Population Projections: Stochastic Simulation Techniques & Applications

Edited by

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Editors' Preface

A. DHARMALINGAM*
IAN POOL**

Demography is a very highly applied subject. It was called "Political Arithmetick" in the early days of the Royal Society. Perhaps its most applied form is in the construction and interpretation of models and projections for policy purposes.

Policy makers cannot carry out "experiments" of the sort that are conventional in the laboratory sciences. Thus they turn to models to simulate possible consequences of policy initiatives, and to see how changes in the society or population will affect the achievement of these policies. Fundamental to policy models are demographic methodologies termed projections, both macro and micro.

Demographic projection techniques had taken a similar form, with what is termed cohort-component techniques, for a long time. These methods are arithmetically rather simple but involve large data sets, and detailed and time-consuming computations, albeit that the new generation computers make this far less laborious. Attempts to provide the same results using, say, more parsimonious mathematical or statistical models have proved futile.

But there is a nagging concern. Forecasts in demography, as in related fields, have traditionally given two mis-impressions: that they provide exact future numbers, and that the trajectories they portray are deterministic, rather than the balance of probabilities. Agencies attempt to avoid the appearance of determinism by computing a series of different projections with varying assumptions. But recently there has been dissatisfaction expressed about this approach and empirical papers in journals such as *Nature* have shown the problems that have been engendered.

The response has been to turn to what are called "stochastic" or "probabilistic" projection techniques. They may result in more macro-level outputs, or they may draw on micro-simulation techniques. These yield an

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infinite number of parameters, but the results are then couched in terms of the probability that a trajectory or range of trajectories is likely to occur in the future.

Stochastic population projection is a rapidly expanding field, particularly in the social and economic areas. There is a need to bring the purveyors of these methodologies (typically social scientists) and users (typically the policy community) up-to-date with emerging techniques and the data sources they draw on. Ian Pool, Professor of Demography, at Waikato University's Population Studies Centre organized an international workshop towards this end in December 2004. It brought together domestic and overseas academics, and senior practitioners from the New Zealand policy community to share the state-of-the-art developments in stochastic projection. A follow-up seminar held in Wellington allowed this work to be presented to a wider audience of officials.

The seminar also brought back to New Zealand three overseas experts in the field. Beyond that, two very senior officials, Brian Pink, Government Statistician, and Roger Hurnard of The Treasury, reviewed the seminar's discussions and verbally presented papers on the applications of the methods to policy analyses in New Zealand, discussing, *inter alia*, the data and other needs. Officials from a wide range of "population-oriented" policy ministries also presented papers, and/or intervened in the discussions. This allowed a major objective – a roundtable review of the use of such methods and an exchange of information about them to be diffused not only to academics but also to officials.

The papers included in this special issue of *New Zealand Population Review* were presented at this international workshop. This Issue leads with an article on the likely benefits of using stochastic projections. Using New Zealand data to illustrate his argument, John Bryant makes a strong case for why, despite the huge investment it entails, stochastic population projection is worth considering. He discusses in simple terms the practical and methodological benefits that could accrue from using stochastic rather than conventional population projections.

A dominant approach to forecast mortality in demographic projections is Lee-Carter method. Of the two suggested variants to this approach, one was developed by Health Booth and her colleagues. In their paper, Booth, Tickle and Smith evaluate the two variants and the original Lee-Carter method of mortality forecasting. They test the three methods against time series data from 10 countries with reliable data series commencing in 1941 or earlier. Their analysis shows that two variants are better than the original method in both forecast accuracy and width of prediction interval.

Nico Keilman examines the impact of demographic uncertainty on future old age pensions in Norway. Keilman shows that not only is the net present value of old age pension likely to increase in the future, but also the uncertainty around the central values (eg. median net present value). More importantly, by 2050, the uncertainty in population size in Norway would be twice that of the net present value of old age pension.

One of the first attempts at a comprehensive stochastic population projection for New Zealand, covering mortality, fertility and migration, is provided by Tom Wilson. His results show that future population size of New Zealand is hard to forecast with any degree of certainty. For instance, the 80% confidence interval for population size in 2026 ranges from 4.4 to 5.1 million (an interval of 0.7 million), and by 2051 the interval widens further to 1 million.

In the last paper, Frans Willekens presents a new method for population projection. This is, unlike the macro stochastic population projection models used in other papers, based on a micro-simulation model. The new model combines demographic changes at the macro (or population level) and at the micro level. It uses the theoretical and methodological elements of multistate demography. Willekens presents the various approaches to functional population projection and provides a thick description of the multistate model.

We are delighted to be able to bring these papers to a wider research and policy community through the *New Zealand Population Review.* The international workshop at which earlier versions of the papers were presented was generously supported by a grant from SPEaR (Ministry of Social Development, Wellington), which also arranged and sponsored the larger, very heavily subscribed, public meeting of officials at the Royal Society of New Zealand's meeting room, and at which several of the overseas participants presented their papers. Additional financial support was provided by Waikato University, and from a FoRST research Grant, New Demographic Directions. An earlier version of part of this preface appeared in *SPEaR Bulletin.* We are grateful to the Population Association of New Zealand for providing space and support for this *Special Issue.*

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What Can Stochastic Population Projections Contribute to Policy Analysis?

JOHN BRYANT*

Abstract

The paper describes five ways in which stochastic population projections can contribute to policy analysis: (1) stochastic population projections provide a much richer characterization of demographic uncertainty than conventional projections; (2) stochastic projections are less likely than conventional projections to yield misleading results; (3) the results from stochastic projections are easier to explain to lay people; (4) stochastic projections permit a clear distinction between demographic uncertainty and policy options; and (5) stochastic population projections permit an appropriate division of responsibility between technical experts and policy practitioners.

Replacing conventional population projections with stochastic ones is a significant investment. Software needs to be written or modified. The technical, and rapidly evolving literature on stochastic projections needs to be read and absorbed. Formal analyses of historical demographic trends need to be carried out. Ways need to be found for managing and disseminating the voluminous output that stochastic population projections produce.

Statistical and policy agencies have alternative uses for their time. Rather than investing in stochastic population projections, statistical agencies could produce conventional projections more frequently, or for smaller geographical units. Policy agencies could analyse non-demographic determinants of social trends and fiscal pressures. Statistical and policy agencies need to be sure that stochastic population projects deliver benefits as least as great as these alternative activities.

This presents the promoters of stochastic projections with something of a Catch-22 situation. Stochastic projections are a new and largely untried

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technology, and many of their uses will only become apparent once they have been put to work on real policy issues. Nevertheless, by looking at examples of policy analyses using conventional projections, and the limited examples of analyses using stochastic projections, it is possible to identify some of the major potential advantages of stochastic projections. This paper discusses five potential advantages: (1) stochastic population projections provide a much richer characterization of demographic uncertainty than conventional projections; (2) stochastic projections are less likely than conventional projections to yield misleading conclusions; (3) the results from stochastic projections are relatively easy to explain to lay people; (4) stochastic projections permit a clear distinction between background uncertainty and policy options; and (5) stochastic population projections permit an appropriate division of responsibility between technical experts and policy practitioners.

Stochastic Population Projections Provide a Richer Characterization of Demographic Uncertainty

For policy analysts carrying out technical studies, an important advantage of stochastic projections is that they contain a great deal more information than traditional deterministic projections.

Stochastic projections yield thousands of realistic population scenarios that can be analysed much like a survey. To obtain the median expected population size in 2050, for instance, the analyst calculates population size in 2050 for each of the thousands of scenarios, and takes the median. To obtain the probability that the population size will be more than five million, the analyst calculates the proportion of projected population sizes that are more than five million.

In contrast, conventional population projections contain at most 10-20 stylized scenarios or “variants”, obtained by systematically varying fertility, mortality, and migration. One scenario (in recent Statistics New Zealand publications, Series 5) is designated as the “median” or “preferred” scenario. Rather than calculating a median or mean population size, the analyst looks at the “median” scenario. By identifying which scenarios produce 2050 populations over five million, the analyst can gain some sense of the fertility, mortality, and migration rates necessary to obtain a population of five million, and hence whether a population of five million is likely or not. But the degree of likelihood and the precise reasoning behind the evaluation is typically left ambiguous.

Policy analysts can add assumptions about non-demographic parameters, such as labour productivity or pension eligibility rules, to stochastic population projections to obtain probability distributions for policy outcomes. Lee and Tuljapurkar (2001), for instance, present a bar chart showing a probability distribution for the date that the US Social Security Trust Fund is exhausted. Lee's and Tuljapurkar's forecast assumes existing legislation will not change. The probability of the trust fund being exhausted between 2025 and 2035 (conditional on no changes in legislation) is about 50 per cent.

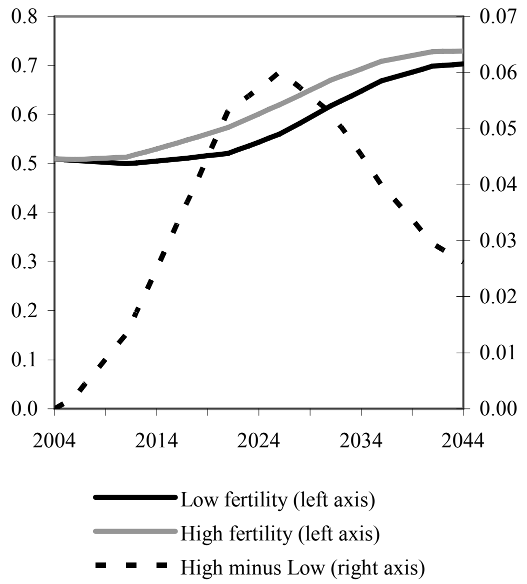
Analogous models can be built using conventional population projections. For instance, most analyses of the US Social Security Trust fund have been based on models that combine conventional population projections with non-stochastic versions of the assumptions made by Lee and Tuljapurkar. The New Zealand Treasury's Long-Term Fiscal Model is constructed along similar lines (Woods 2000). These models allow analysts to make the same sorts of conditional statements as conventional population projections. They allow analysts to say, for instance, that the health expenditure would be X per cent of GDP in 2051 if fertility were to stabilize at two births per woman, labour productivity were to grow at 1.5 per cent per annum, and so forth.

Models based on conventional population projections can provide important insights. For instance, the discovery that current fiscal trajectories in most developed countries are unsustainable was made using conventional models. Nevertheless, a statement that "under current policies, and assuming fertility rate a, mortality rate b, labour force participation rate c, productivity growth e, and expenditure adjustment f, outcome X will occur" contains a lot less useful information than a statement that "under current policies, outcome X has a 10 per cent chance of occurring". The second type of statement can only be produced by models that use stochastic population projections.

