883	2869	3095	2507
32.5	2398	2324	2308	2135	2100	2310	2881	3136	2865	2871	2464
37.5	2308	2349	2281	2281	2135	2107	2302	2856	3107	2846	2292
42.5	2082	2263	2305	2250	2270	2129	2090	2273	2821	3071	2264
47.5	1866	2030	2214	2260	2214	2239	2095	2047	2229	2770	2453
52.5	1618	1801	1962	2146	2198	2155	2173	2027	1982	2163	2105
57.5	1413	1538	1713	1868	2042	2095	2051	2059	1923	1883	1634
62.5	1210	1305	1424	1584	1720	1880	1930	1884	1890	1772	1392

Modelling rates

There are three separate issues to consider when using a statistical model to describe rates from a disease register (observations in a Lexis diagram):

Data: How should data be tabulated: Should we use 1-year intervals or 5-year intervals? Should the tabulation be by age and period, by age and cohort, by period and cohort or should it be by all three: age, period and cohort?

Model: How should we model the effects of age, period and cohort: Use a factor model (one parameter per level) or smooth functions of the three variables? Should the smoothing be parametric or non-parametric?

Parametrization: How should we parametrize the estimated effects: What constraints should be used and how is it made clear which ones we have used? What is a sensible graphical display?

Note that I have separated the model and the parametrization of it. A (linear) model in my terminology is synonymous with the linear subspace spanned by the columns of the model matrix (a.k.a. the design matrix). Some authors (e.g. Clayton and Schifflers [4, 5]) have referred to different parametrizations of the same model as different models.

3 Data

In principle the entire population could be regarded as a cohort, and data analysed in continuous time. However this will rarely be feasible, so in practise data will be tabulated. The analysis dataset will have one record per subset of the Lexis diagram, with number of events and risk time as outcome variables, and mean age, period and cohort as explanatory variables.

Any tabulation of data represents an information loss (rounding of age and date of diagnosis), so the tabulation should be as detailed as possible, it should only be limited by the availability of population figures. Cells with 0 cases will not invalidate the analysis, so there is no lower limit to the tabulation intervals (except for computing capacity).

Cases

If disease cases are taken from a register, cases can be tabulated arbitrarily fine by age at diagnosis, date of diagnosis (period) and date of birth (cohort). It will for example be possible to enumerate cases for each $1 \times 1 \times 1$ -year triangle of the Lexis diagram as illustrated for Danish testis cancer cases in figure 2. In principle it would even be possible to produce a tabulation of data by single months as well.

Person-years

Population figures are needed to produce rates, and the availability of these will normally be the limiting factor. In most countries, population figures in 1-year age classes for each calendar year are available. Such figures of population prevalence can be used to compute the risk time (person-years) in triangular subsets of the Lexis diagram.

For the sake of simplicity, the following formulae are given for one-year age-classes and 1-year periods¹. Specifically, let $L_{a,p}$ be the population size in age a , at beginning of year p , see the left part of figure 3, where $a = 61$ and $p = 1980$. The risk time in age class a , during year p , among those aged a at the beginning of year p (i.e. born in year $p - a - 1$, triangle **A** in figure 3) is estimated as:

$$y_{a,p,p-a-1} = \frac{1}{3}L_{a,p} + \frac{1}{6}L_{a+1,p+1}$$

and in the corresponding lower triangle (i.e. among those born in year $p - a$, triangle **B** in figure 3):

$$y_{a,p,p-a} = \frac{1}{6}L_{a-1,p} + \frac{1}{3}L_{a,p+1}$$

¹Strictly speaking these formulae are wrong as they give *number* of cases rather than *risk time*. In order to make them correct all quantities must be multiplied by the interval length, in this case 1 year.

These formulae are based on an assumption of constant mortality in each triangle of the Lexis diagram. The derivation of these formulae are to my knowledge first seen in a set of lecture notes from Oslo University by Erling Sverdrup[14]. A precise derivation of the formulae and further details can be found in [3]

The formulae should also be used in calculation of risk time in rectangles of the Lexis diagram as well. The total risk time in **AUB** is best estimated by:

$$y_{a,p} = \frac{1}{6}L_{a-1,p} + \frac{1}{3}L_{a,p} + \frac{1}{3}L_{a,p+1} + \frac{1}{6}L_{a+1,p+1}$$

and not by $\frac{1}{2}L_{a,p} + \frac{1}{2}L_{a,p+1}$ as is commonly used.

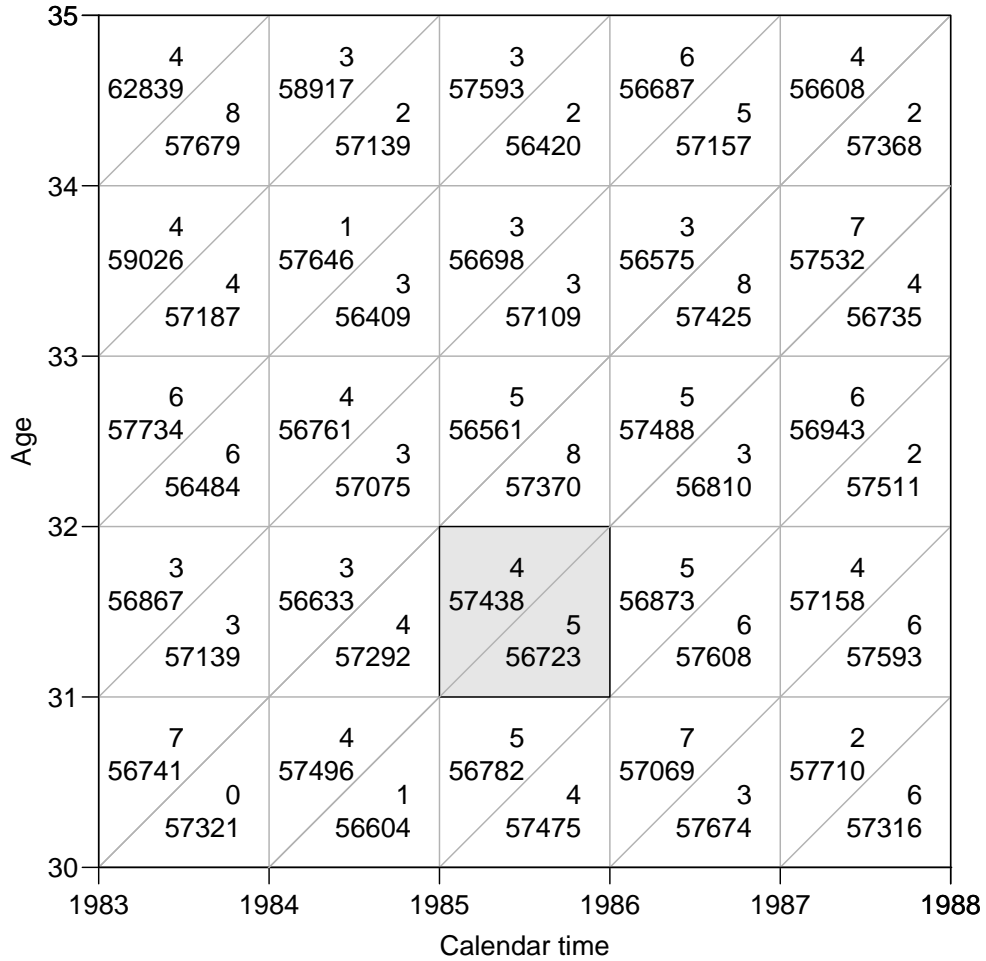


Figure 2: Danish testis cancer cases and male person-years in ages 30–34 and period 1983–1987, subdivided by age, period and cohort in 1-year classes (subdivision of the bold face entry in table 1). For example, in the highlighted square, there were 9 cases diagnosed in age 31 in the year 1985; 4 born in 1953 (upper triangle, persons who cross the 32 age line in 1985) and 5 born in 1954 (lower triangle, persons who cross the 31 age line in 1985).

The first age-category

The risk time in the first age-category, i.e. among 0-year old in the year of birth (\triangle), cannot be computed with the formulae above. One possible estimate is $\frac{1}{2}L_{0,p+1}$ for those born in year p , disregarding those dead in the year born, another alternative is to take a weighted average of $\frac{1}{2}L_{0,p+1}$ and half the number of births in the year, $\frac{1}{2}b_p$. Since the mortality is largest in early months, b_p should be given the smallest weight, but the actual weights to use is matter of taste.

