

# On Age Structures and Mortality

Nico Keilman

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The age structure of any population is shaped by the processes of fertility, mortality and migration, and for a human population it reflects the net effect of those processes during the previous 100 years. When the levels of fertility, mortality and migration have been constant for a long time, the age distribution is also constant. Numbers in each age group may grow or fall over time, depending on the balance between fertility and immigration on the one hand, and mortality and emigration on the other – but their relative share in the total population remains unchanged. When the age distribution varies over time, it signals changing levels of fertility, mortality and migration. The purpose of the present paper is to review the literature that deals with the following question: What lessons can we draw from changes in the age structure of the populations in industrialized countries? Given the interest in the industrialized world for issues connected to the *elderly*, the focus will be on what we can learn about the level of mortality, and changes therein, based on age-structural transitions.

Given the sum of two numbers A and B, we cannot infer A and B from that sum alone. Only by adding extra information can we compute them, for instance when their difference is also given, or their product. Similarly, since the current age structure is the *net result* of historical age-specific fertility, mortality and migration, we are unable to infer the levels of the components of change from the age structure alone. Extra information is needed, for instance:

1. The population is closed to migration.
2. Fertility and mortality rates have been constant for a long time.
3. Growth rates are the same for each age group and they are independent of time.
4. Growth rates are constant in time, but differ between age groups.
5. The age patterns of fertility and mortality are known, but not their levels (e.g. TFR or life expectancy).

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Frequently, the extra “information” is merely an assumption, sometimes a very strong one. For instance, the combined assumption that a closed population (no. 1) has constant growth rate (no. 2) and constant age distribution (no. 3) defines a stable population. This assumption may be realistic in some cases, but more often, it is not. A population in which the growth rates of age groups are independent of time, but differ across age groups is called a variable growth rate population. The assumptions underlying this model are weaker than those for the stable population, and therefore more realistic when one knows that the population is not stable. Yet, the assumption of a stable population is widely used in demography for the following two reasons.

1. Because the assumption is such a strong one, there are also strong mathematical relationships between population size, age structure and fertility and mortality levels in a stable population. These relationships can be used to arrive at powerful conclusions that would be impossible with a weaker assumption.
2. The mathematical relationships mentioned above are good approximations in many cases, in particular when deviations from stability are the result of changing mortality levels, with the changes more or less evenly spread over many age groups.

Information or assumptions of the types 1–5 above may be used in combination as already mentioned in connection with the notion of a stable population. Similarly, we may have more than one observation of the age structure and combine those data with one or more assumptions. Examples of such combinations will be given in the sections that follow. The first section discusses stable population theory and shows how an age structure may be used to infer mortality levels. Most of the theory was developed before 1960 and has been widely applied up to today. The variable growth rate method of the second section emerged in the 1980s and relaxes some of the strong assumptions of a stable population. It is much less used than the methods of stable population theory, not only because it is of more recent date, but also because it allows less powerful conclusions. Two entirely different techniques, that of inverse projection and the closely connected method of back projection were developed in the 1970s and 1980s. They are presented in the third section on “Inverse projection, back projection and generalizations”, together with a recent generalization that encompasses both: generalized inverse projection. Next, the section on “Errors in historical projections of age structures” discusses what we can learn about mortality when we compare age structures observed in the recent past with historical *projections* of those age structures. The accuracy of age structure projections for the elderly leads us in a natural way to the question of how we can improve the accuracy of mortality forecasts. In the section on “Improving forecasts for the elderly”, causality runs from (future) mortality to (future) age structures.

Important applications of stable population theory and variable growth rate theory involve checking the quality of the available data. When a population is known to be stable, but its data cannot be fit to the stable model, one should suspect incomplete registration. Applications of this kind will not be given in the first and second sections, as the focus is on industrialized countries. In other words, unless explicitly stated, it is assumed that all data used in the empirical examples are of sufficient quality.

## Stable Population Theory

Alfred Lotka developed stable population theory in the first half of the previous century<sup>1</sup>, although Leonard Euler (in 1760) and Joshua Milne (in 1815) made early contributions. Ansley Coale (1987) gives an overview. A population is said to be stable when:

- It is closed to migration, i.e. when net migration is zero at all ages
- Both its crude birth rate and crude death rate are independent of time
- Its age distribution is independent of time

A large number of mathematical relationships have been derived between indicators for fertility, mortality and the age distribution of a stable population. These expressions, some of which will be given below, have been used to estimate demographic measures from incomplete data and to adjust inaccurate population statistics.

The relationship between the age distribution of a stable population and its levels of fertility and mortality is

$$c(a) = be^{-ra}p(a), \quad (1)$$

where  $a$  represents age,  $r$  is the growth rate of the stable population,  $c(a)$  is the share of the population aged  $a$ ,  $b$  is the birth rate and  $p(a)$  is the share of the population that survives from birth until age  $a$  (“probability of surviving to age  $a$ ”). Since age is defined here as a continuous variable,  $c(a)da$  is the population’s share aged between  $a$  and  $a + da$ , to be more precise. Integration of (1) gives the following expression for the life expectancy at birth  $e_0$ :

$$e_0 = \frac{1}{b} \int_0^{\infty} c(a)e^{ra} da. \quad (2)$$

In empirical applications, data for the age structure  $c(a)$  alone are obviously not sufficient to determine the characteristics of the stable population. But given an initial estimate of  $p(a)$ , (1) can be rewritten as

$$\ln\left(\frac{c(a)}{p(a)}\right) = \ln(b) - ra, \quad (3)$$

and a regression over  $a$  results in estimates for  $b$  and  $r$  (Keyfitz et al. 1967). However, an approach that avoids regression has become more popular. It is based on tabulated values of the age distribution  $c(a)$  of stable populations with varying levels of the growth rate  $r$ , the birth rate  $b$ , the life expectancy  $e_0$  and the age pattern