Stochastic Projections are Less Likely to Lead to Misleading Policy Conclusions

Consider a policy analyst who wants to assess the sensitivity of fiscal variable to demographic uncertainty. The analyst knows that the variable is affected by age structure, and recalls from some basic demographic training that age structure is strongly affected by fertility. The analyst therefore plugs the Statistics New Zealand high-fertility and low-fertility projections into the policy model to see what happens. The analyst uses results 40 years into the projection period, so that the differences in fertility rates will have time to take effect. The precise results from the model depend on which fiscal variable is used, but most fiscal variables are highly correlated with the dependency ratio, so the results for most fiscal variables will resemble the results for the dependency ratio shown in Panel (a) of Figure 1. Having examined a graph like Panel (a), a policy analyst is likely to conclude that the fiscal variable is insensitive to demographic uncertainty.

Figure 1: Projected dependency ratios



Source: Calculated from Series 2 (low fertility) and Series 8 (high fertility) of the Statistics New Zealand 2004-base population projections. The projections available at the Statistics New Zealand website www.stats.govt.nz.

Note: In the figure the dependency ratio is defined as the number of people aged 0-14 or 65 over, divided by the number aged 15-64.

As Panel (b) demonstrates, this conclusion is only partly correct. The difference between the high and low variants is only a third as large in the 2040s as it had been in the 2020s. In the decades after 2040, difference will eventually reach zero and then become strongly negative. These complicated dynamics reflect the fact that a rise in fertility raises the population's overall dependency in the short-term, by increasing the number of children, but lowers it in the long-term, by increasing the number of working-age adults. Comparing high and low variants 40 years into the future gives a highly misleading impression of the nature and magnitude of the effects of fertility on dependency.

Population dynamics are full of counter-intuitive effects such as these. A very common error, for instance, is to assume that two scenarios that differ substantially in terms of population size must also differ substantially in terms of age structure (Lee 1998). Having observed, that different migration rates lead to very different population sizes, it is easy to assume that different migration rates lead to very different age structures, which generally they do not.

Experience analysing population dynamics can help protect against the more obvious errors. But many policy analysts never have a chance to gain this experience. Careful checking can uncover idiosyncrasies in the population dynamics. For example, examining all available variants, rather than just the median and a couple of alternatives, can reveal which variants in fact have the biggest impact on outcomes. Constructing detailed graphs, like Panel (b) in Figure 1, can reveal patterns that are obscured by simple graphs like Panel (a). However, time is often short, and, when assumptions about policy variable are also included, the number of variants that need to be checked can become unmanageably large.

Stochastic population projections do not present the same sort of traps for the unwary. With conventional population projections, analysts have to draw conclusions from a few stylised variants; with stochastic projections, they have thousands of realistic variants. The possibility of being misled by quirks in individual variants is eliminated. When thousands of variants are used, all with fertility constantly varying, there is no chance that dependency ratios will appear less sensitive to fertility rates in 40 years time than they do in 20 years time. Similarly, there is no need to guess which variants have the greatest effect on age structure, since a stochastic projection derives results from all variants.

The reason why a dozen or so variants from a conventional projection are unmanageable while (with appropriate software) a few thousand variants from a stochastic projection are not is that variants from stochastic projections can be summarized using summary statistics. It makes no sense to calculate means, medians, quartiles or other summary statistics for conventional projections, since the variants from a conventional projection are not a representative sample of anything. Instead, the analyst has to examine all the individual variants. It does make sense to calculate summary statistics for stochastic projections since the variants in a stochastic projection are designed to be a representative sample of possible population futures. It is therefore quite appropriate to summarize results using, say, the median and 95 per cent prediction interval.

Results from Stochastic Projections are Easier to Explain to Lay People

The advantages discussed above are relevant mostly to technical analyses. These advantages are important to technical specialists carrying out research on policy issues. However, one of the distinguishing features of policy research, as opposed to academic research, is that the whole exercise is pointless unless the results can be disseminated to a lay audience. This audience includes government ministers, other officials, and the general public.

Few ministers, officials, and members of the general public have the appetite or the time for extended technical presentations. Results of an analysis often have to be boiled down to single paragraph and a single chart -- or less. A model or a method is therefore much more valuable to policy analysts if its findings can be easily explained.

At first sight, the need for simplicity might seem to count against stochastic projections. Constructing a stochastic population projection requires more complicated statistics and computer programming than constructing a conventional projection. The notion of using thousands of randomly generated scenarios is somewhat daunting.

Harder to construct does not, however, mean harder to understand. In fact, results from stochastic population are easier to understand than results from conventional projections. A statement that the New Zealand population has a 40 per cent probability of surpassing X million in the next 25 years is easier to understand, for instance, than a statement that if fertility was 2.2 births per woman and net migration was 10,000 per year, or if fertility was 2.0 births per woman and net migration was 15,000 per year, then the New Zealand population would surpass X million in the next 25 years. Thanks to weather forecasts, sports analyses, and even high school statistics, most people have become increasingly comfortable with probabilistic forecasts like the ones produced by stochastic population projections. In contrast, the conditional statements produced by conventional projections are unavoidably longer and more dependant on technical concepts such as births per woman or net migration.

For researchers, it is natural to assume that the audience will want to know something about the model or the methods of analysis. It is natural to assume, for instance, that the audience will be curious about how the probability distributions were generated. However, the first lesson of presenting technical results to non-technical people is that people are interested in the results but not the model.

It should be emphasized that the difficulty of understanding conventional projections is intrinsic to the method. It does not reflect any failing by Statistics New Zealand. In fact, the population projections produced by Statistics New Zealand are a model of how conventional projections ought to be done. The choice of scenarios is sensible, the explanations are clear, and users can easily obtain detailed information on outputs and inputs if they want it (see www.stats.govt.nz).

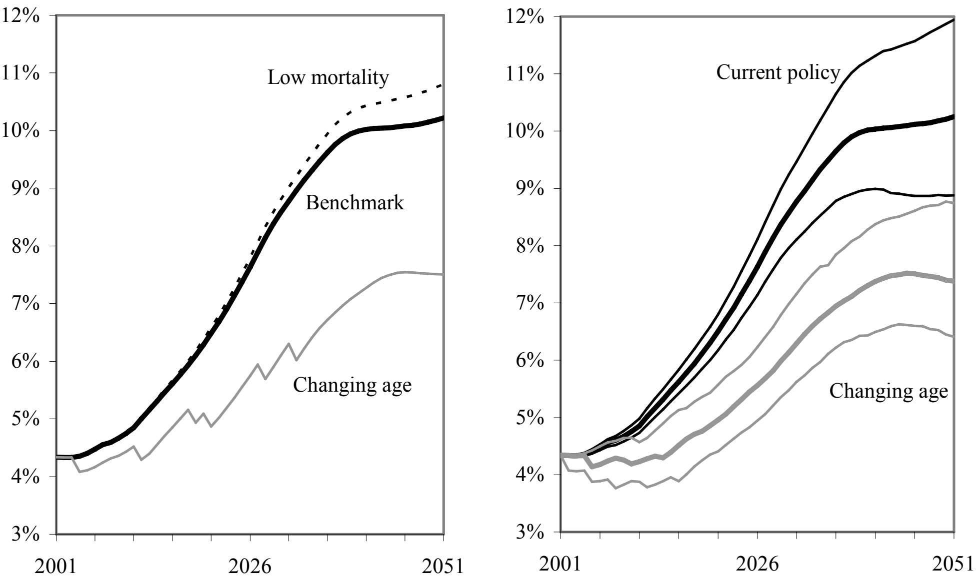
At the meeting where the papers in this volume were first presented, one of the participants noted that many policymakers dislike, or misunderstand, results from surveys that are presented using confidence intervals. The participant suggested that policymakers would react similarly to probabilistic forecasts. It is important to recognize, however, that the prediction intervals yielded by stochastic projections are different from confidence intervals, and easier to grasp. A confidence interval is a pair of random numbers that represent uncertainty about a non-random parameter whose true value will never be known. Even research professionals find this idea confusing. A prediction interval is essentially the same as the odds offered by a bookie.

If a policymaker insists on having a single number, then he or she can always be supplied with a mean or median. In some cases, however, it may be appropriate for the analyst to persist -- tactfully -- with efforts to signal the degree of uncertainty. The world is intrinsically uncertain, and good policies take account of this.

Stochastic Projections Permit a Clear Distinction Between Background Uncertainty and Policy Options

Figure 2 presents two graphs that show how tying the age of eligibility to increases in life expectancy would affect total expenditure on New Zealand Superannuation. (New Zealand Superannuation is a tax-funded universal pension currently available at age 65.) The precise details of the modelling do not matter for present purposes. The important point is the contrast between Panel (a), which is based on conventional population projections, and Panel (b), which is based on stochastic projections. Panel (b) is much more successful than Panel (a) at conveying the fundamentally important distinction between background variables and policy variables.

Figure 2: Expenditure on New Zealand Superannuation as a percent of GDP



Panel (a): Results based on conventional population projections
Panel (b): Results based on stochastic population projections
Note: The figure is only illustrative, and little weight should be placed on the precise values shown.

The solid line in Panel (a) represents the benchmark scenario in which all variables are set at their "medium" level and current policies are maintained. The dotted line represents the case where mortality is high, but everything else remains the same. Lines like this are typically included in policy analyses to demonstrate that uncertainty about background variables such as mortality leads to uncertainty about policy outcomes. The grey line represents the policy alternative where the age of eligibility rises with life expectancy, and everything else is the same as the benchmark variant.

The age of eligibility is a policy variable, while mortality is not. Anything a government does probably has some effect on mortality, but the effects are typically indirect, uncertain, and long-delayed. In contrast, the age of eligibility can be altered at will (subject to periodic approval from the electorate.) Policy analyses should always make a clear distinction between policy variables and "background" variables, and should direct the audience's attention towards the policy variables.

Panel (a) fails to do either of these things: it obscures the difference in status of the "low mortality" and "changing age" variants. This is because conventional populations projections give the analyst no choice but to use the same technique—the presentation of alternative variants—to depict background uncertainty and to depict policy options.

Panel (b) shows the sort of graph that can be produced from stochastic population projections. The heavy black line shows median expenditure under current policy; the lighter black lines show the 95 per cent prediction interval around this median. The three grey lines depict the alternative policy, whereby the age of eligibility is tied to life expectancy. Each policy is represented by a group of lines. Uncertainty about the background variables (which covers more than just mortality) is represented by the width of the prediction intervals.

The graph avoids any suggestion that policymakers can choose mortality rates in the same way that they can choose eligibility rules. It captures the idea that policymakers can choose between two policies, each of which leads to a different probability distribution for expenditures.