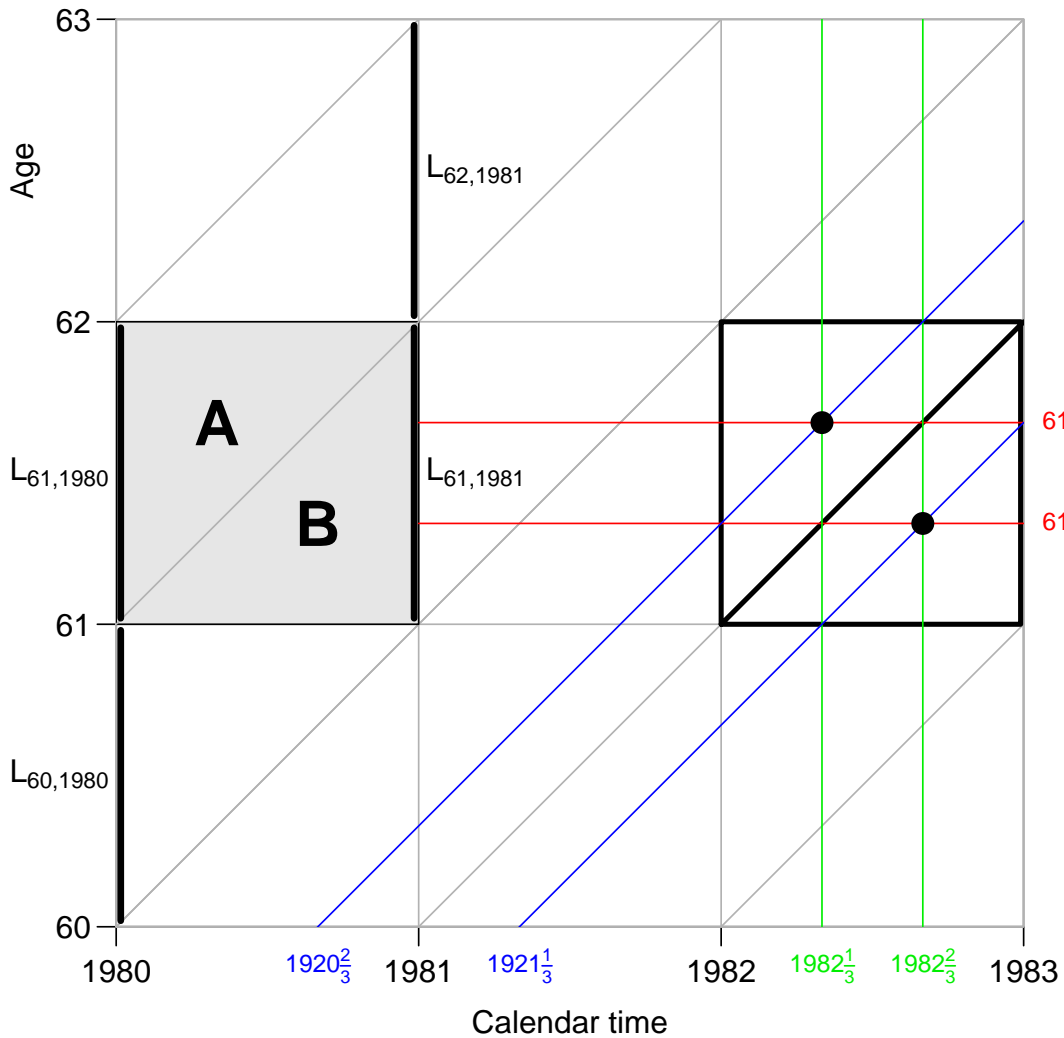


Figure 3: *Lexis diagram.* The thick lines in the left part shows the population figures at the beginning of 1980 and 1981 necessary to estimate the population risk time in the triangles **A** and **B**. The right part of the diagram shows the mean age, period and cohort in the triangular subsets of a Lexis diagram. Note the connection between age, period and cohort: $p = c + a$: $1982\frac{1}{3} = 1920\frac{2}{3} + 61\frac{2}{3}$ and $1982\frac{2}{3} = 1921\frac{1}{3} + 61\frac{1}{3}$.

Mean age, period and cohort in triangular subsets

If a tabulation is by age and period (A-sets: \square), by period and cohort (B-sets: \nearrow) or by age and cohort (C-sets: \swarrow), the mean age, period and cohort in each set is simply the mean for the corresponding tabulation intervals for each of the two tabulation variables. The mean for the third variable is obtained using the relation $p = c + a$.

But when subdividing the Lexis diagram in triangles, the mean age, period and cohort in a given set is not equal to the mean of the classes chosen for tabulation. The means are offset by $\frac{1}{6}$ of the tabulation interval, as shown in the right part of figure 3, see e.g. [15]; a formal derivation of the formulae is given in [3]. These values should be used when modelling rates based on a tabulation in triangles. Note in particular that the relationship $a = p - c$ must hold for all subsets of the Lexis diagram (and hence for all units in the dataset).

In the following there will be no assumptions about the particular shape of the subsets of the Lexis diagram used for tabulation, neither w.r.t. the number of tabulation variables, whether the tabulation intervals are equally long for different variables nor whether all subsets have the same shape.

4 Models

The general form of a multiplicative age-period-cohort model for rates $\lambda(a, p)$ at age a in period p for persons in birth cohort $c = p - a$ is:

$$\log[\lambda(a, p)] = f(a) + g(p) + h(c) \quad (1)$$

Here it is assumed that a , p and c represent the *mean* age, period and cohort for the observational units. The model allows the effects of each of the three variables to be non-linear (on the log-rate scale). The particular parametric form chosen for the functions f , g and h is immaterial at this point.

“Poisson” model

For tabulated data, one must assume that the rate is constant within each tabulation category (subset of Lexis diagram). The log-likelihood contribution from observation of the random quantity (D, Y) in one subset is:

$$l(\lambda|D, Y) = D \log(\lambda) - \lambda Y$$

Except for a constant ($D \log(Y)$) not involving the rate parameter this is the same as the log-likelihood for an observation of a random variable D from a Poisson distribution with mean λY . The log-likelihood for the entire table of (D, Y) is the sum of such terms, because individuals are assumed independent, and the contributions to different cells from one individual are *conditionally* independent. Hence, models for λ can be fitted using a program for Poisson regression for independent observations, that allows for an *offset* term to separate the person-years from the rate in the expression for the mean.

However the fact that the Poisson model and the constant rate model has the same likelihood does not mean that the number of cases is Poisson distributed, and in

particular not that the amount of risk time is fixed. The Poisson machinery should only be used for making likelihood based inference. Inference based on the *distributional* properties of the Poisson is not necessarily correct.

The information about $\theta = \log(\lambda)$ is computed as minus the second derivative of the log-likelihood evaluated at the ML-estimate:

$$l(\theta|D, Y) = D\theta - e^\theta Y, \quad l'_\theta(\theta|D, Y) = D - e^\theta Y, \quad l''_\theta(\theta|D, Y) = -e^\theta Y$$

so $I(\hat{\theta}) = e^{\hat{\theta}}Y = \hat{\lambda}Y = D$. Note that this is the *observed* information *not* the Fisher information which is the *expected* information. In the Poisson model the expected information is λY (because Y is assumed known in the Poisson model), but in the constant rate model further assumptions about the observation plan is required to compute the expected value of D .

Submodels

One may argue that test of the terms in model (1) is irrelevant as it is a descriptive model. However it has been customary to make formal tests of the effects.

The relevant submodels can conveniently be arranged in a sequence which gives all the relevant tests as comparisons between adjacent lines :

Model	$\log[\lambda(a, p)]$
Age	$f(a)$
Age-drift	$f(a) + \delta c$
Age-Cohort	$f(a) + h(c)$
Age-Period-Cohort	$f(a) + g(p) + h(c)$
Age-Period	$f(a) + g(p)$
Age-drift	$f(a) + \delta p$

Note that the two drift models (i.e. with a log-linear trend in period resp. cohort) are identical: Since $p = a + c$, a term δa can be separated from δp and absorbed into $f(a)$ giving the cohort drift model. Thus the age-drift model is the intersection of the age-period and the age-cohort model.

The deviance as output from most programs can be used to derive the likelihood-ratio test for the model reductions. The deviance statistic is also commonly used in isolation to judge whether a particular model provides an adequate fit to the data. The deviance statistic is the likelihood ratio test against the model with a completely freely varying interaction between age and period (or cohort). This is a meaningful test if the data represents a meaningful tabulation of the underlying process, but since any tabulation used for observations in a Lexis diagram is arbitrary so is the interaction model. Thus the formal goodness of fit tests does not have an interpretation in terms of the original model for the rates as function of age, period and cohort in continuous time, and so is largely meaningless.

Classical approach to modelling effects

As an extreme way of accommodating the non-linearity of the effects of age, period and cohort, the usual approach to modelling effects uses one parameter per distinct value of a , p and c , by defining the variables as “factors” (class variables).

As the tabulation of data becomes finer, the age-period-cohort modelling by one factor level for each distinct value of the three factors becomes unfeasible. This problem in age-period-cohort modelling emerges because the “factor” approach insists that effects be modelled by one separate parameter for each distinct value of the tabulation factors age, period and cohort. The factor models are thus effectively models that let the tabulation induce the model.

The classical approach (which has largely emerged from cancer epidemiology) has been to define a tabulation sufficiently coarse to avoid an excess amount of parameters in the modelling; keeping the number of parameters of the models at a reasonable level has lead to a coarse tabulation of data, typically in 5-year intervals. Thus there has been a feed-back loop between the tabulation of data and the modelling approach based on the concept of piecewise constant rates — the “factor”-modelling approach. This may have been induced by limited availability of population figures or by limited computing capacity (initially the need to compute standardized rates by hand before the advent of proper modelling hard- and software).

Tree-way tabulated data and the factor model

If data are tabulated by age, period and cohort, and the factor coding of effects is used, the model will fall into two disjoint parts, in the sense that the likelihood function will be a product of two terms, one only involving data from upper triangles (∇) and one only involving data from lower triangles (Δ), with separate sets of parameters. This was pointed out by Osmond and Gardner [9], but to my knowledge no one has suggested a way to remedy this problem, other than pooling the triangular subsets to quadrangular.

Smoothing with parametric functions

Since the three variables age, period and cohort are originally continuous variables it seems natural to model their effects by parametric smooth functions of the class means, for example:

- splines, i.e. 1st, 2nd or 3rd degree polynomials in predefined intervals, constrained to have identical values and derivatives at interval boundaries (knots).
- natural splines, 3rd degree splines constrained to be linear beyond the outermost knots.
- fractional polynomials, combination of polynomials of various powers, including non-integer powers.

Any of these approaches gives columns of the model matrix for age, period and cohort effects, and as such are just linear models.

If sufficient data is available there will be little difference between these approaches, the major question to address is the number of parameters to use for modelling each time-scale. Moreover, all the standard paraphernalia of penalizing the roughness of the effects is available for fine-tuning the number of parameters and the location of knots. However, penalizing the roughness is not necessarily desirable in a descriptive demographic model where sudden changes in effects may be perfectly sensible, for example due to changes in diagnostic practice.

Parametric smoothing avoids the problem of two separate models when using a factor model for data tabulated by age, period and cohort. Any factor model uses one parameter per cohort, even for the youngest and oldest where usually little data is present. With a parametric function it is possible to let the model reflect the information available in different cohorts.

If the number of parameters in the terms describing an effect equals the number of categories, then the model will be the same as the factor model, albeit parametrized differently. Hence the parametric models are submodels of the classical “factor” model.

Non-parametric smoothers

If a non-parametric smoothing is used it is difficult to keep strict control over the parametrization. From the next sections it will be clear that access to the model matrix is essential for handling the parametrization of the effects of age, period and cohort. Therefore this option is not considered further here.

5 Identifiable linear trend?

Holford [7] suggested to extract the linear trends from the age-, period- and cohort-parameters respectively, by regressing each set of estimates on the mean age, period and cohort, and then report the residuals as age, period and cohort effects. This would give a display of the identifiable quantities on a recognizable scale. The three remaining parameters would then be the age-slope and the period/cohort slope and the intercept. The intercept would depend on the choice of reference point for the age and period or cohort.

Regression of the estimates for the age, period and cohort classes on age, period and cohort and extraction of the linear trend produces a set of parameters (functions) \tilde{f} , \tilde{g} and \tilde{h} that are 0 on average with 0 trend and are connected to the original parameters by:

$$\begin{aligned} f(a) &= \tilde{f}(a) + \mu_a + \delta_a a \\ g(p) &= \tilde{g}(p) + \mu_p + \delta_p p \\ h(c) &= \tilde{h}(c) + \mu_c + \delta_c c \end{aligned}$$

Holford notes that $\delta_a + \delta_p$ and $\delta_p + \delta_c$ are invariants in the sense that regardless of the initial parametrization of f , g and h , they will have the same values, because any other

parametrization (\check{f} , \check{g} , \check{h}) can be obtained by a suitable choice of μ_a , μ_c and γ :

$$\begin{aligned}\check{f}(a) &= f(a) - \mu_a - \gamma a \\ \check{g}(p) &= g(p) + \mu_a + \mu_c + \gamma p \\ \check{h}(c) &= h(c) - \mu_c - \gamma c\end{aligned}$$

It is easily verified that $\check{f}(a) + \check{g}(p) + \check{h}(c) = f(a) + g(p) + h(c)$ for any value of $(a, p, c = p - a)$, and that the regression slopes of \check{f} , \check{g} and \check{h} differ from those for f , g and h with the same numerical quantity (γ), but that the quantities $\delta_a + \delta_p$ and $\delta_p + \delta_c$ are the same.