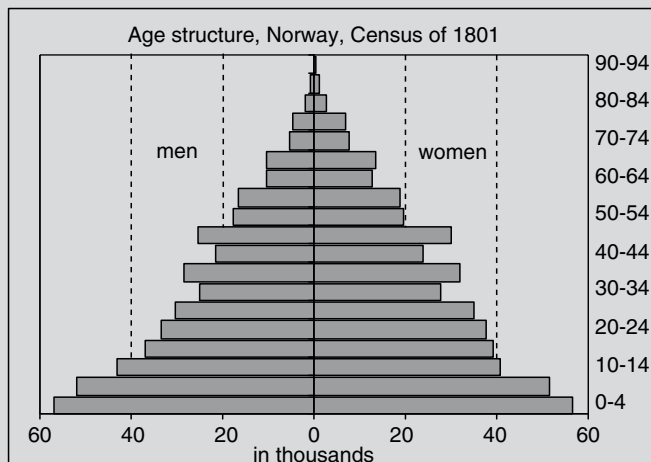
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<sup>1</sup>Lotka and Sharpe (1911). See also Lotka’s *Analytical theory of biological populations*. New York: Plenum Press, 1998 (Plenum Series on Demographic Methods and Population Analysis). This is an English translation of the work that Lotka published in the two-part *Théorie Analytique des Associations Biologiques* in 1934 and 1939, and represents Lotka’s contributions to the field of demographic analysis.

of mortality  $p(a)$  (see Coale and Demeny 1983). The idea is, first, to select an initial model life table (i.e. an age pattern  $p(a)$  and a mortality level  $e_0$ ) and next to find a stable population for which the age structure closely resembles that of the empirical population<sup>2</sup>. The goodness of fit indicates whether or not one should choose a different life table. When the stable population has been identified in Coale and Demeny's extensive tabulations, the corresponding growth rate  $r$  and birth rate  $b$  can be read off, as well as numerous other quantities for this particular population. Box 1 contains an empirical example for Norway with data from its population census of 1801.

**Box 1** Application of stable population theory to Norway's age distribution in 1801

The Population Census of 1801 in Norway is generally believed to be of high quality (Drake 1969). The age pyramid below suggests that the population might have been nearly stable. Norwegian crude birth and death rates were rather constant at 30–32 and 24–26 per 1,000, respectively, in the period 1735–1801 (Drake 1969, Table 3.6). Age groups between 25 and 45 signal non-stability, although some digit preference probably also contributed to the irregularities. By working with cumulated age groups, this problem will have only minor impact on the findings.



(continued)

<sup>2</sup>In practice one does not work with the age distribution  $c(a)$ , but with the cumulative distribution  $C(a) = \int_0^a c(\alpha) d\alpha$ . This way one avoids problems caused by irregularities in the empirical age structure due to digit preference, age heaping and shifting. Probably this is an important reason why the regression approach is not widely used.

**Box 1** (continued)

I compared the cumulated age distributions  $C(a)$  for men and women to those of stable populations based on Regional Life Tables Model North of levels 11–15, i.e. life expectancy values of 45–55 for women and 41.8–51.4 for men. For successive values of  $a$ , I found the stable growth rate by interpolation between tabulated growth rates. A perfectly stable population should result in the same interpolated growth rate for each  $a$ . In empirical applications, interpolated rates vary by age. Variation across levels was lowest for level 12, the standard deviation in the rate over ages 15–70 being 1.1 and 0.7 per thousand for the two sexes. The mean interpolated growth rates were equal to 12.2 and 10.2 per thousand for men and women, respectively. This suggests a life expectancy of around 45 years before 1801.

For men aged 35–39 or 65–69, and women aged 30–34, 40–44, or 70–74, the estimated growth rates were remarkably lower than those for other age groups. Exceptionally low birth rates and high death rates in the 1740s and 1770s explain some of these effects (Drake 1969).

The approach outlined above starts from an assumed level and age pattern of mortality. Thus an important issue is how sensitive the results are for the choice of a particular life table. In other words, how do the characteristics of the stable population change when the mortality pattern changes? There is no general analytical answer to this question, but the effects are probably not large for actual populations. Coale (1972) and Keyfitz (1985) have analysed the case in which the mortality change is the same for all ages. Assume that all age-specific death rates are reduced by an amount  $k$ . In that case, it can be shown that the age distribution of the population is not affected, that the growth rate increases by  $k$ , that the birth rate is unchanged and that the death rate reduces by  $k$ .<sup>3</sup>

Closely related is the concept of a quasi-stable population, defined as a population, in which fertility has been approximately constant, while mortality has steadily declined over the past few decades (Bourgeois-Pichat 1958). Such a population has an age distribution, which differs little from that of the stable population implied by current fertility and mortality schedules.

When a population's age distribution is measured at two successive censuses, two sets of fertility and mortality indicators can be inferred, one for each census. Next, we can combine the birth rate from the first census with the life table from the other. This will tell us to what extent the mean age, or the dependency ratio, or any other indicator derived from the age structure, has changed over the period between

<sup>3</sup> When the reduction of the death rates varies by age, the age distribution of the stable population is changed in such a way that age segments with the strongest mortality reduction get more weight. The typical mortality decline has been strongest below age five. As a result, mortality declines have, throughout human history, tended to make populations younger (Preston et al. 2001, p. 160).

the two censuses as a result of changes in mortality or in fertility (Keyfitz and Flieger 1969). An important assumption is, of course, that the population be stable at both points in time. Such an analysis requires that one calculate a hypothetical age distribution based on a given birth rate and a certain life table. This can be done based on expression (1), provided one knows the intrinsic growth rate  $r$  of the stable population. The latter is achieved by solving  $r$  from Lotka's fundamental equation

$$\int_{\alpha}^{\alpha} \phi(x) e^{-rx} dx = 1, \quad (4)$$

where  $\phi(x) = m(x)p(x)$  represents the net female fertility rate at age  $x$ . Coale (1957) describes an iterative algorithm for determining  $r$ , which converges quickly.

## Variable Growth Rate Method

The methods outlined in the previous section assume that the population is stable, quasi-stable, or nearly stable. For industrialized countries nowadays, this is an unreasonable assumption. Following low fertility levels in the 1930s, many of these countries experienced a baby boom in the first two decades after the Second World War and a drop in fertility in the 1970s. At the same time, female life expectancy increased continuously – for men there was a temporary stagnation in the 1960s. Industrialized countries in Eastern Europe showed dramatic declines in fertility around 1990, and life expectancies improved hardly or not at all between 1985 and 1995, in particular for men. Because of these developments, fertility and mortality cannot be assumed to be constant, which means that the assumption of a stable population is too strict. The variable growth rate method relaxes that assumption. Whereas a stable population displays a growth rate that is constant, both with respect to age and time, the variable growth rate method assumes rates that may be dependent on age.