Stochastic Population Projections Permit an Appropriate Division of Responsibility

Conventional population projections are conditional. They show what would happen if fertility, mortality, and migration were to follow the assumed paths. The producers of the projections typically indicate that the median variant is more likely than the other variants, in the sense that actual fertility, mortality, and migration rates are more likely to resemble the rates assumed by the median variant than to resemble the rates assumed by the other variants. But it is up to the end user to decide whether a particular outcome has, say, a 10 per cent probability or a 50 per cent probability.

Policy analysts normally have to provide policy makers with unconditional recommendations such as “the existing number of maternity hospitals is sufficient”. When presented with a conventional population projection, analysts must therefore convert it into a forecast. For instance, when assessing future needs for maternity hospitals they need to decide whether it is plausible that fertility will remain at approximately two births per woman.

In most cases, policy analysts prefer not to make these sorts of decisions. They prefer to borrow other people’s published assumptions about uncertain variables rather than construct their own assumptions. Partly, this is a matter of expertise. Generalist policy analysts are wise to defer to technical specialists. However, a more fundamental motivation is the possibility that the analyst, or the analyst’s minister, may have to defend the analysis if it is criticized. Analyses are easier to defend when the assumptions about key variables were borrowed from reliable external sources. Conventional population projections deprive analysts of this source of protection.

In contrast to conventional projections, producers of stochastic population projections usually put their necks on the line and claim that their estimated probabilities are good approximations of the true probabilities. For instance, in their seminal paper presenting stochastic projections of US mortality, Lee and Carter (1992:659) write that they “intend [their] forecasts to be more than illustrative”. Similarly, in their article on global population growth, Lutz, Sanderson, and Scherbov (2001:543) state without further qualification that “there is around an 85 per cent chance that the world’s population will stop growing before the end of the century”. From a policy analyst’s point of view, this is an attractive division of responsibility. It is much easier, and safer, if the producers of the projections, rather than the users, assign probabilities.

Conclusion

Stochastic population projections offer significant advantages for conducting policy analyses and for explaining these analyses to others. Technical analyses are easier and safer when based on a large sample of realistic population variants, as produced by stochastic projections, rather than a handful of stylised variants, as produced by conventional projections. Although stochastic population projections are more difficult to carry out than conventional projections, their results are more intuitive. They also minimize confusion between policy choices and background uncertainty. Finally, stochastic population projections relieve users of the need to assess the plausibility of alternative outcomes.

These advantages mean that stochastic population projections are likely to become increasingly popular and influential. That does not mean that conventional population projections will disappear entirely. Experience may show that for some tasks conventional projections work best. But it does mean that policy analysts who currently use conventional population projections needs to start paying attention to stochastic projections.

Acknowledgements

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Evaluation of the Variants of the Lee-Carter Method of Forecasting Mortality: A Multi-Country Comparison

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LEN SMITH

Abstract

The Lee-Carter (LC) method of mortality forecasting is well known and widely used. Two recent variants are the Lee-Miller (LM) variant and the Booth-Maindonald-Smith (BMS) variant. Both aim to improve the performance of the method. These two variants and the original Lee-Carter method are evaluated using data for twenty populations for 1900-2001, with the fitting period ending in 1985 and the forecast period beginning in 1986. Forecast errors are compared and decomposed, and uncertainty is examined. For these short-term forecasts, the two variants are generally more accurate than the LC method with narrower prediction intervals; and BMS marginally outperforms LM on these criteria overall. Further evaluation using different fitting periods is required.

As Keyfitz observed in 1981, one might have thought that population forecasters would be obsessed with eagerness to see how well they have done in the past, and that users would demand reports on the error of current forecasts; but "no such obsession or demand is to be seen" (Keyfitz 1981:580). Population futures have always been a central concern of demographers and those who use their work, from the studies of Malthus in the eighteenth century to those of Pearl and Reed in the twentieth. But, perhaps as a result of the failure of these and other authors to correctly foretell the demographic future, demographers for most of the last century retreated into non-committal scenario-building projections: demographic forecasting based on formal statistical methods has developed only in the last two decades. Actuaries similarly are centrally concerned with the future survival of current lives, but again formal

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statistical methods of mortality forecasting are a comparatively recent development.

The publication of the Lee-Carter method (Lee and Carter 1992) marked the beginning of a new era of interest in mortality forecasting. Since then several other methods have been developed, but the Lee-Carter method is still regarded as among the best currently available and is now widely used. On the basis of this method, Tuljapurkar, Li and Boe (2000) identified a universal pattern of constant rates of mortality decline in the world's most developed countries, with rates of decline higher than those incorporated in official projections, leading to higher forecast levels of life expectancy.

The Lee-Carter method uses matrix decomposition to reduce annual age-specific death rates to a time-dependent index of level of mortality, and a set of time-independent parameters which modify the overall level at particular ages. It uses standard time series methods to model and forecast the level index over time. As with time-series-based forecasting in general, the philosophy of the Lee-Carter approach is that the past is the best guide to the future. Thus accurate modelling of past trends is an essential basis for forecasting future levels of mortality, and accurate modelling of the past variability of mortality is an essential basis for estimating the uncertainty of the forecast. In this context, a central issue is: *how much* of the past provides the best guide to *how much* of the future? Even in the context of a statistical forecast, judgment will be required to answer this question, but the objective is to minimise the role of judgement and maximise the role of formal theory on the one hand, and formal evaluation on the other.

Modifications to the Lee-Carter method have been proposed by Lee and Miller (2001) and Booth, Maindonald and Smith (2002). These address the choice of fitting period, the method for the adjustment of the level parameter and the choice of jump-off rates. The three variants of the Lee-Carter method have not been comprehensively evaluated. This paper presents the results of an evaluation of the Lee-Carter, Lee-Miller and Booth-Maindonald-Smith variants based on data by sex for ten countries. The evaluation involves fitting the different variants to data up to 1985, forecasting for the period since that date, and comparing the forecasts with actual mortality in that period.

The Three Variants

The Lee-Carter (LC) Method

The Lee-Carter method of mortality forecasting combines a demographic model of mortality with time-series methods of forecasting. The method is generally interpreted as making use of the longest available time series of data. The Lee-Carter model of mortality is

$$\ln m_{x,t} = a_x + b_x k_t + \varepsilon_{x,t} \qquad (1)$$

where $m_{x,t}$ is the central death rate at age *x* in year *t*, k_t is an index of the level of mortality at time *t*, a_x is a general pattern of mortality by age, b_x is the relative speed of change at each age, and $\varepsilon_{x,t}$ is the residual at age *x* and time *t*. The a_x are calculated as the average of $\ln m_{x,t}$ over time, and the b_x and k_t are estimated by singular value decomposition.

A second-stage estimation is then undertaken; this involves adjusting k_t by refitting to total observed deaths, D_t. This adjustment gives greater weight to ages at which deaths are high, thereby partly counterbalancing the effect of using logratres in the Lee-Carter model. After adjustment, k_t is extrapolated using the time series model

$$k_t = k_{t-1} + d + e_t \qquad (2)$$

where *d* is constant annual change in k_t, and e_t are uncorrelated errors. The combination of the standard errors in *d* and e_t represents the uncertainty associated with a one-year forecast. This is used to produce probabilistic prediction intervals for the forecast values of k_t. Forecast age-specific death rates are obtained using extrapolated k_t and fixed a_x and b_x. In this case, the jump-off rates (i.e. the rates in the last year of the fitting period or jump-off year) are fitted rates.

It should be noted that the Lee-Carter method does not prescribe the linear time series model of a random walk with drift for all situations. However, this model has been judged to be the most appropriate in almost all cases; even where a different model was indicated, the more complex model was found to give results which were only marginally different to the random walk with drift (Lee and Miller 2001). Further, Tuljapurkar *et al.* (2000) found that the decline in mortality was constant, i.e. k_t was linear, for the G7 countries, reinforcing the use of a random walk with drift as an integral part of the Lee-Carter method.

The Lee-Miller (LM) Variant

The Lee-Miller variant differs from this basic Lee-Carter method in three ways:

1. the fitting period is reduced to commence in 1950;
2. the adjustment of k_t involves fitting to e(0) in year t;
3. the jump-off rates are taken to be the actual rates in the jump-off year.

In their evaluation of the Lee-Carter method, Lee and Miller (2001) noted that for US data the Lee-Carter model did not perform particularly well when using the fitting period 1900-1989 to forecast the period 1990-1997. The main source of error was the mismatch between fitted rates for the last year of the fitting period (1989) and actual rates in that year; this jump-off error or bias amounted to 0.6 years in life expectancy for males and females combined (Lee and Miller:2001:539). Jump-off bias was avoided by constraining the model such that k_t passes through zero in the jump-off year.

It was also noted that the pattern of change in mortality was not fixed over time, as the Lee-Carter model assumes. Based on different age patterns of change (or b_x patterns) for 1900-1950 and 1950-1995, Lee and Miller (2001) adopted 1950 as the first year of the fitting period. This 'simple and satisfactory solution' (Lee and Miller 2001:545) to changing age patterns of change had been adopted by Tuljapurkar *et al.* (2000).

The adjustment of k_t by fitting to e(0) was adopted to avoid the use of population data as required for fitting to D_t (Lee and Miller 2001).

The Booth-Maindonald-Smith (BMS) Variant

The Booth-Maindonald-Smith variant also differs from the Lee-Carter method in three ways:

1. the fitting period is chosen based on statistical goodness-of-fit criteria under the assumption of linear k_t;
2. the adjustment of k_t involves fitting to the age distribution of deaths;

3. the jump-off rates are taken to be the fitted rates based on this fitting methodology.

Booth, Maindonald and Smith (2002) fitted the Lee-Carter model to Australian data for 1907-1999 and found that the 'universal pattern' (Tuljapurkar *et al.* 2000) of constant mortality decline as represented by linear k_t did not hold over that fitting period. In addition, problems were encountered in meeting the assumption of constant b_x in the underlying Lee-Carter model. Taking the assumption of linearity in k_t as a starting point, the Booth-Maindonald-Smith variant seeks to maximise the fit of the overall model by restricting the fitting period, which also results in the assumption of constant b_x being better met. The choice of fitting period is based on the ratio of the mean deviances of the fit of the underlying Lee-Carter model and of the overall linear fit: this ratio is computed for all fitting periods (that is for all years marking the start of periods, which always end in the jump-off year) and the period for which this ratio is substantially smaller than that for periods starting in previous years is chosen.

The procedure for the adjustment of k_t was modified. Rather than fit to total deaths, D_t, the Booth-Maindonald-Smith variant fits to the age distribution of deaths, $D_{x,t}$, using the Poisson distribution to model the death process and the deviance statistic to measure goodness of fit (Booth, Maindonald and Smith 2002). The jump-off rates are taken to be the fitted rates under this adjustment.