As Holford showed, the “detrended” period estimates can be obtained directly in the model fitting by replacing the part of the design matrix corresponding to period by a matrix with columns orthogonal to the intercept column and the (period) drift column. This matrix is found by taking the original columns and projecting them on the orthogonal complement to the space spanned by the constant and the drift.

However, the uniqueness of the overall secular trend $\delta_p + \delta_c$ depends on the definition of “orthogonal” or “0 on average with 0 slope”. The formulae devised by Holford are based on orthogonality w.r.t. the usual inner product:

$$\langle \mathbf{x} | \mathbf{y} \rangle = \sum x_i y_i$$

However this is not the only way of defining the drift, instead we could use an inner product of the type:

$$\langle \mathbf{x} | \mathbf{y} \rangle = \sum x_i w_i y_i$$

with some pre-defined weights. One obvious choice would be to take the w_i s proportional to the number of cases in each record (tabulation cell), i.e. using the observed information about the log-rate as weights.

Hence, the linear components ($\delta_a + \delta_p$ and $\delta_p + \delta_c$) devised by Holford are just as arbitrary as any other set of extracted linear trends. The size of extracted linear trends are not a feature of the *model*; they are a feature of the model *and* the (arbitrarily) chosen method for extracting the linear trends.

6 Parametrization of the age-period-cohort model

Since the aim is modelling rates as a function of age, period and cohort, the logical approach to parametrization is to formulate the problem in continuous time, i.e. by a model for the rate at any point (a, p) in the Lexis diagram. A general formulation of the model is:

$$\log[\lambda(a, p)] = f(a) + g(p) + h(c) \quad (2)$$

for three functions, f , g and h . The model predicts the rates at any point in the Lexis diagram. Applied to tabulated data the rates are assumed constant in each of the subsets in the Lexis diagram. The general form of the model makes parametric assumptions about the rates in these subsets. Note that the classical factor approach to

modelling also falls under this formulation — the functions are just assumed piecewise constant in larger intervals.

The challenge is to choose a parametrization of these three functions in a way that:

1. is meaningful,
2. is understandable and recognizable,
3. is practically estimable by standard software.
4. allows reconstruction of the fitted rates from the reported values.

The only components of the model (2) that can be uniquely determined are the second derivatives of the three functions, and yet the relevant representation of the model is by graphs of three functions f , g and h that sum to the predicted log-rates. The first derivatives as well as the absolute levels can be moved around between the functions. One choice is only to show the second derivatives, but as the scale for these is not easily understandable this is not an option in practise, although it has been used [12].

Choice of parametrization

For the sake of the argument, consider first the age-cohort model:

$$\log[\lambda(a, c)] = f(a) + h(c)$$

In this model only the *first* derivatives (contrasts) of f and h are identifiable. This is traditionally fixed by choosing a reference cohort c_0 , say, and constrain $h(c_0) = 0$. This will make $f(a)$ interpretable as the age-specific log-rates in cohort c_0 and $h(c)$ as the log rate ratio of cohort c compared to cohort c_0 .

The formalism behind this is to write:

$$\log[\lambda(a, c)] = \tilde{f}(a) + \tilde{h}(c) = (f(a) + \mu) + (h(c) - \mu)$$

and by choosing $\mu = h(c_0)$ we get the desired functions as:

$$\tilde{f}(a) = f(a) - h(c_0) \quad \tilde{h}(c) = h(c) - h(c_0)$$

which indeed has the property that $\tilde{f}(a) + \tilde{h}(c) = f(a) + h(c)$ and $\tilde{h}(c_0) = 0$. In practise this can be implemented by choosing the parametrization of the model carefully. In the case of a factor model for the effect of cohort, this is known as choosing the reference cohort to be c_0 . This is a standard procedure when fitting linear models, but it is rarely recognized as the solution to an identifiability problem.

A similar machinery can be invoked to explicitly move the three unidentifiabilities in an age-period-cohort model around between f , g and h by choosing μ_a , μ_c and δ so that the resulting functions, $\tilde{f}(a)$, $\tilde{g}(p)$ and $\tilde{h}(c)$ meet some desired constraints:

$$\begin{aligned} \log[\lambda(a, p)] = \tilde{f}(a) + \tilde{g}(p) + \tilde{h}(c) = & f(a) - \mu_a && - \gamma a + \\ & g(p) + \mu_a + \mu_c + \gamma p + \\ & h(c) && - \mu_c - \gamma c \end{aligned}$$

In the age-period-cohort model with three terms and where only the *second* derivatives of the effects are identifiable, two levels and one value of the *first* derivative must be fixed. This is frequently done by fixing one value on the cohort scale to be 0 and two points on the period scale to be 0, thereby fixing the overall slope of the period parameters, but a less technical principle for the choice of parametrization is desirable.

A principle for parametrization

Any parametrization of the age-period-cohort model fixes two levels and a slope among the three functions, but different principles can be invoked to accomplish this.

One principle for choice of parametrization is based on an extension of the assumptions behind way the age-cohort model was parametrised:

1. The age-function should be interpretable as log age-specific rates in 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).

Alternatively, the period function could be constrained to be 0 at a reference date, p_0 . In this case the age-effects at $a_0 = p_0 - c_0$ would equal the fitted rate for period p_0 (and cohort c_0), and the period effects would be residual log-RRs relative to p_0 .

The first choice fixes one constant (0 at c_0), and the third fixes a level (0 on average or 0 at p_0) and a slope (0 slope for the period function). The inclusion of the slope (drift) with the cohort effect makes the age-effects interpretable as cohort-specific rates of disease (longitudinal rates). Depending on the subject matter, the role of cohort and period could be interchanged, in which case the age-effects would be cross-sectional rates for the reference period.

In practise this can be implemented as follows. Suppose functions \hat{f} , \hat{g} and \hat{h} have been estimated from data. Then we fix a reference cohort c_0 , and extract the linear part from \hat{g} , for example by regressing the values of $\hat{g}(p)$ on p :

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

where μ is chosen to make $\tilde{g}(p)$ equal to 0 on average. The log-rates can then be expressed in three new terms:

$$\log[\lambda(a, p)] = \tilde{f}(a) + \tilde{g}(p) + \tilde{h}(c)$$

where

$$\begin{aligned} \tilde{f}(a) &= \hat{f}(a) + \mu + \beta a + \hat{h}(c_0) + \beta c_0 \\ \tilde{g}(p) &= \hat{g}(p) - \mu - \beta p \\ \tilde{h}(c) &= \hat{h}(c) + \beta c - \hat{h}(c_0) - \beta c_0 \end{aligned}$$

The functions $\tilde{f}(a)$, $\tilde{g}(p)$ and $\tilde{h}(c)$ defined this way fulfils the requirements above. If we prefer to fix the the period function to 0 at a given date p_0 , we just use $\mu = \hat{g}(p_0) - \beta p_0$, instead of using the estimated μ from the regression.

Note that in the derivation above, we have used no assumptions about the algorithm used to extract the linear trends. It was only assumed that it was possible to de-trend g and h in some way.

Explicit drift parameter

A variant of the above approach is to extract the drift entirely and report it as a separate parameter and then report both cohort and period effects as “residuals”. This would correspond to the partitioning of the model into terms:

$$\begin{aligned}\log(\lambda(a, p)) &= \tilde{f}_c(a) + \delta(c - c_0) + \tilde{g}(p) + \tilde{h}(c) \\ &= \tilde{f}_p(a) + \delta(p - p_0) + \tilde{g}(p) + \tilde{h}(c)\end{aligned}$$

where $\tilde{g}(p)$ and $\tilde{h}(c)$ are “de-trended”, i.e have 0 slope. $\tilde{f}_c(a)$ are the age-specific rates in the reference cohort c_0 and $\tilde{f}_p(a)$ the age-specific rates in the reference period p_0 . Thus age-specific rates can be chosen to refer refer to either a specific cohort (longitudinal rates) or a specific period (cross-sectional rates). Note that $\tilde{f}_c(a) = \tilde{f}_p(a) + \delta(a - (p_0 - c_0))$, so if there is a positive drift ($\delta > 0$) the cohort (longitudinal) age-curve will be steeper than the period (cross-sectional) age curve.

Parametric models in practise

The parametrization outlined above can be implemented in practise as follows:

1. Set up model matrices for age, period and cohort, M_a , M_p and M_c , each including the intercept term. If a factor model is used these will have columns of indicators of levels, if a spline model is used the matrices will be columns of base vectors for the splines.
2. Extract the linear trend from M_p and M_c , by projecting their columns onto the orthogonal complement of $[1|p]$ and $[1|c]$, respectively. The resulting matrices \tilde{M}_p and \tilde{M}_c have two fewer columns than the original M_p and M_c .
3. Center the cohort effect around c_0 : First take a row from \tilde{M}_c corresponding to c_0 . Form a matrix of the same dimension as \tilde{M}_c with all rows equal to this, and subtract it from \tilde{M}_c to form \tilde{M}_{c_0} .
4. The parametrization above can now be obtained by using the M_a for the age-effects, \tilde{M}_p for the period effects and $[c - c_0|\tilde{M}_{c_0}]$ for the cohort effects. Note that since the intercept is assumed to be included in M_a , the age-effects are automatically adjusted for the centering of the cohort-effect around c_0 , so they represent log-rates for the cohort c_0

5. Suppose the subsets of the estimated parameter vector corresponding to M_a , \tilde{M}_p and $[c - c_0 | \tilde{M}_{c_0}]$ are $\hat{\beta}_a$, $\hat{\beta}_p$ and $\hat{\beta}_c$. The value of $\hat{f}(a)$ at the a s actually present in the dataset is $M_a \hat{\beta}_a$, and similarly for the other two effects. The variance of it is found by $M_a^T \hat{\Sigma}_a M_a$, where $\hat{\Sigma}_a$ is the variance-covariance matrix of $\hat{\beta}_a$.

It is clear from the above that it will be convenient to have tools that can generate model matrices for the type of model used, as well as facilities for matrix operations.

7 Fitting models sequentially

It is possible to obtain an approximation to the parametrization outlined above using a small trick: First fit the age-cohort model. By omitting an explicit intercept and choosing a suitable reference for the cohort, the age-effect will be log-rates for the reference cohort and the cohort effect will be log RRs relative to this. $\hat{f}(a)$ and $\hat{h}(c)$ are then used as age and cohort effects.