Various authors have contributed to the theory around the variable growth rate method, in a series of papers that were published in the first half of the 1980s (Bennett and Horiuchi 1981; Preston and Coale 1982; Arthur and Vaupel 1984). These papers followed on the work of McKendrick (1926) and Von Foerster (1959), among others. Bennett and Horiuchi started from the McKendrick-Von Foerster partial differential equation, which relates the rate of change in population size with respect to age and time to the force of mortality at that time. Preston et al. (2001) give a useful overview of the theory and various applications. For the purpose of the present paper it suffices to note that Eq. 1 for the age distribution of a stable population, which is closed to migration, is modified to<sup>4</sup>

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<sup>4</sup>Expression (5) can be generalized to include migration, by incorporating an age-specific net migration rate. The net migration rate is the difference of the immigration rate and the emigration rate. Note that the immigration rate is not a rate in the demographic (occurrence-exposure) sense, as the population exposed to the risk of immigration to the country is not included in the immigration rate.

$$c(a,t) = b(t) \exp \left[ - \int_0^a r(x,t) dx \right] p(a,t), \quad (5)$$

where  $p(a,t)$  is now an expression of the proportion that would survive to age  $a$  according to the mortality schedule at the moment  $t$  for which  $c(a,t)$  is the proportion at age  $a$ . The growth rate  $r(x,t)$  expresses population growth during an infinitesimally short time interval from  $t$  to  $t+dt$  for the fixed age group  $x$ . Note that when the growth rates are independent of age and time ( $r(a,t)=r$  for all  $a$  and  $t$ ), the integral in (5) reduces to  $r a$ , cf. expression (1). In order to infer a mortality schedule from an observed age structure, both sides of Eq. 5 are multiplied by total population size at time  $t$  and solved for  $p(a,t)$ . The result is

$$p(a,t) = \frac{N(a,t)}{N(0,t)} \exp \left[ \int_0^a r(x,t) dx \right]. \quad (6)$$

Expression (6) tells us that a mortality schedule can be derived from knowledge of the age pyramid  $N(a,t)$  and the age-specific growth rates  $r(x,t)$ .  $N(0,t)$  denotes births at time  $t$ . For an actual population the rates can be computed based on the age pyramid of two subsequent years. Box 2 illustrates the method for the case of Norway 1850–1995.

**Box 2** Mortality schedules computed on the basis of the variable growth rate method, Norway, 1850–1995

Statistics Norway generously provided me with unpublished data on the population of Norway by 1-year age group and sex at 1 January of each calendar year beginning in 1846. First, I used the discrete-time version of expression (6), i.e.

$$\frac{L_a}{l_0} = \frac{N_{a,t}}{B(t)} (1+r_{1,t})(1+r_{2,t})\dots(1+r_{a,t}).$$

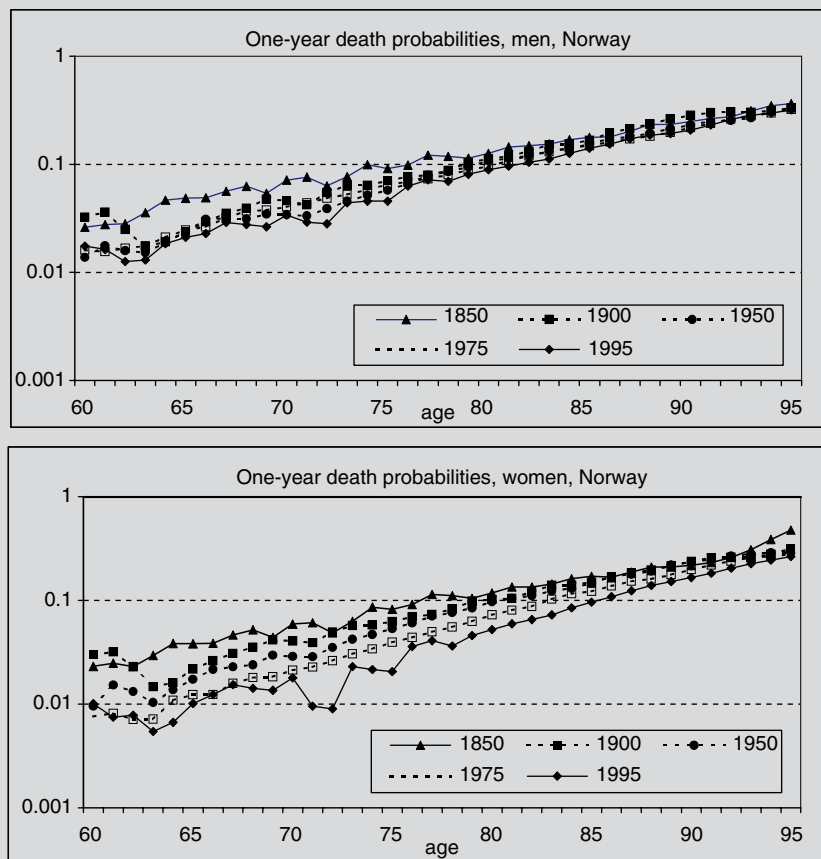
Here  $N_{a,t}$  represents the population in age group  $(a, a+1)$  at time  $t$ ,  $r_{a,t}$  is the growth rate for age group  $(a, a+1)$  at time  $t$ ,  $L_a$  represents the life table stationary population in age group  $(a, a+1)$  at time  $t$ , and  $B(t)$  is the number of births in year  $t$ . Assuming that the life table radix  $l_0$  equals 1 (i.e. scaling  $L_a$  such that it is expressed per one person), and furthermore assuming that  $l_a = \frac{1}{2}[L_{a-1} + L_a]$ ,  $a > 0$ , I found for the 1-year probability of dying  $q_a$  at time  $t$  the following expression:

$$q_a = 1 - \frac{l_{a+1}}{l_a} = \frac{N_{a-1,t} - N_{a+1,t} (1+r_{a,t})(1+r_{a+1,t})}{N_{a-1,t} + N_{a,t} (1+r_{a,t})}, a > 0.$$

(continued)

**Box 2** (continued)

Next, I computed the growth rates as  $r_{a,t} = [N_{a,t+1}/N_{a,t-1}]^{1/2} - 1$ , and inserted these in the expression above. The growth rates are the net result of mortality, immigration, and emigration. Migration can be disregarded for ages 60 and over, but not for younger ages. Therefore, I limited myself to the elderly.