Data

The data for this study are taken from the Human Mortality Database (<http://www.mortality.org> or <http://www.humanmortality.de>) and the Australian Demographic DataBank (Australian Centre for Population Research). Ten countries were selected giving 20 sex-specific populations for analysis. The ten countries selected are those with reliable data series commencing in 1941 or earlier. It was desirable to use only countries for which the available time series of data commenced somewhat earlier than 1950 in order to maintain the full and consistent comparison of the three variants. Lee and Carter (1992) used US data for the full period available, 1900-1989. Therefore this multi-country analysis uses data for the period commencing in 1900 where possible. Though for some countries the data extend back to the nineteenth century, these were truncated at 1900. The Lee-Carter method could be interpreted as using all available data for the fitting period, but the use of pre-1900 data would both reduce comparability of methods across countries and necessitate a time series model with a non-linear trend which falls outside the scope of both applications to date and the current analysis. The selected countries are shown in Table 1 along with the dates used to define the fitting periods. The dates defining the start of the BMS fitting period were determined as part of the fitting procedure (Booth *et al.* 2002).

Table 1: Countries and years defining fitting and forecasting periods

Country	Start year				End year
	LC	LM	BMS [m]	BMS [f]	
Australia	1921	1950	1968	1970	2000
Canada	1921	1950	1974	1976	1996
Denmark	1921	1950	1968	1967	2000
England and Wales	1900	1950	1968	1972	1998
Finland	1941	1950	1971	1971	2000
France	1900	1950	1971	1969	1997
Italy	1906	1950	1968	1968	1999
Norway	1900	1950	1969	1963	2000
Sweden	1900	1950	1976	1969	2001
Switzerland	1900	1950	1962	1962	2001

Note: The fitting period is defined by start year to 1985; the forecasting period is defined by 1986 to end year.

The data consist of central death rates and mid-year populations by sex and single years of age to 110 years (except Australia to 100 years). For this analysis, data at older ages (age 90 and above) were grouped in order to avoid problems associated with erratic rates at these ages.

Methods and Measures

The three variants were fitted to periods ending in 1985 and used to forecast death rates from 1986 to the last year of available data (1996 to 2001, depending on the country). The variants are evaluated by comparing forecast and actual log death rates, forecast and actual life expectancy and forecast uncertainty.

For log death rates, forecasting error is measured in terms of absolute error (| forecast – actual |) and error (forecast – actual). These are averaged over forecast years to produce mean (absolute) errors indexed by age, and averaged over age to produce mean (absolute) errors indexed by year. Averaging over both year and age produces overall (absolute) error. Error in life expectancy (forecast – actual) is indexed by year, and averaging over years produces mean error in life expectancy. These overall measures may be further averaged across countries.

Components of differences in error are identified by comparing results based on relevant combinations of fitting period, adjustment method and jump-off rates. For example, the effect of jump-off error is measured by comparing two forecasts that are identical except for jump-off rates, one fitted and the other actual.

Uncertainty in the forecasts is derived from the standard error of k_t in the time series model (equation 2). Two components of uncertainty are distinguished: uncertainty due to innovation, in other words e_t, and uncertainty in the drift. From equation (1), the standard error of $\ln m_{x,t}$ is equal to the standard error of k_t multiplied by the constant b_x. (Note that Lee and Carter (1992:670) found the standard errors of a_x and b_x to become less significant over forecast time in comparison to the standard error of k_t and that by 10 years into the forecast of US mortality 98 per cent of the standard error of e(0) was accounted for by uncertainty in k_t.) As $\ln m_{x,t}$ are on a common scale for given age, it is possible to compare standard errors in $\ln m_{x,t}$ between variants, sex and countries for given ages, and hence for derived statistics covering the entire age range. Such comparisons are only slightly affected by the differing levels of mortality among the 20 populations and different fitting periods of the three variants.

Each $\ln m_{x,t}$ is a stochastic process determined by the stochastic process k_t. Hence, ignoring error terms, $\varepsilon_{x,t}$, the variations in $\ln m_{x,t}$ are perfectly correlated across age. (Errors in a_x and b_x are not taken into account.) This means that the prediction interval for life expectancy and other life table functions can be derived directly from the prediction interval for k_t without having to worry about the cancellation of errors. The approach adopted to comparing uncertainty in life expectancy is to take their 95 per cent prediction intervals. These are asymmetric due to the log transform and the transformation involved in the life table. Again, these prediction intervals are roughly comparable among populations.

In what follows, the three variants are referred to as LC, LM and BMS. The three fitting periods are referred to by "long", "1950" and "short", reflecting the variable length in the LC and BMS variants and fixed length in LM. The three adjustment methods are referred to by "D_t", "e(0)" and "$D_{x,t}$" (see above).

Forecast Evaluation of the Three Variants

Findings based on overall absolute error in log death rates for the 20 populations considered (Table 2) show that LM and BMS are more accurate than LC. Relative to LC (Table 3), most overall absolute errors are in the range 30 to 70 per cent. Of the three variants, BMS has the lowest error for 15 of the 20 populations, as well as the lowest average error for both females and males.

An additional finding is that LC consistently underestimates mortality, especially for females, as indicated by the negative average overall error (Table 4). LM and BMS do not show a marked tendency to over- or under-estimate, and have overall errors closer to zero.

Across the age range, patterns of error in the log death rates are similar across different countries so an average of all countries is shown in Figure 1. Errors are small and show no consistent age pattern for LM and BMS apart from a tendency to overestimate for males at ages 45+. The LC method produces large negative mean errors at the younger ages, particularly for females, and small positive mean errors at the older ages. This is due to the fact that the longer LC fitting period produces estimates of b_x that do not reflect the age pattern of change in the forecasting period. The dominance of the large negative errors at the younger ages accounts for the overall underestimation observed for LC in Table 4.

Table 2: Overall absolute error by sex, variant and country

Country	Female			Male		
	LC	LM	BMS	LC	LM	BMS
Australia	0.306	0.149	0.120	0.485	0.178	0.136
Canada	0.242	0.094	0.107	0.296	0.097	0.105
Denmark	0.307	0.238	0.215	0.184	0.217	0.190
England and Wales	0.272	0.114	0.095	0.384	0.132	0.107
Finland	0.667	0.276	0.265	0.559	0.207	0.193
France	0.360	0.100	0.093	0.361	0.123	0.118
Italy	0.355	0.152	0.151	0.258	0.177	0.189
Norway	0.733	0.190	0.180	0.217	0.201	0.178
Sweden	0.708	0.189	0.192	0.254	0.212	0.177
Switzerland	0.529	0.208	0.186	0.266	0.191	0.172
Average	0.448	0.171	0.160	0.326	0.174	0.156

Note: Overall absolute error is the mean over age and year of the absolute error in log death rates.

Table 3: Overall absolute error relative to LC by sex, variant and country

Country	Female			Male		
	LC	LM	BMS	LC	LM	BMS
Australia	1.00	0.49	0.39	1.00	0.37	0.28
Canada	1.00	0.39	0.44	1.00	0.33	0.35
Denmark	1.00	0.77	0.70	1.00	1.18	1.04
England and Wales	1.00	0.42	0.35	1.00	0.34	0.28
Finland	1.00	0.41	0.40	1.00	0.37	0.34
France	1.00	0.28	0.26	1.00	0.34	0.33
Italy	1.00	0.43	0.42	1.00	0.69	0.73
Norway	1.00	0.26	0.25	1.00	0.93	0.82
Sweden	1.00	0.27	0.27	1.00	0.83	0.70
Switzerland	1.00	0.39	0.35	1.00	0.72	0.65
Average	1.00	0.38	0.36	1.00	0.53	0.48

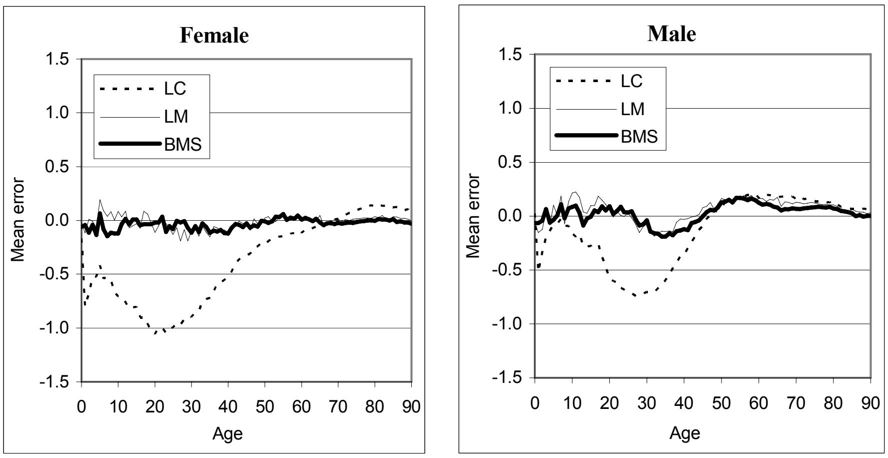
Note: Overall absolute error is the mean over age and year of the absolute error in log death rates. The country average is the ratio of the average errors.

Table 4: Overall error by sex, variant and country

Country	Female			Male		
	LC	LM	BMS	LC	LM	BMS
Australia	-0.170	0.052	0.004	-0.256	0.102	0.042
Canada	-0.221	-0.022	-0.058	-0.146	0.026	-0.055
Denmark	-0.231	0.040	0.038	0.074	0.133	0.111
England and Wales	-0.221	0.002	0.016	-0.247	0.035	0.030
Finland	-0.614	-0.167	-0.168	-0.410	0.004	-0.044
France	-0.272	0.020	0.030	-0.208	0.064	0.058
Italy	-0.265	-0.059	-0.083	-0.078	-0.001	-0.032
Norway	-0.675	-0.001	-0.041	0.121	0.094	0.106
Sweden	-0.644	-0.006	-0.047	-0.094	0.075	-0.006
Switzerland	-0.461	-0.015	-0.020	-0.121	0.027	0.029
Average	-0.377	-0.016	-0.033	-0.136	0.056	0.024

Note: Overall error is the mean over age and year of the error in log death rates.

Figure 1: Mean error by age, by sex and variant, averaged across countries



Note: Mean error is the mean over years of error in log death rates.

Although LC underestimates overall mortality when measuring error in log death rates, this does not necessarily translate into an overestimate of life expectancy, due to the variation in the magnitude and sign of errors over age. Table 5 shows that LC and, to a lesser extent, BMS do overestimate female life expectancy. All variants underestimate male life expectancy, due to the overestimation of mortality at the older ages observed in Figure 1. For this measure, in contrast to the overall absolute error measure, LC results do not appear to be substantially inferior to those for LM and BMS: this is because the large negative and positive errors in different parts of the age range partly cancel.