The log of the fitted values from this model is then used as offset variable in a model with period-effect:

$$\log[\lambda(a, p)] = [\hat{f}(a) + \hat{h}(c)] + g(p)$$

The period effects from this model (also omitting an explicit intercept) are then used as the residual log RRs by period.

The estimates obtained by this sequential procedure are not the ML-estimates from the age-period-cohort model, they are marginal age-cohort estimates and period estimates *conditional* on the estimates from the age-cohort model, but in practise they will be very similar to the ML-estimates.

Usually the estimates from this approach will be close to the ML estimates, and the advantage is that the parametrization is very simple, no special manipulations are required to reparametrize and obtain standard errors. There are obvious extensions of this trick: First fit the age-drift model, and then sequentially cohort and period as “residual” effects.

A variant of this procedure has been used by some authors as a way of fixing the age-effects to obtain identifiability [1]. The procedure has been implemented in the function `apc.fit` in the `Epi` package for **R** too.

8 Graphical display of effects

For any chosen constraints there will be three functions, $f(a)$, $g(p)$ and $h(c)$ which sum to the log-rates. These effects should be shown in one figure, with same equidistance for the horizontal scale for age, period and cohort. Also the relative extent for the rate-scale for age-effects and relative risk scale for period and cohort effects should be the same. This will put all three effects on a directly comparable scale and allow the slopes of the effects to be compared.

The figure must have the horizontal scale divided in two; one for age and one for cohort / period; the latter two will often cover overlapping calendar periods. The

vertical scale will be a rate scale for the age-effect and a relative risk scale for the period and cohort effects. If a reference cohort or period is chosen a dot should be placed at $(c_0, 1)$ or at $(p_0, 1)$ to indicate this.

This is shown in figure 4 for the Danish testis cancer data.

9 Application of natural splines to Danish testis cancer data.

The ideas in this paper are implemented in the `Epi` package in **R**. The classical displays shown in figure 1 were produced with the function `rateplot`.

Testis cancer cases in Denmark 1943–96 were tabulated in 1-year classes by age, period and cohort. Population figures in 1-year age-classes at 1 January each year was obtained from Statistics Denmark. The risk rime was computed as outlined in section 3. The analysis is restricted to the age-classes 15–64 years.

The age-period-cohort model was fitted with `apc.fit`, which allows various models (linear splines, cubic splines, factors) and parametrizations to be used. The displays in figures 4–7 shows a model where natural splines with 15 parameters for each of the effects were used, these were plotted with the functions `apc.frame` and `apc.lines`.

From the curves it is clear that there is a “dip” in rates for the birth cohorts born during the first and second world war. Such a dip is a second order feature of the curve and is therefore not an artifact of the parametrization. These two dips in the cohort effects are brought out clearly by a combination of the detailed tabulation of data, and the detailed parametrization of the cohort effect. Modelling the effects with fewer parameters would overlook the dip around the first world war.

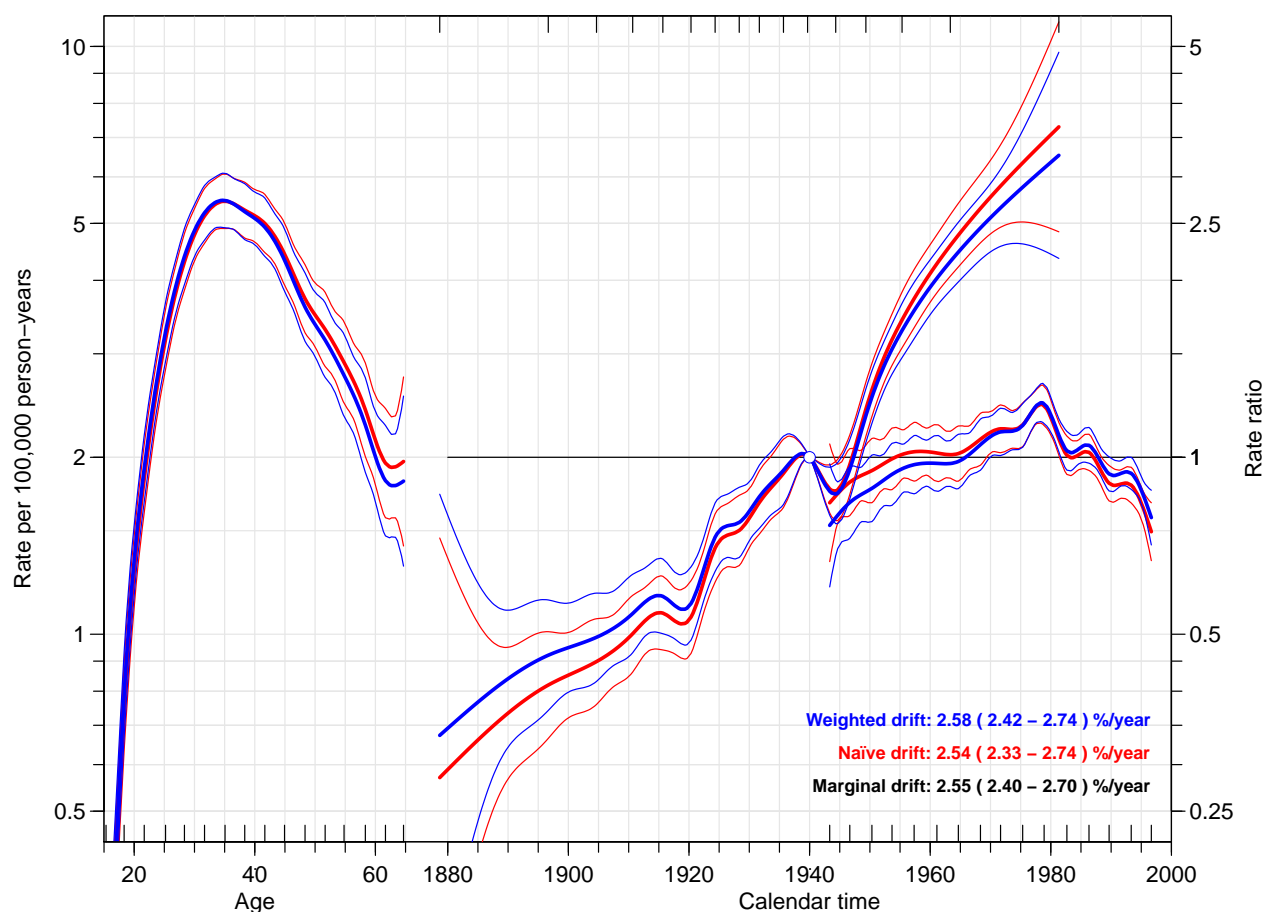


Figure 4: The estimated effects using the weighted and the naïve approach to extracting the drift. For both approaches the drift is included with the cohort effect. The fit to the data is the same. The marginal drift is the drift estimate from the age-drift model. The inside tickmarks at the bottom and top indicate the placement of the knots for the natural splines.

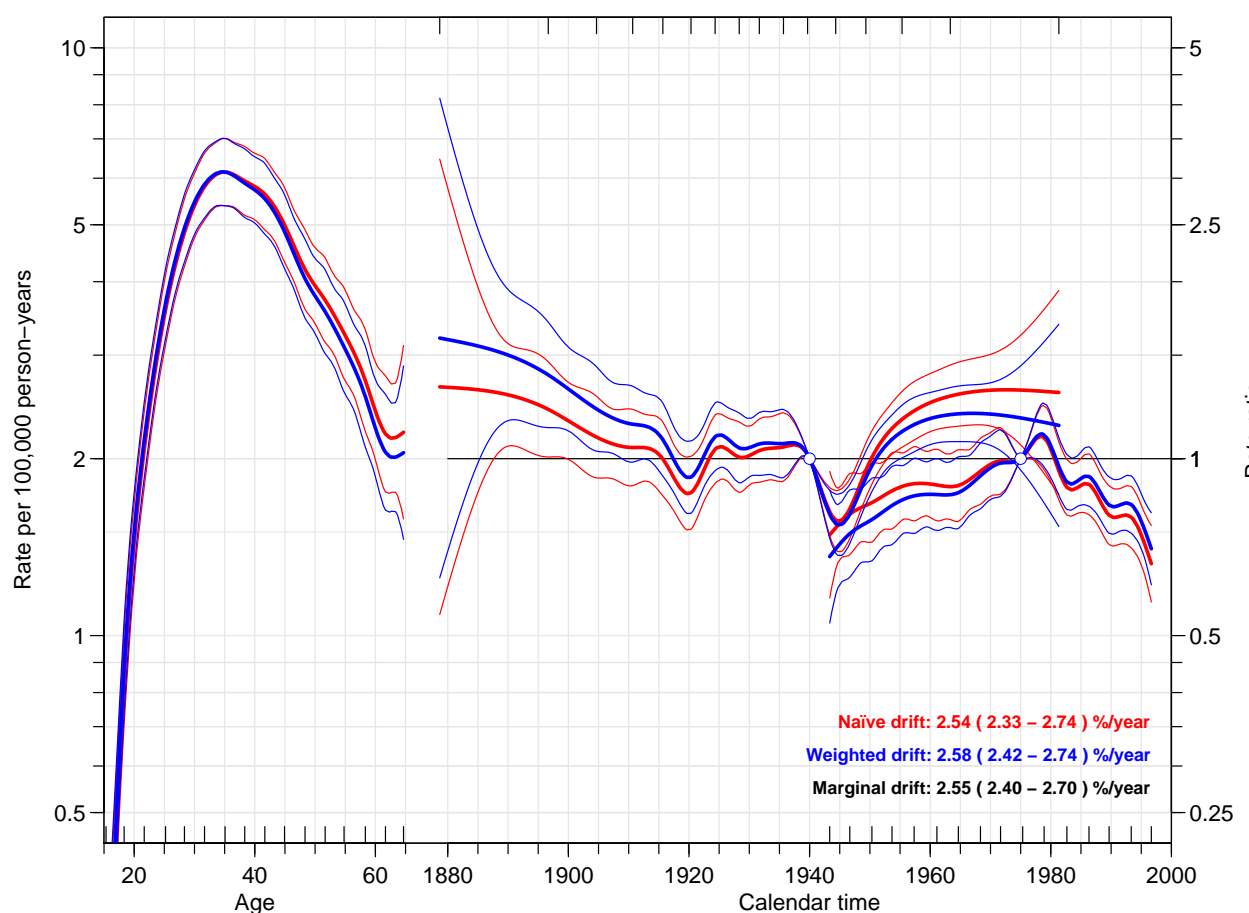


Figure 5: *The estimated effects using the weighted and the naive approach to extracting the drift. The age-effect refers to the 1940 cohort and the 1975 period. The fit to the data is the same, but to reconstruct the rates the estimates shown in the curves must be multiplied by the drift term $(c - c_0) \times \delta = (c - 1940) \times \delta$.*