The graphs plot 5-year moving averages. They show two distinct features. First, the relative mortality reduction since 1850 was stronger for the youngest than for the oldest old. This led in turn to a rectangularization of the survival curves for both sexes (Mamelund and Borgan 1996, 39–40). Second, the decrease over time was quite uniform for women, although accelerating during the past 50 years. For men the strongest reductions occurred in the second half of the nineteenth century.



## Inverse Projection, Back Projection and Generalizations

Several methods have been used by historical demographers to infer time series of vital rates and age structures from a known or assumed age structure, together with time series of annual or quinquennial births and deaths. Ronald Lee introduced in 1974 a technique called ‘inverse projection’. Given an age and sex structure at time  $t = 0$ , and a series of birth and death counts for the period  $(0, T)$ , the method computes mortality rates, fertility rates and age structures for the years  $(0, T)$ . It assumes that the age schedules of both fertility and mortality depend on a single parameter and that the population is closed to migration. The method proceeds from one time interval unit (1 or 5 years) to the next. For each interval, it computes a preliminary number of deaths based on the starting population by age and an initial schedule of age-specific death rates. The mortality schedule is scaled up or down on the basis of the observed number of deaths. The death rates thus obtained are used to survive the population to the end of the interval. Finally, birth rates are applied to the mid-period female population of reproductive ages, and these rates are adjusted so as to produce the correct number of births. The assumption of a closed population has been relaxed in later versions of the method (Brunborg 1976, 1992; Lee 1985): when population counts are known from more than one census, migration is determined by comparing intercensal population growth with natural growth. McCaa (1989, 1993) has developed the PC program ‘Populate’ which includes these and other features. Box 3 gives a summary of Brunborg’s application of the inverse projection method to the case of Norway, 1736–1970.

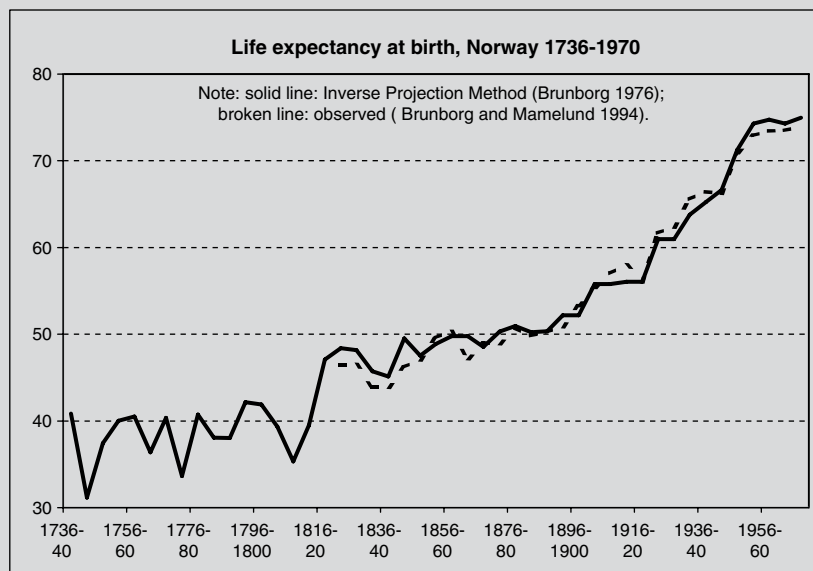
### **Box 3** Brunborg’s application of the IP-method to Norway, 1735–1974

Brunborg (1976) used annual data on births and deaths from Drake (1969) for the years 1735–1769, and official data for the period 1770–1974 (Statistics Norway 1994). Both series suffer probably from underregistration and other errors. Norway’s first census was held in 1769, but the recorded age distribution is inaccurate (Drake 1969). Brunborg computed total population in 1735 on the basis of birth and death counts for the period 1735–1769, and total population in 1769. An assumed stable age distribution corresponding to level 8 Model North mortality, with crude birth and death rates equal to 31 and 26 per 1,000 resulted in an estimated age distribution for 1735. The choice of the stable age distribution is not crucial for the results after ca. 1800, see footnote 5. Brunborg selected Model North life tables at levels 7 ( $e_0 = 33.5$  for men and women combined) and 24 ( $e_0 = 75.9$ ) as the basis for the range of mortality schedules. The fertility schedule was an average for 1874–1876 and 1889–1892 (the oldest available schedules at that time), with a mean age at childbearing of 33.2 years, and the migration schedule was based on data from 1866–1895. The general pattern for the life expectancy

(continued)

**Box 3** (continued)

(and the Net Reproduction Rate) is reproduced well compared to observed values. Brunborg found also that estimated proportionate age distributions in 1801, 1875, and 1966 were very close to observed values: most differences (10-year age groups) were smaller than 0.4% points, and none exceeded 1.2% points. One may conclude that life expectancy was between 35 and 40 years in the eighteenth century, and considerably lower in crisis periods (1741–1745: 31.2; 1771–1775: 33.6).



Brunborg's life expectancy values are 5–10 years lower than those obtained on the basis of stable population theory (Box 1). Several explanations are possible.

1. Brunborg's birth data may suffer from underregistration. McCaa (1989) analyses the sensitivity of Brunborg's life expectancy estimates for underregistration of vital events. From McCaa's Figure 1 I estimate that a continuous underregistration of births by 10% implies life expectancy values that are too low by 3–5 years in the last three decades of the eighteenth century. Although this explanation in itself is plausible, one may object that the most likely source of birth underregistration is infant mortality, which must have resulted in too low counts for deaths as well. McCaa finds that a 10% underregistration of deaths counteracts the effect of too low birth counts by about the same number of years of life expectancy. On the other hand, stillbirths unduly registered as deaths but not as births, may have led to too low life expectancies.

(continued)

**Box 3** (continued)

2. The 1769 census (723,000) may have underreported total population size. Drake (1969) assumes that the official figure was too low by about 19,000, or 2.6%. If the error is the same for all ages and the number of deaths is fixed, the one-parameter mortality schedule results in death rates that are too high by 2.6%. This means that the life expectancy is too low by an amount of  $0.026.H.e_0$ , where  $H$  is Keyfitz' concentration index (Keyfitz 1985). By definition,  $H$  is lower than 1 – for pre-industrial Norway it is probably around 0.5 (Model North at level 12 gives  $H$ -values equal to 0.52 for men and 0.48 for women). With a life expectancy of around 40 years, the undercount in the census of 1769 explains roughly half a year of the life expectancy difference, but certainly not more than 1 year.
3. Brunborg's results are not entirely reliable before 1800, due to the arbitrary choice of the age distribution for 1735 (Model North, level 8). After 1800, the initial age distribution is washed out. Unfortunately, we do not know how sensitive the life expectancy estimates before 1800 are for different choices of the stable age distribution in 1735.
4. The 1801 population was not stable. Fertility and mortality levels between 1735 and 1801 do not indicate any severe deviation from stability (Box 1), but there was probably some emigration (around 270 persons per year, or 0.3 per thousand, according to Drake's estimates). If this is accepted, the stable population estimate for the life expectancy in Box 1 should even be *higher*, but only slightly so.