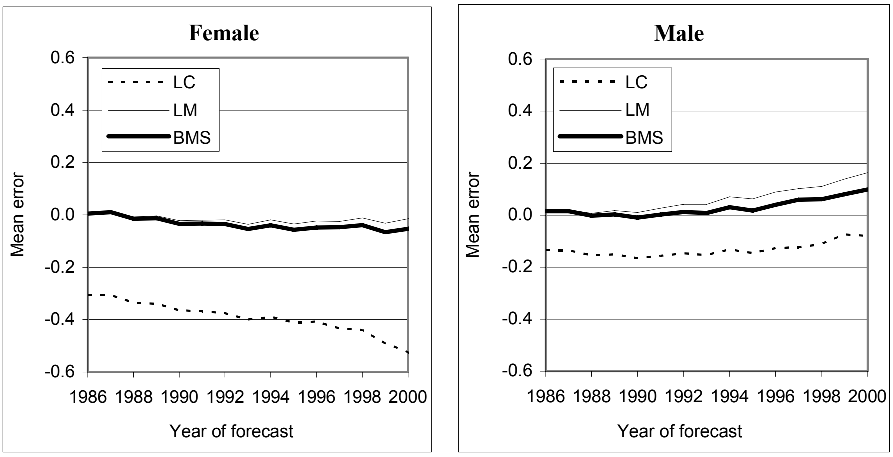
Table 5: Mean error in life expectancy by sex, variant and country

Country	Female			Male		
	LC	LM	BMS	LC	LM	BMS
Australia	-0.70	-0.77	-0.11	-1.06	-1.53	-0.59
Canada	0.33	0.30	0.32	-0.49	-0.53	0.18
Denmark	1.26	0.49	0.40	-0.73	-1.10	-1.18
England and Wales	0.04	-0.46	-0.42	-0.48	-0.97	-0.78
Finland	0.79	0.48	0.82	0.14	-0.61	-0.11
France	-0.32	-0.43	-0.29	-0.40	-0.88	-0.76
Italy	-0.65	-0.52	-0.26	-1.24	-1.06	-0.74
Norway	0.90	0.10	0.44	-1.33	-1.50	-1.13
Sweden	0.61	0.12	0.15	-0.73	-1.33	-0.64
Switzerland	0.76	0.33	0.57	-0.03	-0.46	-0.32
Average	0.30	-0.04	0.16	-0.64	-1.00	-0.61

Note: Mean error in life expectancy is error averaged over years.

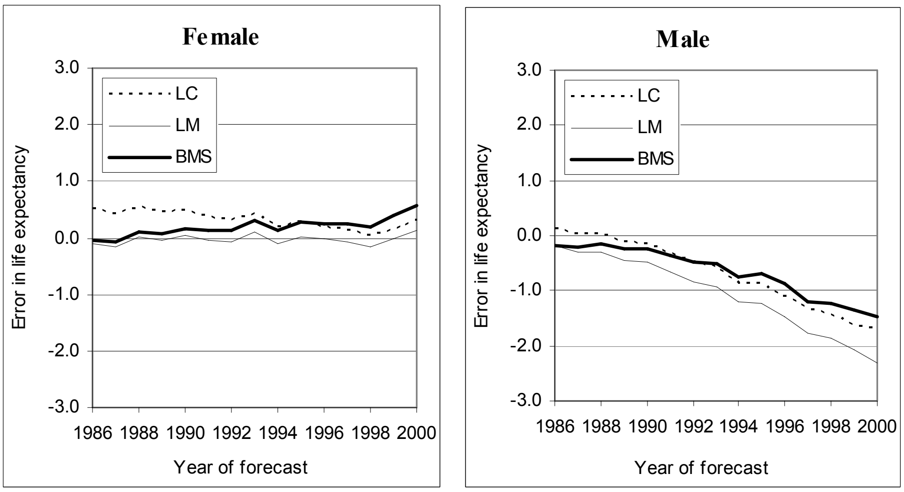
Over time, the pattern of mean error varies by population. However, some consistent trends can be discerned. LC errors almost always start with a sizeable negative in the first year and remain negative throughout the entire duration of the forecast. BMS errors are typically very close to zero in the first year of the forecast, indicating minimal jump-off error. Both LM and BMS usually remain reasonably close to zero for the duration of the forecast (though this is not the case for all populations). Figure 2 averages across countries, but gives a sense of the general pattern. All three variants give a reasonably good approximation of life expectancy for females over the forecast period (Figure 3). The 1950 start year for LM gives the most appropriate rate of improvement in life expectancy: LC gives a slightly too gradual improvement (and also has a significant positive jump-off error) and BMS is slightly too steep. The rate of improvement in male life expectancy is underestimated by all three variants: the shorter fitting period for BMS gives the best results except in the very early years.

Figure 2: Mean error by forecast year, by sex and variant, averaged across countries



Note: Averages from 1996 to 2000 include a decreasing number of populations (see Table 1). Since only two countries have data to 2001, results have been shown to 2000 only.

Figure 3: Error in life expectancy by forecast year, by sex and variant, averaged across countries

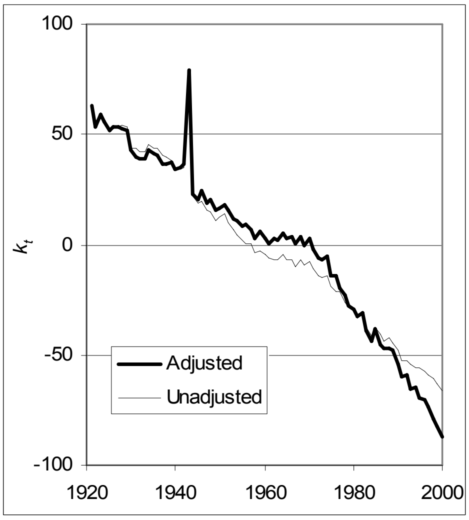


Decomposition of Differences among the Three Variants

Differences in error between variants can be decomposed into three components corresponding to the source of error: fitting period, method of adjustment and jump-off rates. These are inter-related. The choice of method of adjustment is independent of the two other components. Choice of fitting period (or start year) is independent of other considerations for LC and LM, but for BMS is dependent on the shape of fitted k_t, which in turn is influenced to a small extent by the method of adjustment particularly where deviations from linearity occur (see Figure 4). For LC and BMS, jump-off error or bias is dependent on both fitting period and method of adjustment (see below).

These error components are examined in order of dependence. The most dependent component, jump-off error is discussed first. After its removal, the effect of fitting period is discussed. Finally the net effect of adjustment method is considered.

Figure 4: k_t and adjusted k_t (by fitting to $D_{x,t}$) for Australia, both sexes combined, 1921-2000



Jump-off Bias

Jump-off bias derives from the error in the fit of the underlying Lee-Carter model after adjustment of k_t. In terms of log death rates (see equation 1), it is equal to $\varepsilon_{x,t}$ in the jump-off year (i.e. 1985). For the LM variant, this error is zero because actual rates are used as jump-off rates. In the LC and BMS variants, the size of $\varepsilon_{x,t}$ in the jump-off year is determined by the goodness of fit of the Lee-Carter model which is dependent on the fitting period (or start year) as well as the adjustment of k_t.

Jump-off error is thus a constant quantity over forecast years in terms of log death rates and death rates. It results in a bias in life expectancy in the jump-off year (termed jump-off bias); however, the size of this effect will not remain constant over forecast years because of entropy of the life table.

Figure 5 shows size of jump-off bias in life expectancy for LC and BMS for the 20 populations. The bias is much greater for LC than BMS, and greater for females than males. For females, LC bias is as large as 1.19 years (for Norway), whereas BMS bias is at most 0.15 years. While in most cases jump-off bias for the LC variant is positive, it is less consistent in direction for BMS.

Figure 5: Jump-off bias in life expectancy by sex and country, LC and BMS variants

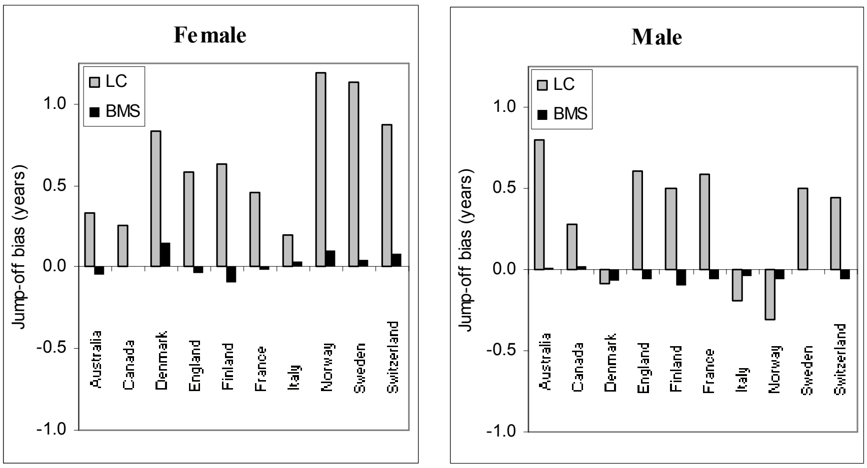


Table 6 shows the effect of jump-off bias on overall absolute error for the LC and BMS variants. The magnitude of the average effect of bias is greatest for LC: the effect for BMS is only 4-7 per cent of that for LC. Jump-off bias also accounts for a greater proportion of average overall error in the LC variant than in the BMS variant: for LC, jump-off bias accounts for 57 per cent of overall error for females and 42 per cent for males compared with 11 and 4 per cent respectively for the BMS variant. Unlike LC, however, in the case of BMS jump-off bias serves to reduce average overall error, indicating that for absolute error, at least, fitted rates provide a better jump-off point than actual rates.