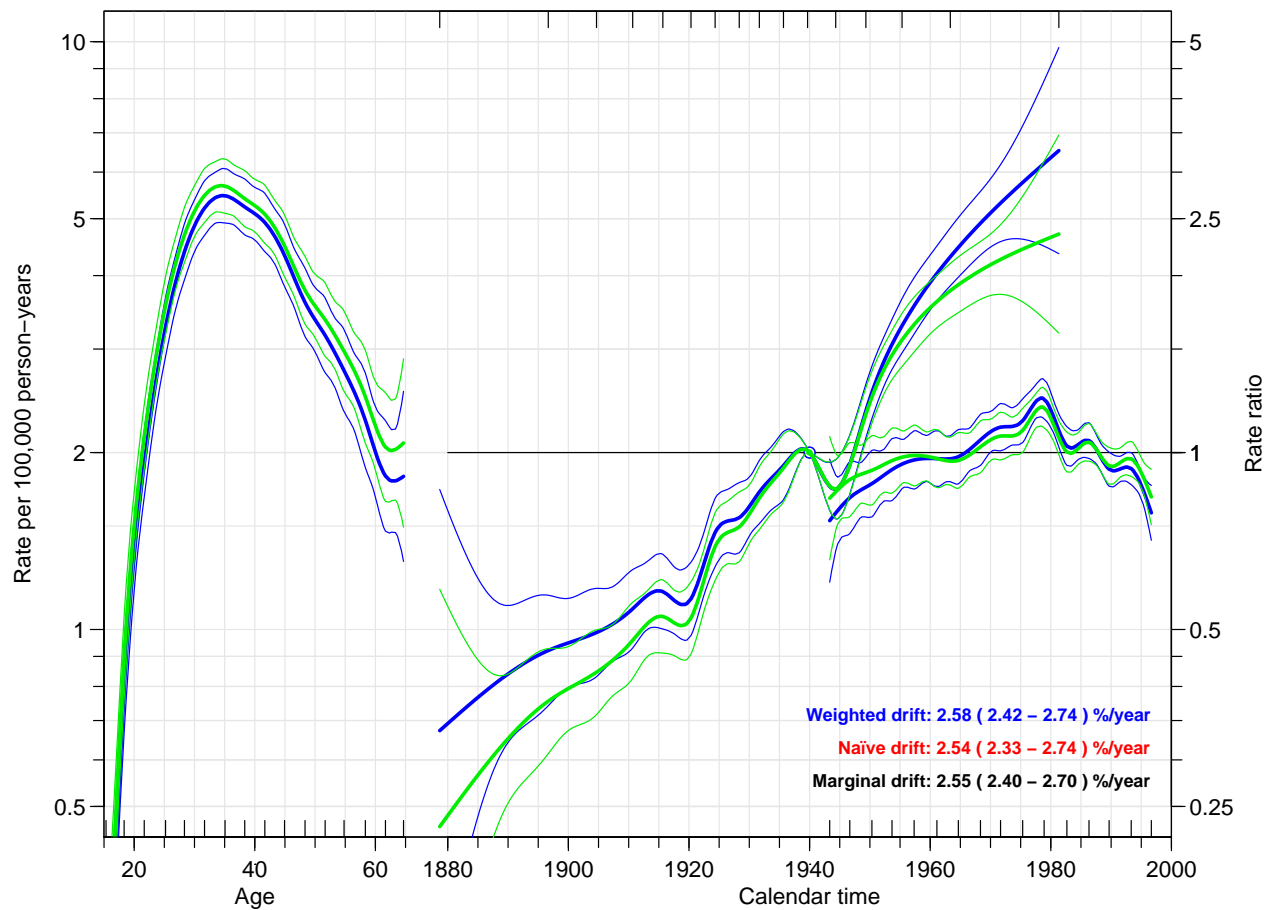


Figure 6: *The estimated effects using the weighted approach to extracting the drift, contrasted with the sequential approach by first fitting the age-cohort model and the the period model to the residuals. The age-effect refers to the 1940 cohort. The fit to the data is the not same for the two sets of estimates.*

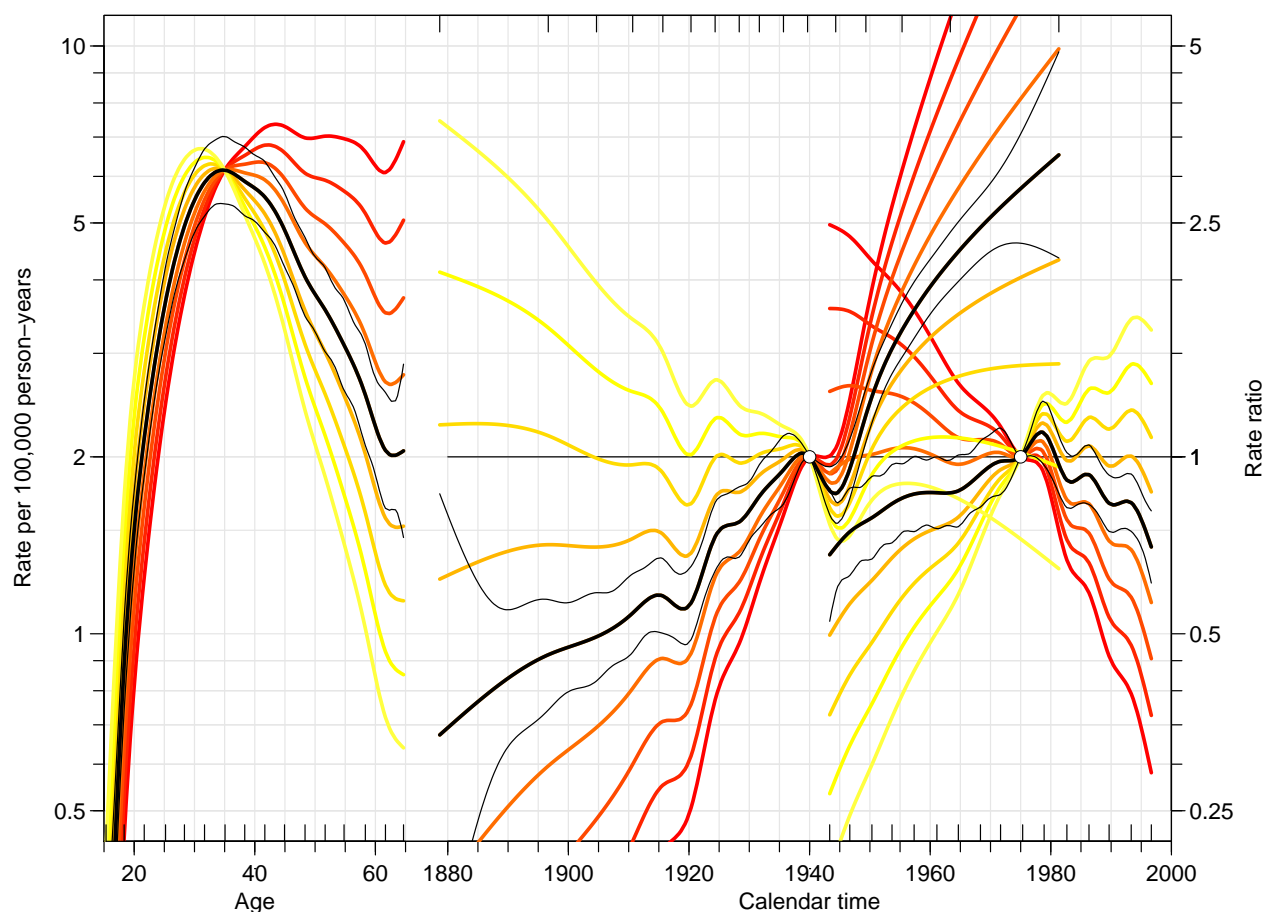


Figure 7: *The estimated effects using the weighted approach to extracting the drift (black) and allocating it with the cohort, and using the 1940 cohort and 1975 period as references. Curves with added annual period drifts of $-4, -3, \dots, 4\%$ are shown as well. The rates predicted from curves of like colours are the same. A film-like version can be found at www.biostat.ku.dk/~bxc/APC/Testis-film.pdf.*

10 Discussion

Age-period-cohort models are descriptive tools for rates observed in a Lexis diagram. Proper analysis of rates should use the maximally available information. Therefore tabulation in very coarse groups of age, period and cohort should be avoided. Whenever possible tabulation by all three variables should be done.

In the epidemiological literature overly coarse tabulation of data is abundant, where for example rates of childhood diabetes (ages 0-14 years) is commonly modelled using three 5-year age classes [6, 10, 11, 2]!

At least for countries in western Europe, data on population size in 1-year age-classes will usually be available. The United States of America seems in general to maintain a higher level of ignorance about the population structure. The tabulation of data should be by age, period *and* cohort in as small intervals as possible.

Large parts of the literature on the age-period-cohort models is difficult to read because of overly complicated notation, e.g. use of indexing of age, period and cohort groups by i , j and k running from 1 to I , J and K , giving rise complicated indexing formulae, involving the total number of categories that are otherwise only relevant when specifying computer code. It seems more straightforward to use mnemonics like a , p and c and letting the indices be the mean of these continuous variable in each cell of the tabulation, even if takes much of the magic out of the subject.

Effectively only the factor model induced by the tabulation of data have been used in age-period-cohort modelling and it is also largely the only one addressed in the theoretical papers. Therefore the parametrization problems have only been addressed within the framework of the factor model. This has lead to a plethora of suggestions for parametrizations with little view to the principal aspects of the subject matter, see e.g. [13].

The modelling tools available for age-period-cohort modelling have by and large been Poisson-modelling by programs that produce a standard parametrization of factors such as `proc genmod` from SAS or the `glm` command from Stata. In many papers the authors have shied away from graphical reporting of the estimates [6, 8, 10]. This may be an indication of the technical problems associated with transforming the default parametrization from the statistical packages to a useful parametrization. Particularly the derivation of standard errors of estimates can be a complicated task with mid-20th century software as Stata and SAS.

In this paper I reiterated the basic fact for the parametrization of the age-period-cohort model: Arbitrary decisions on the allocation of two absolute levels and one drift must be taken in order to report the estimated effects. Arbitrary in this context means unrelated to the model, impossible to derive from data or design. Choice of parametrization should of course not be unrelated to the subject matter.

Since the substance is description of disease rates in populations over time, the major variable is age. Therefore the reporting of the models should be based on age-specific rates. It is impossible to give universal guidelines as to whether they should be reported as cohort-rates (longitudinal) in which case the drift should be included with the cohort-effect, or as period-rates (cross-sectional) in which case the drift should be included with the period effect.