In spite of the fact that IP rests on weaker assumptions than stable population theory, all in all I assume that Brunborg's life expectancy estimates are too low, for two reasons. First, because the deaths data he used included stillbirths. The effect on life expectancy is stronger than McCaa suggested, because the overregistration of deaths was concentrated in the first few weeks of the life span. McCaa used a one-parameter life table, and thus he assumed implicitly that the overregistration was evenly spread over the entire age span. Second, because the choice of level 8 Model North stable age distribution in 1735 was too pessimistic.

Unlike projection by the traditional cohort-component method (CCM), inverse projection (IP) starts from birth and death counts and infers age-specific vital rates. CCM computes births and deaths on the basis of age-specific vital rates. Both methods proceed forward in time. 'Back projection' (BP) goes backward. The method was developed by Wrigley, Schofield and Oeppen, see Wrigley and Schofield (1982). It starts with a known age structure at time  $T$  and births and deaths counts for an *earlier* period  $(0, T)$ . Next, using a number of assumptions, it calculates age structures for that period, as well as age-specific vital rates and net-migration. Unlike IP, where population totals are specified externally (so that migration can be handled),

BP computes population totals within the model. BP has been criticized on two grounds (Lee 1985). First, the model is underidentified: for  $T$  periods, the BP-model has  $T$  more unknowns than equations. Therefore *ad hoc* assumptions are necessary. Second, the weak ergodicity principle states that any two age structures, however different, that are submitted to the same series of fertility and mortality rates will eventually converge towards the same age structure<sup>5</sup>. This implies that BP selects one path of the demographic variables from among an infinity of reasonably smooth paths, and thus any number of alternative but equally plausible paths may be constructed.

Further work by Jim Oeppen (1993a, b) attempted to respond to Lee's critique, in particular the first point. This resulted in a general method called Generalized Inverse Projection (GIP), which can be related to both IP and BP. Like IP, GIP assumes one-parameter families of age schedules for mortality and migration. The aim of GIP is to estimate a series of mortality and migration parameters that correspond to the period for which birth and death counts are available and, simultaneously, a series of population age structures that are consistent with the data and the parameters. (Fertility schedules are not required for computing age structures – births are given.) First, Oeppen expresses the general equations for population movement, defining the population aged  $a$  at time  $t$ ,  $N_{a,t}$ , as a function of  $N_{a-1,t-1}$  together with the death probability and the emigration rate, both at age  $a$ . Births in  $(t-1, t)$  are related to  $N_{0,t}$  by means of the appropriate survival probability and migration rate. Next, migrants result from the migration rate and the mid-period population, while deaths are computed based on the death probabilities, the population at the beginning of the period and the number of migrants. Starting from an assumed initial population  $N_{a,0}$ , subsequent application of these equations results in a system of non-linear equations with the totals of births and deaths for each of the  $T$  periods and age groups at time  $T$ , as given. For  $K$  age groups, there are  $T + K$  equations and there are  $2T$  parameters to be estimated – a scaling constant for mortality and one for migration in each period. The GIP-method estimates these parameters, given the constraints, by minimizing a penalty function which contains three terms: one for the relative deviations in estimated and observed deaths, one for the deviations in the age structure at time  $T$  and a third one with period-to-period fluctuations in the migration scale parameter. Thus, the method obtains an optimal fit of the model to the data on deaths and final age structure, while at the same time the migration parameter changes as little as possible. Additional information, for example, known population sizes or age structures for censuses before time  $T$ , can easily be included in the penalty function. If the initial population structure  $N_{a,0}$  is given, instead of the final structure  $N_{a,T}$ , the method solves the IP problem (GIP-IP). If the final structure is given, GIP is reduced to BP (GIP-BP).

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<sup>5</sup> This is exactly the reason why the starting age structure of IP is not critical. For example, starting from two very different stable populations (female, North,  $e_0 = 47.5$ ,  $r = 0$ ; and female, North,  $e_0 = 27.5$ ,  $r = 0.01$ ) for the case of England in the period 1540 to 1871, Lee (1985) finds converging IP-results after a few decades already.

Oeppen has tested the BP-version of the method on various data sets, including Brunborg's data for Norway since 1735. Total population was estimated very accurately, even on the basis of the *total* population for *only 1* year (1980), together with quinquennial births and deaths counts. I compared Oeppen's unpublished estimates for the Norwegian population by 5-year age groups for the years 1850, 1870, 1890, ..., 1970<sup>6</sup> with official data and found that errors in the proportionate age structure never were larger than 1.2% points. Averages over the age groups for the absolute errors ranged from 0.19% to 0.33% points for these 7 years. Thus for this particular data set, GIP-BP reproduced observed age structures very accurately. The net migration estimates were considerably smoother than the 'observed' values, but this can be improved by giving less weight to the migration smoothness in the penalty function. Similar conclusions hold for data from England 1801–1871. It turns out that Oeppen's GIP-BP estimates are very close to the original ones of Wrigley and Schofield obtained by BP. Other applications that produced excellent fits for the age structure are those for Denmark 1665–1840 and Amsterdam 1681–1920 (see Johansen and Oeppen 2001; Van Leeuwen and Oeppen 1993).

GIP-BP does not resolve the problem connected to weak ergodicity. Oeppen assumed that the initial population is stable and estimated its growth rate from the series of births. Alternatively, it could be estimated from the deaths series, or it could be made endogenous and estimated by the method. Different estimates of the growth rate will produce different initial populations. In one application (England 1540–1871; see Oeppen 1993b Table. 2.1<sup>7</sup>), the initial population estimated by GIP-BP fell linearly by 36% when the growth rate was increased from zero to 10%, with strong implications for the estimates of the first decades after 1540. After about 50 years, the initial differences were washed out. In other words, GIP-BP results are not reliable for roughly the first 50 years, due to the weak ergodicity principle. GIP-BP shares this characteristic with IP, unless the initial age structure is known for IP.