Table 6: Magnitude and relative size of effect of jump-off bias on overall absolute error by sex, variant and country

Country	Female				Male			
	Bias		% of total error		Bias		% of total error	
	LC	BMS	LC	BMS	LC	BMS	LC	BMS
Australia	0.139	-0.021	45.4	-17.1	0.283	-0.004	58.5	-3.2
Canada	0.132	-0.012	54.5	-11.6	0.184	0.002	62.3	1.9
Denmark	0.085	-0.031	27.8	-14.2	-0.009	-0.028	-4.8	-14.6
England and Wales	0.145	-0.018	53.4	-18.9	0.220	-0.008	57.2	-7.4
Finland	0.308	-0.036	46.2	-13.7	0.222	-0.015	39.7	-7.7
France	0.247	0.002	68.7	1.8	0.225	0.012	62.4	10.5
Italy	0.184	0.008	51.7	5.0	0.078	0.023	30.4	12.4
Norway	0.507	-0.023	69.2	-13.0	0.032	0.000	14.8	-0.2
Sweden	0.495	-0.023	69.9	-12.1	0.062	-0.021	24.3	-12.0
Switzerland	0.300	-0.025	56.7	-13.7	0.071	-0.017	26.7	-9.9
Average	**0.254**	**-0.018**	**56.8**	**-11.3**	**0.137**	**-0.006**	**42.0**	**-3.6**

Country comparison shows that there is general consistency within variant in the direction of the effect of jump-off bias, especially for LC and females, but considerable variation in magnitude. For males, the effect of bias for LC ranges from –0.009 for Denmark to 0.283 for Australia, while for BMS the range is –0.028 for Denmark to 0.023 for Italy. Corresponding ranges for females are 0.085 for Denmark to 0.507 for Norway, and –0.036 for Finland to 0.008 for Italy. On average bias is greater for females than males. For LC, there is no pattern between the sexes, but for BMS there is a tendency for the sexes to follow similar patterns across countries.

Fitting Period

The effect of different fitting periods is essentially measuring the effect of different trends in k_t. Average overall absolute errors net of jump-off bias are shown in Table 7. The marginal effects due to fitting period are small in comparison with jump-off bias for LC but are commensurate with jump-off bias for BMS. It is seen that average overall absolute error is greatest for the long fitting period; in other words, reducing the fitting period results in reduced error. Whether the 1950 or short fitting period is most advantageous is unclear: for females, error is smallest for the fitting period starting in 1950 while for males error is smallest for the short fitting period.

Table 7: Average overall absolute error net of jump-off error by sex and variant

Fitting period	Female			Male		
	Adjustment			Adjustment		
	D_t	e(0)	$D_{x,t}$	D_t	e(0)	$D_{x,t}$
Long	0.194	0.189	0.190	0.189	0.187	0.186
1950	0.171	0.171	0.171	0.175	0.174	0.174
Short	0.180	0.178	0.179	0.167	0.162	0.162

The short period would be expected to produce smaller errors if the short term trend were a better guide than the longer term trend to the future. Thus, use of the short period might be expected to result in smaller errors than use of 1950. The fact that this is not the case for females (in absolute error terms) suggests that the post-1985 trend differed from that up to 1985.

Country comparisons shown in Table 8 show that the reduction in overall absolute error due to the use of a fitting period starting in 1950 or a short fitting period is fairly consistent across countries. Of the 20 populations, 14 show reductions in error due to reductions in length of fitting period, and in nine of these the short fitting period gives greater reductions in error. Denmark is a notable exception for both sexes, with both increases in error and greater increases for the short fitting period than the 1950 fitting period. It should be noted, however, that there were difficulties in using the method for Denmark with the chosen fitting and forecasting periods due to the erratic nature of k_t in the later part of the fitting period. For Swedish males, the reduced period also resulted in greater error; in this case the 1950 fitting period produced the greater effect. In a further three cases, inconsistent results were obtained: for Canadian and Swedish females, the 1950 fitting period improved forecast accuracy, while the short fitting period resulted in greater error; and for Norwegian males the reverse was true.

Table 8: Effect of fitting period relative to LC on overall absolute error by sex, country and method of adjustment

Adjustment:	D_t		e(0)		$D_{x,t}$	
Fitting period:	**1950**	**Short**	**1950**	**Short**	**1950**	**Short**
			Female			
Australia	-0.0169	-0.0265	-0.0182	-0.0260	-0.0169	-0.0262
Canada	-0.0163	0.0149	-0.0148	0.0121	-0.0154	0.0110
Denmark	0.0166	0.0253	0.0179	0.0231	0.0164	0.0246
England & Wales	-0.0131	-0.0136	-0.0101	-0.0097	-0.0103	-0.0104
Finland	-0.0888	-0.0566	-0.0706	-0.0442	-0.0754	-0.0481
France	-0.0125	-0.0213	-0.0112	-0.0198	-0.0113	-0.0200
Italy	-0.0201	-0.0256	-0.0186	-0.0286	-0.0177	-0.0269
Norway	-0.0345	-0.0218	-0.0246	-0.0135	-0.0226	-0.0102
Sweden	-0.0240	0.0037	-0.0156	0.0072	-0.0169	0.0090
Switzerland	-0.0210	-0.0170	-0.0162	-0.0123	-0.0177	-0.0140
Average	**-0.0231**	**-0.0138**	**-0.0182**	**-0.0112**	**-0.0188**	**-0.0111**
			Male			
Australia	-0.0215	-0.0615	-0.0229	-0.0596	-0.0233	-0.0614
Canada	-0.0145	-0.0092	-0.0137	-0.0080	-0.0115	-0.0059
Denmark	0.0276	0.0694	0.0252	0.0285	0.0251	0.0271
England & Wales	-0.0312	-0.0500	-0.0291	-0.0464	-0.0269	-0.0447
Finland	-0.1305	-0.1292	-0.1143	-0.1128	-0.1116	-0.1104
France	-0.0113	-0.0298	-0.0119	-0.0297	-0.0098	-0.0281
Italy	-0.0004	-0.0092	-0.0029	-0.0147	-0.0035	-0.0139
Norway	0.0188	-0.0083	0.0164	-0.0075	0.0173	-0.0063
Sweden	0.0195	0.0067	0.0193	0.0056	0.0207	0.0052
Switzerland	-0.0032	-0.0058	-0.0037	-0.0058	-0.0034	-0.0057
Average	**-0.0147**	**-0.0227**	**-0.0138**	**-0.0250**	**-0.0127**	**-0.0244**

Adjustment Method

Table 7 also allows comparison by method of adjustment. For the average overall absolute error measure, the effect of adjustment method is small compared with the effect of fitting period and jump-off bias, and in some cases is extremely marginal. For females, adjustment by e(0) produces least error for long and short periods while there is no difference for the fitting period starting in 1950. For males, adjustment by $D_{x,t}$ is marginally superior for the long fitting period. It can be concluded that adjustment method makes virtually no difference to the overall absolute error. This raises the question as to the usefulness of adjustment per se and the possibility that none of the adjustments improves the forecast over using unadjusted k_t.

Country comparisons again indicate a high degree of consistency in the direction of effect, but considerable variation among countries. There is no consistency in patterns between the sexes. Taking all comparisons across the 20 populations and three fitting periods, the D_t adjustment gives the lowest error in 13 cases, the e(0) the lowest error in 23 cases and the $D_{x,t}$ the lowest error in 24.

Uncertainty

Uncertainty is examined by comparing the 95 per cent prediction intervals for life expectancy. Table 10 shows lower and upper interval width in 1996, the latest year for which data are available for all countries, for LM and BMS relative to LC. For most countries, the intervals are reduced in width for both LM and BMS, despite the smaller number of observations. For females, the intervals are reduced on average by 20-40 per cent with the LM reduction being about 10 percentage points greater than the BMS reduction. For males, the reduction is as great as 60-70 percent with the BMS reduction being greater.

Table 9: Effect of adjustment method relative to D_t on overall absolute error by sex, country and fitting period

Fitting period:	Long		1950		Short	
Adjustment:	e(0)	$D_{x,t}$	e(0)	$D_{x,t}$	e(0)	$D_{x,t}$
			Female			
Australia	-0.0002	-0.0002	-0.0014	-0.0002	0.0003	0.0001
Canada	-0.0009	-0.0013	0.0005	-0.0005	-0.0038	-0.0053
Denmark	-0.0018	-0.0005	-0.0005	-0.0006	-0.0040	-0.0012
England & Wales	-0.0028	-0.0027	0.0002	0.0000	0.0011	0.0005
Finland	-0.0126	-0.0094	0.0056	0.0039	-0.0002	-0.0009
France	-0.0015	-0.0013	-0.0002	-0.0001	0.0000	0.0001
Italy	-0.0010	-0.0016	0.0006	0.0008	-0.0040	-0.0029
Norway	-0.0104	-0.0122	-0.0005	-0.0002	-0.0021	-0.0006
Sweden	-0.0083	-0.0071	0.0002	0.0000	-0.0048	-0.0018
Switzerland	-0.0048	-0.0036	0.0000	-0.0003	-0.0001	-0.0006
Average	**-0.0044**	**-0.0040**	**0.0004**	**0.0003**	**-0.0018**	**-0.0013**
			Male			
Australia	-0.0003	0.0003	-0.0016	-0.0014	0.0016	0.0003
Canada	-0.0009	-0.0029	-0.0001	0.0001	0.0003	0.0003
Denmark	-0.0008	-0.0011	-0.0032	-0.0036	-0.0417	-0.0434
England&Wales	-0.0036	-0.0051	-0.0015	-0.0008	0.0000	0.0002
Finland	-0.0159	-0.0190	0.0002	0.0000	0.0005	-0.0002
France	-0.0009	-0.0018	-0.0014	-0.0003	-0.0008	-0.0002
Italy	0.0007	-0.0002	-0.0018	-0.0033	-0.0048	-0.0050
Norway	-0.0001	0.0000	-0.0025	-0.0015	0.0007	0.0019
Sweden	0.0003	0.0005	0.0001	0.0017	-0.0008	-0.0010
Switzerland	0.0000	0.0000	-0.0005	-0.0003	-0.0001	0.0001
Average	**-0.0021**	**-0.0029**	**-0.0012**	**-0.0010**	**-0.0045**	**-0.0047**

In general, the smaller the prediction interval the better the method. However, if a variant were to over-fit the data, it would artificially reduce the standard error (it is also possible to underestimate the standard error due to model mis-specification). This is potentially more of a problem for BMS than LC and LM because of the selection of a shorter period in order to maximise the linear fit. However, as Table 10 shows, there is no consistent difference between LM and BMS in the amount of reduction in prediction interval width and the differences between these two variants are not great. Hence, either both BMS and LM over-fit the data or this is not an important issue. The latter view seems likely.