Recommendations

In summary, the following steps should be taken when describing rates based on observations from a Lexis diagram:

0. Do *not* take the table of cases and person-years for granted.
1. Tabulate cases and person-years as detailed as possible, preferably by age, period and cohort.
2. Compute risk time correctly from population data.
3. Use the mean age, period and cohort in each cell of the table as continuous covariates. $p = c + a$ must be met for all analysis units.
4. Use parametric functions to describe the effects. Choose the parametrization (allocation of knots etc.) carefully, so that relevant features can be captured, but modelling of random noise is avoided.
5. Report estimates of three effects that can be combined to the predicted rates.
6. Age should be the primary variable, report age-specific rates, i.e. include the absolute level with the age-parameters.
7. Make an informed choice of the other aspects of parametrization, and state it clearly. This will include:
 - (a) How is the drift extracted.
 - (b) Where is the drift allocated.
 - (c) How are the RRs for period and cohort fixed.
 - (d) What is the interpretation of the age-specific rates.
8. Report estimates as line-graphs with confidence limits.
9. Report the size of the drift, both the extracted value from the age-period-cohort model, but also the unadjusted value from a simple age-drift model.
10. Be careful with firm interpretation of formal tests for period and cohort effects — significant effects may represent clinically irrelevant effects.
11. Do not report goodness of fit tests — they are meaningless.

The possible options for parametrization of the model are summarized in table 2.

The options for model fitting, parametrization and graphical reporting mentioned above are all implemented in the **R**-package `Epi`, in functions `apc.fit`, `apc.frame` and `apc.lines`. The package is available through CRAN (The Comprehensive R Archive Network, <http://cran.r-project.org>) or at the package home page <http://www.biostat.ku.dk/~bxc/Epi>.

Table 2: *Parametrizations for the age-period-cohort model. Two steps are needed: Fixing the drift parameter, and fixing the reference values.*

Drift extraction:	1: Orthogonal projection	a: All units the same weight b: Weight equal to observed information (D)
	2: Equation of two points on period and cohort scales	
Interpretation of effects:		
Age	Period	Cohort
Longitudinal rates for cohort c_0	Residual RR	RR relative to cohort c_0
Cross-sectional rates for period p_0	RR relative to period p_0	Residual RR
Longitudinal rates for cohort c_0 . Fitted rates at $a_0 = p_0 - c_0$.	Residual RR relative to p_0 .	RR relative to cohort c_0 .
Cross-sectional rates for period p_0 Fitted rates at $a_0 = p_0 - c_0$.	RR relative to period p_0 .	Residual RR relative to c_0 .

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11 Appendix

Practicalities

In order to get an estimate of the extracted drift with confidence intervals a function is needed that from a set of say P columns of the model matrix produce a set of $P - 2$ columns orthogonal to the constant and the drift w.r.t. some defined inner product.

So let \mathbf{M} be a $n \times P$ model matrix, and define the relevant inner product between two columns as:

$$\langle \mathbf{m}_j | \mathbf{m}_k \rangle = \sum_i m_{ij} w_i m_{ik}$$

where one typically would use either $w_i = 1$ or $w_i = D_i$, the total number of cases observed in unit i of the dataset. The task is then to produce a basis for the projection of the columns of \mathbf{M} on the orthogonal complement to the two column matrix of the constant and the drift, $[1|p]$ (or $[1|c]$ for the cohort effect).

Projections in matrix formulation

The projection of a vector \mathbf{v} on the column space of the matrix \mathbf{X} with respect to the usual inner product, is $\mathbf{P}\mathbf{v}$ where:

$$\mathbf{P} = \mathbf{X}(\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top$$

and the projection on the orthogonal complement is $(\mathbf{I} - \mathbf{P})\mathbf{v}$.

For a general inner product:

$$\langle \mathbf{x} | \mathbf{y} \rangle = \sum_i x_i w_i y_i = \mathbf{x}^\top \mathbf{W} \mathbf{y}$$

with $\mathbf{W} = \text{diag}(w_i)$, the projection matrix on the column space of \mathbf{X} w.r.t. this inner product is:

$$\mathbf{P}_\mathbf{W} = \mathbf{X}(\mathbf{X}^\top \mathbf{W} \mathbf{X})^{-1} \mathbf{X}^\top \mathbf{W}$$

and the projection on the orthogonal complement is $(\mathbf{I} - \mathbf{P}_\mathbf{W})\mathbf{v}$.

Implementation in R

In the parametrization of the linear trend from the cohort and period effects we use **R** functions (`ns`, `bs`, ...) to generate model matrices using e.g. natural splines. Let this be \mathbf{M} .

Then we project the columns of \mathbf{M} on the orthogonal complement of $[1|p]$ w.r.t. a weighted inner product. This is done using the function `proj.ip` (\mathbf{X} is here playing the role of $[1|p]$):

```
proj.ip <-
function( X, M, orth = FALSE, weight=rep(1,nrow(X)) )
{
  Pp <- solve( crossprod( X * sqrt(weight) ), t( X * weight ) ) %*% M
```

```

    PM <- X %*% Pp
    if (orth) PM <- M - PM
    else PM
}

```

When using tabulation of data in very small intervals the resulting datasets can be quite large; for example the example dataset with testis cancer in ages 15–65 for the period 1943–97 has 50 age classes and 54 periods, i.e. $50 \times 54 \times 2 = 5400$ observations for triangles in the Lexis diagram. Therefore the multiplication \mathbf{XW} is done by multiplying with the *vector* \mathbf{w} (**weight**), using the **R**-feature of recycling and the column-major storage of matrices. If it had been coded `X %*% diag(weight)`, it would require a square matrix of dimension n (the number of units), which is very large ($5400^2 = 2,916,000$ entries). By the same token, the projection matrix $\mathbf{X}(\mathbf{X}^T\mathbf{W}\mathbf{X})^{-1}\mathbf{X}^T\mathbf{W}$ is not computed as it would also have this huge dimension. Instead the last part of the matrix with projected columns, $(\mathbf{X}^T\mathbf{W}\mathbf{X})^{-1}\mathbf{X}^T\mathbf{W}\mathbf{M}$ of dimension $p \times p$ is computed first and then multiplied by \mathbf{X} afterwards to produce the $n \times p$ matrix of projected columns.

The resulting matrix has the same number of columns as \mathbf{M} , so in order to avoid problems with parametrizations, it is shaved down to full rank using `Thin.col`:

```

Thin.col <-
function (X, tol = 1e-06)
{
    QR <- qr(X, tol = tol, LAPACK = FALSE)
    X[, QR$pivot[seq(length = QR$rank)], drop = FALSE]
}

```

These two functions are then used in combination to construct the function **detrend** that de-trends the model matrix \mathbf{M} :

```

detrend <-
function( M, t, weight=rep(1,nrow(M)) )
{
    Thin.col( proj.ip( cbind( 1, t ), M, orth = TRUE, weight = weight ) )
}

```

Thus we can find the projection of the model matrix onto the orthogonal of the constant and the period drift, $[1|p]$, by simply `detrend(M, p)`, and it will give the right parametrization for any kind of choice of \mathbf{M} .

Fixing the reference

To get the cohort effect fixed at c_0 , a row of the model matrix for cohort corresponding to c_0 is generated. This value need not be a value actually present in data. When projecting the cohort part of the model matrix on the orthogonal complement of $[1|c]$ the projected (i.e. de-trended value) for the c_0 -row can be obtained by amending the model matrix by this row and projecting on the orthogonal complement of $[1|c]$ with respect to an inner product which has weight 0 in the first position. The resulting row is

then duplicated to form a matrix of the same size as the model matrix and subtracted from the model matrix. Inside `apc.fit`, the relevant piece of code is:

```
xC <- detrend( rbind( Rc, MC ), c(c0,C), weight=c(0,wt) )
Mcr <- xC[-1,] - ref.c * xC[rep(1,nrow(MC)),]
```

where `MC` is the cohort-model matrix, and `Rc` the row corresponding to c_0 .

Putting it together

In order to obtain parameters corresponding to log-rates by age, a model matrix representing age, including the intercept must be in the model. These will represent log age-specific rates for cohort c_0 if the variable $c - c_0$ is put in the model. If the column $c - c_0$ is merged with the de-trended and c_0 -centered cohort effect model matrix, this will represent the log-RR relative to cohort c_0 . Finally the de-trended period matrix will represent the residual log-RR by period.

12 R-functions

The following sections document the **R**-functions for fitting and reporting age-period-cohort models that are available in the **Epi**-package.

<code>rateplot</code>	<i>Functions to plot rates from a table classified by age and calendar time (period)</i>
-----------------------	--

Description

Produces plots of rates versus age, connected within period or cohort (`Aplot`), rates versus period connected within age-groups (`Pplot`) and rates and rates versus date of birth cohort (`Cplot`). `rateplot` is a wrapper for these, allowing to produce the four classical displays with a single call.

Usage

```
rateplot( rates,
  which = c("ap","ac","pa","ca"),
  age = as.numeric( dimnames( rates )[[1]] ),
  per = as.numeric( dimnames( rates )[[2]] ),
  grid = FALSE,
  a.grid = grid,
  p.grid = grid,
  c.grid = grid,
  ygrid = grid,
  col.grid = gray( 0.9 ),
  a.lim = range( age, na.rm=TRUE ) + c(0,diff( range( age ) )/30),
  p.lim = range( per, na.rm=TRUE ) + c(0,diff( range( age ) )/30),
  c.lim = NULL,
  ylim = range( rates[rates>0] ),
  at = NULL,
```

```

labels = paste( at ),
a.lab = "Age at diagnosis",
p.lab = "Date of diagnosis",
c.lab = "Date of birth",
ylab = "Rates",
type = "l",
lwd = 2,
lty = 1,
log.ax = "y",
las = 1,
ann = FALSE,
a.ann = ann,
p.ann = ann,
c.ann = ann,
xannx = 1/20,
cex.ann = 0.8,
a.thin = seq( 1, length( age ), 2 ),
p.thin = seq( 1, length( per ), 2 ),
c.thin = seq( 2, length( age ) + length( per ) - 1, 2 ),
col = par( "fg" ),
a.col = col,
p.col = col,
c.col = col,
... )

Aplot( rates, age = as.numeric( dimnames( rates )[[1]] ),
per = as.numeric( dimnames( rates )[[2]] ), grid = FALSE,
a.grid = grid, ygrid = grid, col.grid = gray( 0.9 ),
a.lim = range( age, na.rm=TRUE ), ylim = range( rates ),
at = NULL, labels = paste( at ), a.lab = names( dimnames( rates ) )[[1]],
ylab = deparse( substitute( rates ) ), type = "l", lwd = 2, lty = 1,
col = par( "fg" ), log.ax = "y", las = 1, c.col = col, p.col = col,
c.ann = FALSE, p.ann = FALSE, xannx = 1/20, cex.ann = 0.8,
c.thin = seq( 2, length( age ) + length( per ) - 1, 2 ),
p.thin = seq( 1, length( per ), 2 ), p.lines = TRUE,
c.lines = !p.lines, ... )

Pplot( rates, age = as.numeric( dimnames( rates )[[1]] ),
per = as.numeric( dimnames( rates )[[2]] ), grid = FALSE,
p.grid = grid, ygrid = grid, col.grid = gray( 0.9 ),
p.lim = range( per, na.rm=TRUE ) + c(0,diff(range(per))/30),
ylim = range( rates, na.rm=TRUE ), p.lab = names( dimnames( rates ) )[[2]],
ylab = deparse( substitute( rates ) ), at = NULL, labels = paste( at ),
type = "l", lwd = 2, lty = 1, col = par( "fg" ), log.ax = "y",
las = 1, ann = FALSE, cex.ann = 0.8, xannx = 1/20,
a.thin = seq( 1, length( age ), 2 ), ... )

Cplot( rates, age = as.numeric( rownames( rates ) ),
per = as.numeric( colnames( rates ) ), grid = FALSE,
c.grid = grid, ygrid = grid, col.grid = gray( 0.9 ),
c.lim = NULL, ylim = range( rates, na.rm=TRUE ),
at = NULL, labels = paste( at ), c.lab = names( dimnames( rates ) )[[2]],
ylab = deparse( substitute( rates ) ), type = "l", lwd = 2, lty = 1,
col = par( "fg" ), log.ax = "y", las = 1, xannx = 1/20, ann = FALSE,