It is surprising that GIP-BP produces reliable empirical results, in spite of the weak ergodicity problem mentioned above. One possible explanation is that the number of feasible solutions is severely restricted by the fact that age-specific mortality depends on only one scaling parameter.

## Errors in Historical Projections of Age Structures

Age structure forecasts reflect *expected* changes in fertility, mortality and migration levels. Thus, when old forecast results are compared to actual figures, *errors* in projected age structures reflect *unexpected* developments of the components of change.

The cohort component method (CCM) is the standard method for preparing a population forecast. In the CCM-tradition, forecast errors occur for two reasons: assumptions on fertility, mortality and migration may be wrong, or the forecast may be based on inaccurate data. The latter source of forecast errors is frequently

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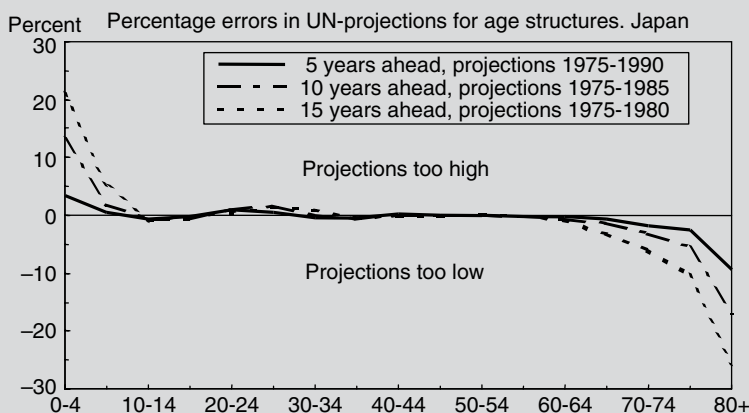
<sup>6</sup>Generously provided by Jim Oeppen (2001) (personal communication).

<sup>7</sup>There is a printing error in Oeppen's Table 2.1: growth rates are too low by a factor ten.

observed for less developed countries, where data quality often is poor (Keilman 2001). In the present paper, the focus is on industrialized countries and, therefore, I shall assume that inaccurate age structure forecasts are only caused by wrong assumptions for the components of change.

Errors in projected age structures for various industrialized countries turn out to have a common pattern. The errors are large and positive for young age groups and more or less equally large but *negative* for the elderly. The overprojections among the young in the 1970s indicated unforeseen sharp declines in birth rates. The elderly were underestimated, because forecasters have been too pessimistic regarding mortality, in particular for women. (There is one exception, however. For middle-aged men in the 1960s, life expectancy forecasts were too *optimistic*, due to unforeseen mortality increases caused by neoplasms, cardiovascular diseases and motor vehicle accidents, see Preston 1974.) This error pattern for age structure projections made by the UN was found for Northern America, Europe, Latin America and Oceania (Keilman 2001), and in projections prepared by statistical agencies in developed countries such as Canada, Denmark, the Netherlands, Norway and the United Kingdom (Keilman 1997). Box 4 illustrates the case of Japan, based on UN projections since 1975. Data from the 1998-round of UN projections were taken as actual.

#### Box 4 Errors in age structure projections



I calculated mean percentage projection errors by age group, the means taken over successive UN projections, controlling for duration. The figure shows a systematic underprojection of the number of elderly, caused by too pessimistic mortality projections. Japan's life expectancy increased from around 75 years in the mid-1970s to almost 80 years, 20 years later. However, UN life expectancy projections were consistently too low by 1.3–1.9 years in that period (Keilman 2001).

## Improving Forecasts for the Elderly

*[Note: The discussion in this section reflects the literature as of early 2002. During the past few years, two important developments have taken place, which are relevant for the conclusions below. First, the findings of a series of reports on mortality forecasting in industrialized countries (Palmer 2003–2007, see Social Insurance Studies volumes 1–5, <http://forsakringskassan.se/sprak/eng/publications/>) suggest that a statistical approach to predicting life expectancy and survival is to be preferred over a causal approach. Second, Alho's approach to stochastic population forecasting (the so-called Program for Error Propagation, or PEP model, see Alho and Spencer 2005) has become the benchmark for preparing and using such forecasts (Tuljapurkar 2008). It has been applied to a large number of individual countries, as well as to a group of 18 European countries (Alho et al. 2006, 2008; Alders et al. 2007). The multi-country setup in this latter project avoided the idiosyncrasies often connected with single-region stochastic and deterministic forecasts].*

The general conclusion that mortality improvements for industrialized countries have been underestimated leads to the question of how mortality projections, and thus forecasts for the elderly population, can be improved. To that end, one first has to understand the reasons why mortality forecasts failed. Broadly speaking, there are two main reasons: assumption drag and inherent uncertainty. First, the extrapolative character of mortality forecasts leads to difficulties each time a trend shift occurs. Empirical studies show that it takes about 10 years before population forecasters acknowledge the new trend (Keilman 1997). Such an 'assumption drag' is clearly visible in life expectancy extrapolations. Second, much of the uncertainty is caused by the fact that experts disagree as to the prospects for further mortality decline. Some assume that there are biological or practical limits to the life expectancy, although these are not necessarily to be reached within the next 50 years (Olshansky et al. 1990; Olshansky and Carnes 1996). Others expect medical breakthroughs in the future, which will lead to rapid mortality decline among the elderly (Vaupel 1997). The empirical evidence is not conclusive either. While human longevity generally improves in industrialized countries, mortality for the oldest old stagnates or even increases slightly in a few countries, such as in Denmark (Denmark Statistik 2000), the USA (Kranczer 1997), the Netherlands and Norway (Nusselder and Mackenbach 2000). At the same time, survival curves show very little or no sign of further rectangularization since the 1950s in some countries (USA, Sweden and Japan; see Wilmoth and Horiuchi 1999), while in other countries the curves continue to become more rectangular, after the rapid developments into that direction until the 1950s (France, England, the Netherlands and Switzerland; see Robine 2001).

How can mortality forecasts be improved, in the sense that they predict the number of elderly more accurately? Several possibilities have been suggested, of which I will mention four.