Table 10: Width of lower and upper prediction intervals in 1996 relative to LC intervals by sex, variant and country

Country	Female				Male			
	Lower interval		Upper interval		Lower interval		Upper interval	
	LM	BMS	LM	BMS	LM	BMS	LM	BMS
Australia	0.95	1.31	1.00	1.36	0.27	0.35	0.36	0.46
Canada	0.79	0.79	0.81	0.81	0.88	0.65	0.91	0.69
Denmark	0.68	0.66	0.72	0.67	1.01	0.07	0.63	0.05
England & Wales	0.50	0.53	0.56	0.59	0.48	0.48	0.55	0.55
Finland	0.87	1.17	0.90	1.25	0.45	0.50	0.53	0.59
France	0.41	0.43	0.45	0.47	0.17	0.12	0.21	0.15
Italy	0.40	0.46	0.44	0.50	0.30	0.26	0.33	0.30
Norway	0.88	0.87	0.95	0.97	0.48	0.39	0.31	0.45
Sweden	0.63	0.77	0.69	0.82	0.37	0.47	0.42	0.55
Switzerland	0.58	0.66	0.62	0.71	0.39	0.43	0.42	0.47
Average	**0.61**	**0.70**	**0.66**	**0.76**	**0.39**	**0.32**	**0.40**	**0.38**

The only true test of the forecast uncertainty is out-of-sample forecast accuracy. Examination of whether actual life expectancy falls within the prediction interval for all years shows that for females there are only eight instances when this is not the case. These all occurred for the lower prediction interval of the LC variant in the first five years of the forecast: Norway in 1986 to 1990, Sweden in 1986 and 1988 and Switzerland in 1986. For males, a different pattern occurs. First the LC prediction interval almost always contains actual life expectancy (except for Canada) while for LM and BMS there are a significant number of exceptions involving almost all countries. These all occur for the upper prediction interval and are mostly in the later years of the forecast. These are due to the unprecedented rapid decline in mortality that occurred among males during the forecast period in the countries concerned. In total, BMS has fewer occurrences than LM and the magnitude of excess over prediction interval is greater.

While for females, these results may indicate that the prediction intervals for LM and BMS could be too wide, for LC and all three variants for males the combination of jump-off bias and bias in estimated drift preclude determination of the accuracy of the prediction intervals.

Conclusion

It has been shown that the LM and BMS variants are superior to LC in both forecast accuracy and width of prediction interval. The decomposition of error has demonstrated that jump-off bias is a significant source of error for LC. These results confirm the findings of Lee and Miller (2001). In addition, the LC adjustment by fitting to D_t has been shown to be marginally inferior to the other two adjustment methods. It has also been shown that in a majority of cases, BMS is marginally superior to LM in accuracy and uncertainty.

These results are limited to the forecasting period and countries adopted. It is likely that they may be generalised to other developed countries. The extent to which they may be generalised to other forecasting periods is less clear. It has been shown that the accuracy of different forecasting methods is highly dependent on the particular period (Keyfitz 1991, Murphy 1995). In this comparison, the variants do not differ substantially, and it remains to be examined whether the details of the basic Lee-Carter method have a different effect in different forecasting periods.

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The Impact of Demographic Uncertainty on Liabilities for Public Old Age Pensions in Norway

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Abstract

The paper analyses the importance of demographic uncertainty for the net present value (NPV) of public old age pension obligations in Norway. A probabilistic population forecast is combined with a deterministic macro model for future pension expenditures. The model is applied to Norwegian data for the period 2003-2100. Under the current pension system, the liabilities are likely to grow by a factor of ten towards the end of the century. The demographic driving force is an assumed increase in the life expectancies of men and women by some 13-16 years over the next 95 years.

The results show also that long-run relative uncertainty is larger for total population than for the NPV, due to the enormous uncertainty in the number of births in the long run. In 2100, the 80 per cent prediction interval of population size is 1.5 times as wide as the median value. For the NPV, this relative uncertainty ratio is 80 per cent. Also for earlier years, the relative uncertainty in the NPV is approximately half that in population size. There is no single broad age group, in which relative uncertainty is similar to that in the NPV during the entire period.

After the Second World War, many Western countries developed general systems for the provision of public old age pensions. At that time, life expectancies for men and women were about ten years lower than nowadays. Falling mortality has led to longer periods over which retirees received their pension benefits. At the same time, early retirement and increased disability among older workers resulted in a fall in the actual age at which workers left the labour market. Shorter periods of active life in the labour market and longer periods of life spent as retiree resulted in problems connected to the sustainability of the public old age pension systems. As a result, a number of countries, including all OECD

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countries, have revised their pension systems, or are currently considering such a reform.

The performance of the public old age pension system depends strongly on the size and the age composition of the elderly population. Thus, any analysis of the future performance of such a system requires a reliable forecast of the elderly. The precise number of elderly in the future cannot be known in practice, but certain numbers are more probable than others. In other words, a probabilistic approach is required, and the population forecast to be used in the pension analysis should be given in the form of prediction intervals.

The purpose of this paper is to analyse how important demographic uncertainty is for the net present value (NPV) of public old age pension obligations of the Norwegian state. The NPV is a major variable in fiscal policy planning. When its value systematically exceeds the expected tax contributions targeted for public pensions, the pension system is not sustainable. In that case, contributions have to be raised, benefits have to be reduced, or both. If such changes in pension parameters are not sufficient or not feasible, the pension system has to be reformed. Whether a reform is necessary or not, an important question is for how long demographically induced uncertainty can be neglected. To put it differently, how long in advance can one discover early signals that warn us that a pension reform is required, or that pension parameters have to be adjusted?

When one assumes fixed benefits under the current pension system in Norway, the average contribution rate of employees has to increase from 10 per cent of current wages to 23 per cent in 2050 and 30 per cent in 2100. Relative to the Mainland GDP (MGDP), old age pension expenditures will grow from currently 6 per cent to 15 per cent in 2050. Other age-related expenditures are also expected to increase -- for instance, an estimated three percentage point increase to 2050 due to health care. It is unrealistic to assume that a stronger tax burden, neither for individual taxpayers nor for the private sector, can be used to avoid a deficit. Thus, in January 2004, the Norwegian Pension Commission proposed a major pension reform (see Pension Commission:2004).[1] In their analysis of the current obligations of the Norwegian state concerning old age pensions, the commission published deterministic projections of the NPV up to 2100. We will take a stochastic perspective, and present the predictive distribution of the future NPV in selected years, resulting from the predictive distribution of the population in those years. Pension variables are deterministic, including the remaining life expectancy at each age (the period over which pension rights are discounted). Only the age pyramid is stochastic.

Under the current system, Norwegian public old age pensions have a strong PAYG-component, and pension rights depend on two factors: work history, and labour income. Contributions come from employers, employees (through general taxes), and directly from the state budget. The legal retirement age is 67. In practice, many workers leave the labour market before that age, due to disability pensions or early retirement.

Stochastic Demographic Forecast to 2100

Point Predictions

Expected values for key parameters to 2100 were borrowed from Statistics Norway's long-term demographic projections (see Brunborg and Texmon: 2003). These projections are of the cohort-component type. TFR, life expectancy and net immigration to 2100 are in principal straight-line extrapolations of assumed values in Statistics Norway's official forecast for the period 2002-2050, published in 2002 (http://www.ssb.no/emner/02/03/ folkfram/). Table 1 summarizes these key parameters. Inger Texmon kindly provided us with unpublished data.

Table 1: Assumptions in Statistics Norway's long-term population projection

	Registered	Low	Medium	High
1. Total Fertility Rate				
2001	1.78			
2002	1.75	1.74	1.75	1.77
2050		1.40	1.80	2.20
2100		1.07	1.80	2.53
2. Life expectancy at birth, men				
2001	76.2			
2002	76.5	76.0	76.3	76.6
2050		81.6	84.2	86.7
2100		87.6	92.1	96.0
3. Life expectancy at birth, women				
2001	81.5			
2002	81.5	81.4	81.6	81.9
2050		86.0	88.1	90.0
2100		90.9	94.8	97.4
4. Net immigration				
2001	7,955			
2002	17,200	16,000	18,000	19,000
2003	11,300	9,000	15,000	20,000
2004-2100		6,000	13,000	20,000

Specification of Demographic Uncertainty

We used uncertainty parameters from the UPE-project "Uncertain Population of Europe" (see http://www.stat.fi/tup/euupe/) in which annual stochastic population forecasts were computed starting on 1 January 2003 (assumed to be known) to the year 2050 for 18 European countries, including Norway. For the purpose of the current paper we extrapolated Norwegian uncertainty parameters until 2100.

UPE obtains quantified uncertainty of a demographic forecast by applying the cohort-component book-keeping model a large number of times, typically 3,000 or 5,000 times, with a deterministic jump-off population, and stochastically varying values for age-specific mortality, age-specific fertility, and net migration. The method is based on the so-called scaled model for error (Alho and Spencer 1997). The main characteristics of the model in the current application are qualitatively as follows:

- Uncertainty in age-specific mortality and age-specific fertility was treated in the relative (logarithmic) scale; for net-migration uncertainty was treated in the additive scale.
- Uncertainty was assumed to increase with forecast year based on empirical analyses. Error increments were scaled such that they represented increasing patterns of error variances.
- Error increments of each age and sex group have a constant non-negative autocorrelation estimated from the data. Similarly, cross-correlation of errors across age were represented by an AR(1) process with empirically estimated correlations between neighbouring ages.
- Correlation between error increments in male and female mortality, in each age, was included.
- Correlation between errors in male and female net migration was included.
- Uncertainty in fertility, mortality, and migration were assumed to be independent of each other.
- A normal distribution was used to represent error increments for each age- and sex-group.

The UPE-forecast assumptions were based on three separate sources.

1. Time series analyses of age-specific (and total) fertility; age- and sex-specific mortality and life expectancy at birth; net migration by age and sex, relative to total population size.
2. Analyses of historical forecast errors for total fertility, life expectancies, and net migration.
3. Interviews with experts for fertility, mortality, and migration.

(See Alders *et al.* (forthcoming) for details on the UPE assumptions).
For Norway, the following specification was chosen in the UPE project.

Mortality
Scales for error increments were specified so they depended both on age and forecast year. The scales were estimated from long-term data series from Austria, Denmark, Finland, France, West Germany, Italy, the Netherlands, Norway, Sweden, Switzerland, and the U.K. The estimates were based on the median level of uncertainty in the past, averaged across countries. Autocorrelation of error increments was 0.05. Cross-correlation across age was 0.95. Cross-correlation across sexes was 0.85.

Fertility
Scales for error increments were specified so they depended on forecast year but not on age. Total fertility rate was used to obtain the estimates. Initial values for the scales were estimated from the data for 1990-2000, by calculating the standard deviation of first differences (log-scale). Eventual value for the scales was obtained from long-term data series for Denmark, Finland, Iceland, the Netherlands, and Sweden. The initial value was limited to the eventual value linearly. Autocorrelation of error increments was zero, ie. log(TFR) was assumed to be a Random Walk. The cross-correlation across age was 0.95.