```



```
cex.ann = 0.8, a.thin = seq( 1, length( age ), 2 ), ... )
```

Arguments

rates	A two-dimensional table (or array) with rates to be plotted. It is assumed that the first dimension is age and the second is period.
which	A character vector with elements from <code>c("ap", "ac", "apc", "pa", "ca")</code> , indication which plots should be produced. One plot per element is produced. The first letter indicates the x-axis of the plot, the remaining which groups should be connected, i.e. "pa" will plot rates versus period and connect age-classes, and "apc" will plot rates versus age, and connect both periods and cohorts.
age	Numerical vector giving the means of the age-classes. Defaults to the rownames of rates as numeric.
per	Numerical vector giving the means of the periods. Defaults to the columnnames of rates as numeric.
grid	Logical indicating whether a background grid should be drawn.
a.grid	Logical indicating whether a background grid on the age-axis should be drawn. If numerical it indicates the age-coordinates of the grid.
p.grid	do. for the period.
c.grid	do. for the cohort.
ygrid	do. for the rate-dimension.
col.grid	The colour of the grid.
a.lim	Range for the age-axis.
p.lim	Range for the period-axis.
c.lim	Range for the cohort-axis.
ylim	Range for the y-axis (rates).
at	Position of labels on the y-axis (rates).
labels	Labels to put on the y-axis (rates).
a.lab	Text on the age-axis. Defaults to "Age".
p.lab	Text on the period-axis. Defaults to "Date of diagnosis".
c.lab	Text on the cohort-axis. Defaults to "Date of birth".
ylab	Text on the rate-axis. Defaults to the name of the rate-table.
type	How should the curves be plotted. Defaults to "l".
lwd	Width of the lines. Defaults to 2.
lty	Which type of lines should be used. Defaults to 1, a solid line.
log.ax	Character with letters from "apcyr", indicating which axes should be logarithmic. "y" and "r" both refer to the rate scale. Defaults to "y".
las	see par .
ann	Should the curves be annotated?
a.ann	Logical indicating whether age-curves should be annotated.
p.ann	do. for period-curves.
c.ann	do. for cohort-curves.

<code>xannx</code>	The fraction that the x-axis is expanded when curves are annotated.
<code>cex.ann</code>	Expansion factor for characters annotating curves.
<code>a.thin</code>	Vector of integers indicating which of the age-classes should be labelled.
<code>p.thin</code>	do. for the periods.
<code>c.thin</code>	do. for the cohorts.
<code>col</code>	Colours for the curves.
<code>a.col</code>	Colours for the age-curves.
<code>p.col</code>	do. for the period-curves.
<code>c.col</code>	do. for the cohort-curves.
<code>p.lines</code>	Should rates from the same period be connected?
<code>c.lines</code>	Should rates from the same cohort be connected?
<code>...</code>	Additional arguments passed on to <code>matlines</code> when plotting the curves.

Details

Zero values of the rates are ignored. They are neither in the plot nor in the calculation of the axis ranges.

Value

NULL. The function is used for its side-effect, the plot.

Author(s)

Bendix Carstensen, Steno Diabetes Center, <http://www.pubhealth.ku.dk/~bxc/>

See Also

[apc.frame](#)

Examples

```
data( blcaIT )
attach(blcaIT)

# Table of rates:
bl.rate <- tapply( D, list(age,period), sum ) /
               tapply( Y, list(age,period), sum )
bl.rate

# The four classical plots:
par( mfrow=c(2,2) )
rateplot( bl.rate*10^6 )

# The labels on the vertical axis could be nicer:
rateplot( bl.rate*10^6, at=10^(-1:3), labels=c(0.1,1,10,100,1000) )

# More bells and whistles
par( mfrow=c(1,3), mar=c(3,3,1,1), oma=c(0,3,0,0), mgp=c(3,1,0)/1.6 )
rateplot( bl.rate*10^6, ylab="", ann=TRUE, which=c("AC","PA","CA"),
          at=10^(-1:3), labels=c(0.1,1,10,100,1000),
          col=topo.colors(11), cex.ann=1.2 )
```

`apc.fit`*Fit an Age-Period-Cohort model to tabular data.*

Description

Fits the classical five models to tabulated rate data (cases, person-years) classified by age and period: Age, Age-drift, Age-Period, Age-Cohort and Age-period.

Usage

```
apc.fit( data,
          A,
          P,
          D,
          Y,
          ref.c,
          ref.p,
          model = c("ns", "bs", "ls", "factor"),
          dr.extr = c("weighted", "Holford"),
          parm = c("ACP", "APC", "AdCP", "AdPC", "Ad-P-C", "Ad-C-P", "AC-P", "AP-C"),
          npar = c( A=5, P=5, C=5 ),
          scale = 1,
          alpha = 0.05,
          print.AOV = TRUE )
```

Arguments

<code>data</code>	Data frame with (at least) variables, A (age), P (period), D (cases, deaths) and Y (person-years). Cohort (date of birth) is computed as $P-A$.
<code>A</code>	Age; numerical vector with mean age at diagnosis for each unit.
<code>P</code>	Period; numerical vector with mean date of diagnosis for each unit.
<code>D</code>	Cases, deaths; numerical vector.
<code>Y</code>	Person-years; numerical vector.
<code>ref.c</code>	Reference cohort, numerical. Defaults to median date of birth among cases. If used with <code>parm="AdCP"</code> or <code>parm="AdPC"</code> , the residual cohort effects will be 1 at <code>ref.c</code>
<code>ref.p</code>	reference period, numerical. Defaults to median date of diagnosis among cases.
<code>model</code>	type of model fitted: <ul style="list-style-type: none"> • bs fits a model with B-splines for each of the terms, with <code>np</code> parameters for the terms. • ns fits a model with natural splines for each of the terms, with <code>np</code> parameters for the terms. • ls fits a model with linear splines. • factor fits a factor model with one parameter per value of A, P and C. <code>np</code> is ignored in this case.
<code>dr.extr</code>	How the drift parameter should be extracted from the age-period-cohort model. weighted (default) lets the weighted average (by marginal no. cases, D) of the estimated period and cohort effects have 0 slopw. Holford uses the naïve average over all values for the estimated effects, disregarding the no. cases.

parm	<p>The parametrization of the effects. The first four all refer to the ML-fit of the Age-Period-Cohort model, the last four give Age-effects from a smaller model and residuals relative to this. If one of the latter is chosen, drift is ignored. Possible values are:</p> <ul style="list-style-type: none"> • ACP: ML-estimates. Age-effects as rates for the reference cohort. Cohort effects as RR relative to the reference cohort. Period effects constrained to be 0 on average with 0 slope. • APC: ML-estimates. Age-effects as rates for the reference period. Period effects as RR relative to the reference period. Cohort effects constrained to be 0 on average with 0 slope. • AdCP: ML-estimates. Age-effects as rates for the reference cohort. Cohort and period effects constrained to be 0 on average with 0 slope. These effects do not multiply to the fitted rates, the drift is missing and needs to be included to produce the fitted values. • AdPC: ML-estimates. Age-effects as rates for the reference period. Cohort and period effects constrained to be 0 on average with 0 slope. These effects do not multiply to the fitted rates, the drift is missing and needs to be included to produce the fitted values. • Ad-CP: Age effects are rates for the reference cohort in the Age-drift model. Cohort effects are from the model with cohort alone, using log(fitted values) from the Age-drift model as offset. Period effects are from the model with period alone using log(fitted values) from the cohort model as offset. • Ad-PC: Age effects are rates for the reference cohort in the Age-drift model. Period effects are from the model with period alone, using log(fitted values) from the Age-drift model as offset. Cohort effects are from the model with cohort alone using log(fitted values) from the period model as offset. • AC-P: Age effects are rates for the reference cohort in the Age-Cohort model, cohort effects are RR relative to the reference cohort. Period effects are from the model with period alone, using log(fitted values) from the Age-Cohort model as offset. • AP-C: Age effects are rates for the reference period in the Age-Period model, period effects are RR relative to the reference period. Cohort effects are from the model with cohort alone, using log(fitted values) from the Age-Period model as offset.
npar	The number of parameters to use for each of the terms in the model. It can be a list of three numerical vectors, in which case these taken as the knots for the age, period and cohort effect, the first and last element in each vector are used as the boundary knots.
alpha	The significance level. Estimates are given with (1-alpha) confidence limits.
scale	numeric(1), factor multiplied to the rate estimates before output.
print.AOV	Should the analysis of deviance table for the models be printed?

Value

An object of class "apc" (recognized by [apc.lines](#)) — a list with components:

Age	Matrix with 4 colums: A.pt with the ages (equals <code>unique(A)</code>) and three columns giving the estimated rates with c.i.s.
Per	Matrix with 4 colums: P.pt with the dates of diagnosis (equals <code>unique(P)</code>) and three columns giving the estimated RRs with c.i.s.