## *Mortality Laws*

Demographers, statisticians and actuaries have long been occupied with finding a suitable ‘law of mortality’, i.e. a mathematical representation of age-specific mortality – most often (but not exclusively) in terms of the death rates. Once such a law is identified, its parameters are estimated for a sufficiently long period and next they are extrapolated. A large number of mortality laws have been proposed, a process that started with De Moivre in 1725 and that continues until the present day (Hannerz 2001). For a recent review, see Tabeau (2001). Some of the laws are restricted to adult or old age mortality (Coale-Kisker, Himes-Preston-Condran, Gompertz, Perks, Weibull). Tabeau (2001) and Boleslawski and Tabeau (2001) compare 27 of such laws. Relational models, such as Brass’ logit model and the Lee-Carter model, are also considered. Among the laws and models, the Heligman-Pollard curve is widely applied (Rogers and Gard 1991; McNown and Rogers 1989; Hartmann 1987; Kostaki 1992a,b). Compared to other models, the H-P curve has the advantage that it pairs accuracy in prediction with flexibility, in particular when describing mortality changes over time. Hartmann (1987) used Swedish mortality data for the period 1900–1970 and concluded that the H-P curve is a useful model for making population projections, one reason being the fact that it accommodates for changing age patterns of mortality as the level of mortality changes. Another popular model, namely the one proposed by Lee and Carter (Lee and Carter 1992; Carter and Lee 1992) apparently is much less flexible than the H-P model (see Büttner 1999). Moreover, it tends to produce extremely low mortality for young age groups when it is forced to project very high levels of the life expectancy. Adding a lower bound to the death rates may solve that problem (Büttner 1999). However, an important advantage of the Lee-Carter model is that it contains, in effect, only one parameter that has to be extrapolated. A detailed comparative study could shed further light on the issue under which circumstances the Lee-Carter model results in better mortality forecasts than the Heligman-Pollard model, and vice versa. This would extend the single-country comparison of the H-P and the L-C models by Bell (1997). For US white male and female mortality 1940–1991, he finds slightly better performance of the H-P model, although certain bias corrections to the L-C model do better than the original H-P model.

## *Cause of Death*

One could include cause of death (c.o.d.) in the mortality extrapolations. While c.o.d. is useful when analysing historical mortality, it is doubtful that it will help to predict future mortality more accurately. In addition, c.o.d. registration for the elderly is thought to be rather unreliable. Following are two reasons for this, an empirical one and a statistical one. (1) Tabeau et al. (2001a) found very similar life expectancy extrapolations to 2020 with and without c.o.d. in an empirical study for



France, Italy, the Netherlands and Norway, using data for the period 1950–1994. Wilmoth (1995) showed analytically for linear extrapolation models that including c.o.d. will result in lower future life expectancy than ignoring c.o.d. Thus the fact that c.o.d. has been omitted in most official forecasts cannot have been the reason for the underprojection of the life expectancy. Finally, three Dutch c.o.d. mortality forecasts made between 1970 and 1975 were less accurate than six other forecasts based upon traditional mortality extrapolations (i.e. by age and sex only) that were made between 1950 and 1980 (Keilman 1990). (2) Traditional models assume that causes of death are independent. This is an unrealistic assumption: persons who are expected to die from a specific cause obviously have an increased risk of dying from other causes, depending on the illness in question. There is no generally accepted way to take the association between causes of death into account in empirical studies (Chiang 1991).

### ***Endogenizing Mortality***

One could include risk factors, life style, health and morbidity status as independent factors in the mortality extrapolations. Marital status, living arrangement, traffic accidents, the introduction of antibiotics and smoking have been used for that purpose (Alderson and Ashwood 1985; Joung 1996; Van Hoorn and De Beer 2001). The simultaneous extrapolation of health, morbidity and mortality has also been suggested (Manton et al. 1992; Murray and Lopez 1997). For a review, see Van den Berg Jeths et al. (2001). The accuracy of such mortality forecasts, as opposed to the rather mechanical ones based on a mortality law, has not been investigated.

### ***Stochastic Mortality Forecasts***

A radically different solution is to quantify uncertainty and accept the fact that forecast errors are unavoidable. In the last decade, a number of stochastic forecast models based on the Cohort Component Method (CCM) have been developed (Lee and Tuljapurkar 1994; Lutz and Scherbov 1998; Alho 1998; De Beer and Alders 1999; Keilman et al. 2001). The basic idea is to think of the population in the future not as one number, but as a whole distribution: some numbers are more likely than others. If life expectancies and numbers of elderly are presented in the form of *predictive* distributions of this kind, the user is forced to take forecast uncertainty into account. At the same time, forecasts of this nature are less vulnerable to sudden changes in real mortality trends than traditional deterministic forecasts. Box 5 gives an empirical illustration for the life expectancy of Norwegian women.

Stochastic population forecasting uses the CCM. But instead of one set of parameters for fertility, mortality and migration, as in the traditional deterministic method (or perhaps three, when a high, a medium and a low forecast variant are computed), one specifies the joint statistical distribution of all input parameters.

Because of the large amount of input parameters (35 fertility rates, 200 death rates and 120 parameters for net migration for each forecast year), simplifying assumptions are used. First, one assumes that fertility, mortality and migrations are independent. For industrial countries, this is a reasonable assumption. Second, one focuses on the distribution of a few summary indicators (for instance total fertility rate, life expectancy at birth, level of net-immigration), thereby ignoring the statistical distributions of the detailed parameters (age-specific rates). Three main methods are in use for computing probabilistic forecasts of the key parameters: time-series extrapolation, expert judgement and extrapolation of historical forecast errors. Time-series methods rely on statistical models that are fitted to historical data. These methods, however, result often in excessively wide prediction intervals when used for long-term forecasting. Judgemental methods can be used to correct or constrain such broad prediction intervals. Expert judgement is also used when expected values and corresponding prediction intervals are hard to obtain by formal methods. A group of experts is asked to indicate the probability that the key parameter in some future year falls within a certain pre-specified range. A weakness of this approach is that experts, often being unduly confident, tend to give overoptimistically high probabilities. Finally, empirical errors observed for past forecasts may be extrapolated to predict the expected errors for the current forecast. A problem here is that forecasts prepared in the 1960s or earlier were poorly documented, so that data on historical errors do not stretch back as far as one would like.

In practice, elements of the three methods are used in combination. For instance, time-series often result in unrealistically wide intervals on the long term, which may be reduced judgementally based on expert knowledge. Moreover, the intervals, whether obtained by time-series methods or expert opinion, can be checked against historical error patterns, in particular in the short term.

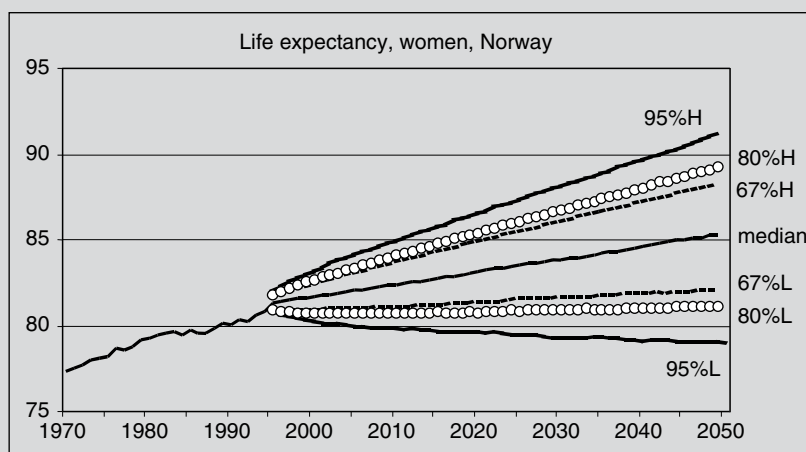
Irrespective of the method used, probabilistic forecasts of the youngest and oldest age groups show the most uncertainty, because fertility and mortality are hard to predict. In addition, prediction intervals are often narrower when variables are aggregated (for example, when 1-year age groups are combined into 5-year age groups, or when the populations for the two sexes combined is analysed), rather than looked at individually, because the errors tend to cancel each other out. These kinds of uncertainty assessments are crucial, and statistical agencies would do a great service to users of forecasts if they would adopt probabilistic methods rather than methods that are more traditional, which do not take uncertainty into account.

## Conclusions

This paper shows various ways to infer mortality levels in a population from information about the age structure, and changes therein. The age structure alone cannot be used for such a purpose. Additional data, or assumptions, are necessary. Stable population theory builds on strong assumptions, but has been used successfully for

### Box 5 Prediction intervals for future life expectancy and elderly women in Norway

A bivariate ARIMA (2,0,0) model was estimated for the logs of annual life expectancies at birth for men and women in Norway 1950–1995, see Keilman et al. (2001). The model was used to predict future life expectancy after 1995, with targets of 80 and 84.5 years in 2050 for men and women, respectively. The figure below gives the prediction intervals for the female life expectancy. There is an expected 95% probability that the female life expectancy will be between 79 and 91 years of age in 2050. The correlation across the sexes was estimated as 0.65.



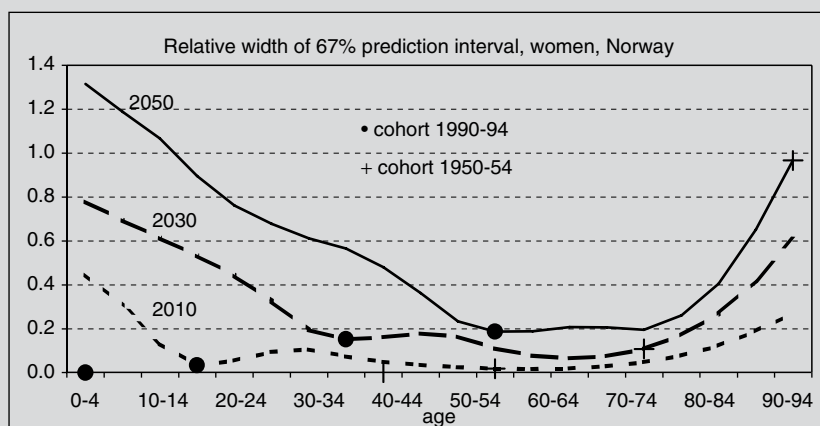
Our results indicate similar uncertainty for the life expectancy at birth as those obtained by De Beer and Alders (1999) for the case of the Netherlands. These authors found a 95% prediction interval of 12 years wide in 2050, both for men and for women. Intervals presented by Tuljapurkar et al. (2000) for the G7 countries (Canada, France, Germany, Italy, Japan, the United Kingdom, and the United States) are much smaller than ours. The width of their 90% intervals of combined-sex life expectancy at birth in 2050 ranges from a minimum of 2.8 years for Canada to a maximum of 7.5 years for the UK. The intervals are based on a one-parameter Lee-Carter model for age-specific mortality for the two sexes combined, which is fitted to an abridged life table with 5-year age classes up to 80–84. Ages 85 years and higher were lumped into one age class (except for Japan). The age- and sex aggregation, which reduces random fluctuations, may have resulted in these relatively narrow intervals.

The stochastic forecast resulted in prediction intervals for the population by age up to 2050. For the elderly, these intervals were rather narrow, not

(continued)

**Box 5** (continued)

because mortality is easy to predict, but simply because there are so few elderly. For purposes of comparison, it is instructive to inspect the width of the relative intervals, i.e. the intervals as a ratio of the median. The graph below illustrates that for the oldest old, uncertainty is almost as large as it is for the youngest age groups. The lines for 2010, 2030, and 2050 indicate relative uncertainty in a *cross-sectional* way. They suggest that uncertainty first decreases from birth to middle ages (up to an age equal to the forecast duration), and that it increases thereafter. These cross-sectional patterns do not reflect uncertainty over the life course correctly. The relative intervals for the birth cohort 1950–1954 illustrate that the age gradient for the elderly is much steeper than what the cross-sectional pattern indicates. The plot for birth cohort 1990–1994 shows that uncertainty increases for the youngest age groups as well.



near-stable historical populations. The method is quite robust against changes in mortality. The variable growth rate method rests on much weaker assumptions, but permits less powerful conclusions. The most detailed information on mortality (and fertility) may be derived in the case where one has series of birth and death counts, in combination with one or more age structures. Inverse projection and back projection have been applied to some historical populations. Finally, some qualitative insight can be derived from evaluating historical age structure projections against observed data. A recurrent finding in this connection is that population forecasters in industrialized countries in the past decades have been too pessimistic regarding mortality improvements. This in turn led to substantial underprojections of the number of elderly. Stochastic projections are an appropriate means of improving the quality of forecasts for the elderly (and other age groups as well), because they quantify forecast uncertainty. They force the users to think in uncertainty terms and anticipate unexpected trends.

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