Coh	Matrix with 4 colums: <code>C.pt</code> with the dates of birth (equals <code>unique(P-A)</code>) and three columns giving the estimated RRs with c.i.s.
Drift	A 3 column matrix with drift-estimates and c.i.s: The first row is the ML-estimate of the drift (as defined by <code>drift</code>), the second row is the estimate from the Age-drift model. For the sequential parametrizations, only the latter is given.
Ref	Numerical vector of length 2 with reference period and cohort. If <code>ref.p</code> or <code>ref.c</code> was not supplied the corresponding element is NA.
AOV	Analysis of deviance table comparing the five classical models.
Type	Character string explaining the model and the parametrization.
Knots	If <code>model</code> is one of "ns" or "bs", a list with three components: <code>Age</code> , <code>Per</code> , <code>Coh</code> , each one a vector of knots. The max and the min are the boundary knots.
Powers	If <code>model</code> is "fpol", a list with three components: <code>Age</code> , <code>Per</code> , <code>Coh</code> , each one a vector of the powers used in the fractional polynomials.

Author(s)

Bendix Carstensen, <http://www.pubhealth.ku.dk/~bxc>

See Also

[apc.frame](#), [apc.lines](#).

Examples

```
library( Epi )
data(lungDK)

# Taylor a dataframe that meets the requirements
exd <- lungDK[,c("Ax","Px","D","Y")]
names(exd)[1:2] <- c("A","P")

# Two different ways of parametrizing the APC-model, ML
ex.H <- apc.fit( exd, npar=7, model="ns", dr.extr="Holford", parm="ACP", scale=10^5 )
ex.W <- apc.fit( exd, npar=7, model="ns", dr.extr="weighted", parm="ACP", scale=10^5 )

# Sequential fit, first AC, then P given AC.
ex.S <- apc.fit( exd, npar=7, model="ns", parm="AC-P", scale=10^5 )

# Show the estimated drifts
ex.H[["Drift"]]
ex.W[["Drift"]]
ex.S[["Drift"]]

# First nice plot frame
par( mar=c(3,4,1,4), mgp=c(3,1,0)/1.5, las=1 )
sc <- apc.frame(a.lab = seq( 30, 90, 20 ),
               a.tic = seq( 30, 90, 10 ),
               cp.lab = seq( 1860, 2000, 20 ),
               cp.tic = seq( 1860, 2000, 10 ),
               r.lab = c(1,2,5,10,20,50)*10,
               r.tic = c(1:9*10, 1:5*100),
               rr.ref = 200,
```

```

gap = 22 )

# Reference lines
abline( v=ex.H[[5]][2]-sc[1] )
segments( 1860-sc[1], sc[2], 2000-sc[1], sc[2] )

# Fill in the estimated effects
apc.lines( ex.S, col="green", scale="rates", frame.par=sc, ci=TRUE )
apc.lines( ex.H, col="red", scale="rates", frame.par=sc, ci=TRUE )
apc.lines( ex.W, col="blue", scale="rates", frame.par=sc, ci=TRUE )

# Extract the drifts in % per year
rd <- formatC( (ex.W[["Drift"]][["A-d"],]-1)*100, format="f", digits=2 )
wd <- formatC( (ex.W[["Drift"]][["APC"],]-1)*100, format="f", digits=2 )
hd <- formatC( (ex.H[["Drift"]][["APC"],]-1)*100, format="f", digits=2 )

# Put them on the plot
text( 1999-sc[1], 11,
      paste( "Weighted drift:", wd[1], "(", wd[2], "-", wd[3], ") %/year" ),
      col="blue", adj=c(1,0), font=2, cex=0.8 )
text( 1999-sc[1], 11*1.2,
      paste( "Naïve drift:", hd[1], "(", hd[2], "-", hd[3], ") %/year" ),
      col="red", adj=c(1,0), font=2, cex=0.8 )
text( 1999-sc[1], 11*1.2^2,
      paste( "Raw drift:", rd[1], "(", rd[2], "-", rd[3], ") %/year" ),
      col="green", adj=c(1,0), font=2, cex=0.8 )

```

apc.frame

Produce an empty frame for display of parameter-estimates from Age-Period-Cohort-models.

Description

A plot is generated where both the age-scale and the cohort/period scale is on the x-axis. The left vertical axis will be a logarithmic rate scale referring to age-effects and the right a logarithmic rate-ratio scale of the same relative extent as the left referring to the cohort and period effects (rate ratios).

Only an empty plot frame is generated. Curves or points must be added with `points`, `lines` or the special utility function `apc.lines`.

Usage

```

apc.frame( a.lab,
           cp.lab,
           r.lab,
           rr.lab = r.lab / rr.ref,
           rr.ref = r.lab[length(r.lab)/2],
           a.tic = a.lab,
           cp.tic = cp.lab,
           r.tic = r.lab,
           rr.tic = r.tic / rr.ref,
           tic.fac = 1.3,

```

```

a.txt = "Age",
cp.txt = "Calendar time",
r.txt = "Rate per 100,000 person-years",
rr.txt = "Rate ratio",
gap = diff(range(c(a.lab, a.tic)))/3,
col.grid = gray(0.85),
sides = c(1,2,4) )

```

Arguments

<code>a.lab</code>	Numerical vector of labels for the age-axis.
<code>cp.lab</code>	Numerical vector of labels for the cohort-period axis.
<code>r.lab</code>	Numerical vector of labels for the rate-axis (left vertical)
<code>rr.lab</code>	Numerical vector of labels for the RR-axis (right vertical)
<code>rr.ref</code>	At what level of the rate scale is the RR=1 to be.
<code>a.tic</code>	Location of additional tick marks on the age-scale
<code>cp.tic</code>	Location of additional tick marks on the cohort-period-scale
<code>r.tic</code>	Location of additional tick marks on the rate-scale
<code>rr.tic</code>	Location of additional tick marks on the RR-axis.
<code>tic.fac</code>	Factor with which to diminish intermediate tick marks
<code>a.txt</code>	Text for the age-axis (left part of horizontal axis).
<code>cp.txt</code>	Text for the cohort/period axis (right part of horizontal axis).
<code>r.txt</code>	Text for the rate axis (left vertical axis).
<code>rr.txt</code>	Text for the rate-ratio axis (right vertical axis)
<code>gap</code>	Gap between the age-scale and the cohort-period scale
<code>col.grid</code>	Colour of the grid put in the plot.
<code>sides</code>	Numerical vector indicating on which sides axes should be drawn and annotated. This option is aimed for multi-panel displays where axes only are put on the outer plots.

Details

The function produces an empty plot frame for display of results from an age-period-cohort model, with age-specific rates in the left side of the frame and cohort and period rate-ratio parameters in the right side of the frame. There is a gap of `gap` between the age-axis and the calendar time axis, vertical grid lines at `c(a.lab,a.tic,cp.lab,cp.tic)`, and horizontal grid lines at `c(r.lab,r.tic)`.

The function returns a numerical vector of length 2, with names `c("cp.offset","RR.fac")`. The y-axis for the plot will be a rate scale for the age-effects, and the x-axis will be the age-scale. The cohort and period effects are plotted by subtracting the first element (named `"cp.offset"`) of the returned result from the cohort/period, and multiplying the rate-ratios by the second element of the returned result (named `"RR.fac"`).

Value

A numerical vector of length two, with names `c("cp.offset","RR.fac")`. The first is the offset for the cohort period-axis, the second the multiplication factor for the rate-ratio scale.

Side-effect: A plot with axes and grid lines but no points or curves.

Author(s)

Bendix Carstensen, Steno Diabetes Center, <http://www.pubhealth.ku.dk/~bxc/>

References

<http://www.pubhealth.ku.dk/~bxc/APC/notes.pdf>

See Also

[apc.lines](#), [apc.lines](#)

Examples

```
par( mar=c(4,4,1,4) )
res <-
apc.frame( a.lab=seq(30,90,20), cp.lab=seq(1880,2000,30), r.lab=c(1,2,5,10,20,50),
           a.tic=seq(30,90,10), cp.tic=seq(1880,2000,10), r.tic=c(1:10,1:5*10),
           gap=27 )

res
# What are the axes actually?
par(c("usr","xlog","ylog"))
# How to plot in the age-part: a point at (50,10)
points( 50, 10, pch=16, cex=2, col="blue" )
# How to plot in the cohort-period-part: a point at (1960,0.3)
points( 1960-res[1], 0.3*res[2], pch=16, cex=2, col="red" )
```

apc.lines

Plot APC-estimates in an APC-frame.

Description

When an APC-frame has been produced by [apc.frame](#), this function draws a set of estimates from an APC-fit in the frame. An optional drift parameter can be added to the period parameters and subtracted from the cohort- and age parameters.

Usage

```
apc.lines( A, P, C,
           scale = c("log","ln","rates","inc","RR"),
           frame.par = NULL,
           drift = 0,
           c0 = median( C[,1] ),
           a0 = median( A[,1] ),
           p0 = c0 + a0,
           ci = rep( FALSE, 3 ),
           lwd = c(3,1,1),
           lty = 1,
           col = "black",
           type = "l",
           ... )
```


Arguments

A	Age effects. A 4-column matrix with columns age, age-specific rates, lower and upper c.i. If A is of class apc (see apc.fit , P, C, c0, a0 and p0 are ignored, and the estimates from there plotted.
P	Period effects. Rate-ratios. Same form as for the age-effects.
C	Cohort effects. Rate-ratios. Same form as for the age-effects.
scale	Are effects given on a log-scale? Character variable, one of "log", "ln", "rates", "inc", "RR". If "log" or "ln" it is assumed that effects are log(rates) and log(RRs) otherwise the actual effects are assumed given in A, P and C. If A is of class apc , it is assumed to be "rates".
frame.par	2-element vector with the cohort-period offset, and RR multiplier. This will typically be the result from the call of apc.frame
drift	The drift parameter to be added to the period effect. If scale="log" this is assumed to be on the log-scale, otherwise it is assumed to be a multiplicative factor per unit of the first columns of A, P and C
c0	The cohort where the drift is assumed to be 0; the subtracted drift effect is drift*(C[,1]-c0) .
a0	The age where the drift is assumed to be 0.
p0	The period where the drift is assumed to be 0.
ci	Should confidence interval be drawn. Logical or character. If character, any occurrence of "a" or "A" produces confidence intervals for the age-effect. Similarly for period and cohort.
lwd	Line widths for estimates, lower and upper confidence limits.
lty	Linetypes for the three effects.
col	Colours for the three effects.
type	What type of lines / points should be used.
...	Further parameters to be transmitted to matlines used for plotting the three sets of curves.

Details

The drawing of three effects in an APC-frame is a rather trivial task, and the main purpose of the utility is to provide a function that easily adds the functionality of adding a drift so that several sets of lines can be easily produced in the same frame.

Value

A list of three matrices with the effects actually plotted is returned invisibly.

Author(s)

Bendix Carstensen, Steno Diabetes Center, <http://www.pubhealth.ku.dk/~bxc>

References

See Also

[apc.frame](#), [apc.frame](#)

Examples