Net Migration
Uncertainty in net-migration was specified in terms of total net migration. Scales were determined by connecting an estimate of past variability to a judgmentally chosen ultimate value. Norway relies on population registers as the source of population data, and thus the uncertainty of net migration was set to zero for year $t = 2003$. Autocorrelation of error increments for Norway was 0.56. Cross-correlation in net migration error between males and females, each year, was assumed to be 0.9. A schedule of empirically estimated gross migration levels by age and sex was estimated based on

data from Denmark (1998-2002), Norway (2000, 2002) and Sweden (1998-2002). It was used as a multiplier to derive the proportional level of uncertainty by age and sex. Thus, the cross-correlation across age was 1.0.

Demographic Results to 2100

We used Juha Alho's macro simulation program PEP ("Program for Error Propagation", see http://joyx.joensuu.fi/~ek/pep/pepstart.htm) to compute 5000 simulations of the population of Norway broken down by sex and one-year age groups. Populations as of 1 January 2004 to 1 January 2100 were forecasted. The population as of 1 January 2003 was the latest considered known.

Throughout the paper, we will present uncertainty for a certain forecast variable in terms of the width of the 80 per cent prediction interval for that variable. We prefer to use 80 per cent instead of the usual 95 per cent (at least in many econometric applications), since a 95 per cent prediction interval would reflect all possible values except for outliers, i.e. values that have a predictive value less than 2.5, or more than 97.5 per cent. The 80 per cent interval gives a better impression of where the major part of the probability distribution is located.

Table 2 presents selected results for the years 2050 and 2100. 80% L and 80 % H represent the lower and upper bounds of the 80 per cent prediction intervals. For reasons of comparison, the last column gives corresponding values from Statistics Norway's deterministic forecast to 2050, and the extrapolations by Brunborg and Texmon to 2100 (Medium Variant in both cases).

The central tendency of the predictive distributions for life expectancy is generally in agreement with the values for the medium variant of Statistics Norway's long term forecast, although the long-range life expectancy for men tends to be a bit low. The median population sizes in 2050 and 2100 are very close to the values predicted by Statistics Norway, and also the numbers of elderly agree very well.

Population size in 2100 shows huge uncertainty, with an 80 per cent prediction interval between 3.7 and 14.2 million. The most important factor here is the uncertainty in the number of live births, as reflected in the population aged 0. Young children contribute to the uncertainty, too. Further results are given in the "Results" Section.

Table 2: Results of stochastic population projections

	Mean	Median	Standard deviation	80% L	80% H	Stat Norway (medium)
Life expectancy, men (yrs)						
2050	84.0	84.0	3.38	79.6	88.3	84.2
2100	91.8	91.8	5.06	85.5	97.7	92.1
Life expectancy, women (yrs)						
2050	88.0	88.0	3.20	83.9	92.0	88.1
2100	95.0	94.8	4.96	89.5	100.3	94.8
Population size (mln)						
2050	5.75	5.63	0.87	4.75	6.87	5.6
2100	8.20	6.59	5.53	3.73	14.2	6.5
Population aged 0 (1000s)						
2050	69.5	60.6	38.9	31.7	118.9	59.5
2100	135.8	67.8	214.1	17.2	303.9	N/A
Population aged 67+ (1000s)						
2050	1.24	1.25	0.16	1.02	1.45	1.25
2100	1.76	1.73	0.43	1.24	2.32	1.8

N/A: Not available

Modelling Liabilities

The Pension Commission published the following projections of the Net Present Value of old age pensions.

Table 3: Projections of Net Present Value of old age pension obligations, billion NOK (2003 value)

2003	2004	2005	2010	2020	2030	2040	2050
2948	3074	3204	3917	5520	7295	9235	11554

Source: Pension Commission Table 10.3

The projections were obtained by means of a micro simulation model, which simulates the demographic, labour market, income, and pension histories of individuals. The NPV is based on an assumed discount rate of four per cent per year, and an annual wage increase equal to 1.5 per cent. Note that both the results of the Commission and our results reported below relate to the *current* pension system, not the proposed reform.

Instead of a micro simulation model, we will use a macro model to trace the consequences of population uncertainty for the NPV. We assume that expenses for old age pensions each year are equal to the average pension times the number of pensioners. The net present value of the current pension *obligations*, however, equals this year's pension expenses plus the net present value of all currently known future expenses, arising from the currently earned rights. The NPV is computed specifically for one-year age groups, both for current and for future pensioners.

One important assumption in this calculation concerns the number of years over which expenses are likely to accrue. We have assumed the following.

1. For all current pensioners, we use the 2004-value of the remaining life expectancy at each age. For future pensioners we use an estimate of the future remaining life expectancy for a 67-year old, from the date they reach 67. Because we assume falling mortality, this will be a higher number than today's remaining life expectancy for the 67 years old.
2. Pension rights are earned linearly from the year a person becomes 16, until his 56th year (or up to 70 years for a person earning income later than age 16). This is in accordance with current rules for pension earning time ("trygdetid"), according to which full pension rights are earned after a period of 40 years. We assume that the pension he receives when reaching 67 years of age is based on the average pension that future year. Data on future average pension are taken from table 3.9 of the Pension Commission's report. In case a person has had income over a period shorter than 40 years, the pension is reduced proportionally according to the number of years he has earned pension rights.

The net present value of the obligations is computed as the sum of all age-specific obligations. Let P_t be the average pension in terms of basic pension units in year t, and let G_t be the size in Norwegian Crowns (NOK) of that unit. Let e_x^t be the remaining life expectancy in year t for a person aged x, averaged across sexes, and rounded to the nearest integer. Let N_x^t represent the population aged x in year t, and let NPV_x^t be the net present value of pension obligations for the cohort that is x years old at 1 January of year t. Finally, r is the annual discount rate. Then for current pensioners we have that

$$NPV_x^t = G_t N_x^t P_t \sum_{i=0}^{e_x^t} \frac{1}{(1+r)^i}, \quad 67 \le \mathrm{x} \le 99, \tag{1}$$

where x = 99 indicates the open ended age group 99 and over.

For younger persons, we write k for the number of years until retirement (age 67) for the cohort currently aged x. Let v_x be the fraction of full pension earned, i.e. for a 25-year old v_{25} = (25-15)/40. Then

$$NPV_x^t = G_t N_x^t v_x P_{t+k} \sum_{i=0}^{e_{67}^{t+k}} \frac{1}{(1+r)^{i+k}}, \quad 16 \le x < 67. \tag{2}$$

The net present value of current obligations is then

$$NPV^t = \sum_{x=16}^{99} NPV_x^t. \tag{3}$$

With t =2004, r = 0.04, G_{2004} = 56861 NOK, an annual growth in G_t of 1.5 per cent, P_t from Table 3.9 of the Commission's report (interpolated where necessary), and N_x^t as observed for 1 January 2004, we obtained an NPV-value of 3074 billion NOK, which is the same as predicted by the Commission (see Table 3 above).

Results

Table 4 shows main results: median values, with the relative width of 80 per cent intervals in parentheses. The relative width is defined as the width of the interval divided by the median value. First we will discuss uncertainty, and compare the relative width of prediction intervals across variables and over time.

Of the five variables shown here, uncertainty in 2100 is largest for total population -- its 80 per cent prediction interval that year has a width that is 1.5 times as large as the median forecast. As indicated in Section 2, this is due to the enormous uncertainty in births and young children. Figure 1 shows how quickly the relative width of the 80 per cent prediction interval for age group zero accelerates during this century. This age group concerns the grand-grandchildren of children born today. Such a "multiple generation effect" is clearly less relevant for age groups 67+ and 80+. The relative width of the 80 per cent interval for these two groups is roughly between two-thirds and three-fourths. Yet the uncertainty for the 67+ accelerates somewhat around 2075, when the survivors of children born today disappear from that age group, and uncertainty caused by future fertility adds to that caused by future mortality and migration. The uncertainty connected to the Old Age Dependency Ratio, ie. the number of persons aged 67+ as a ratio of those aged 20-66, increases regularly over time to a level that is somewhat higher than that for the number of elderly. This is because the OADR is much more strongly influenced by immigration than the number of elderly is. Yet uncertainty in the OADR is much lower than that in total population, because the impact of fertility is less.

Table 4: Median values and relative width of 80 per cent prediction intervals (in parentheses) for selected population variables and pension liabilities

	2010	2025	2050	2075	2100
Population size (in millions)	4.73	5.13	5.63	6.10	6.59
	(0.023)	(0.117)	(0.377)	(0.839)	(1.586)
Elderly 67+ (in millions)	0.62	0.90	1.25	1.48	1.73
	(0.045)	(0.142)	(0.341)	(0.408)	(0.627)
Elderly 80+ (100 000)	215	254	522	672	858
	(0.097)	(0.337)	(0.646)	(0.698)	(0.750)
Old Age Dependency Ratio	0.212	0.296	0.395	0.448	0.498
	(0.049)	(0.160)	(0.385)	(0.709)	(0.992)
NPV (in billions NOK)	3 846	6 194	11 486	20 448	35 776
	(0.015)	(0.064)	(0.191)	(0.391)	(0.829)

The uncertainty in the NPV is of a similar magnitude as that in the number of elderly, although it accelerates strongly around 2075. It shares this phenomenon with the number of persons aged 67+, but the acceleration is stronger for the NPV. Figure 2 shows the predictive distributions of the NPV in 2050, 2075 and 2100.

Figure 1: Relative width of 80 per cent prediction interval for population variables

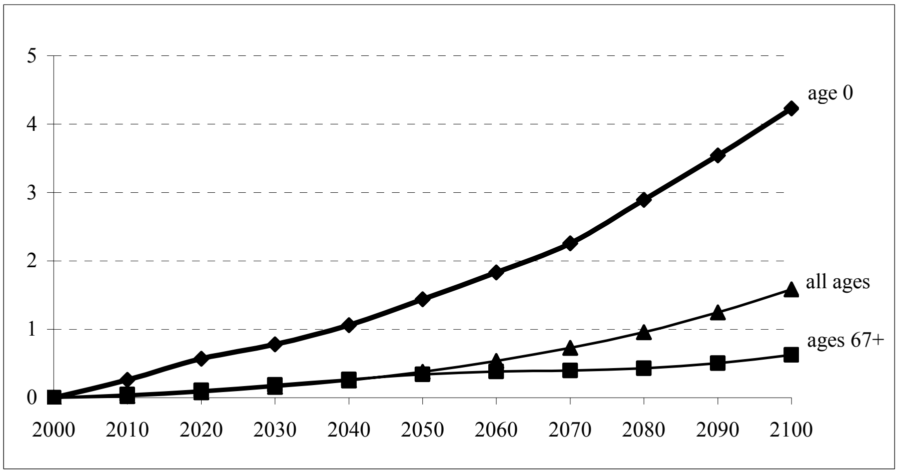
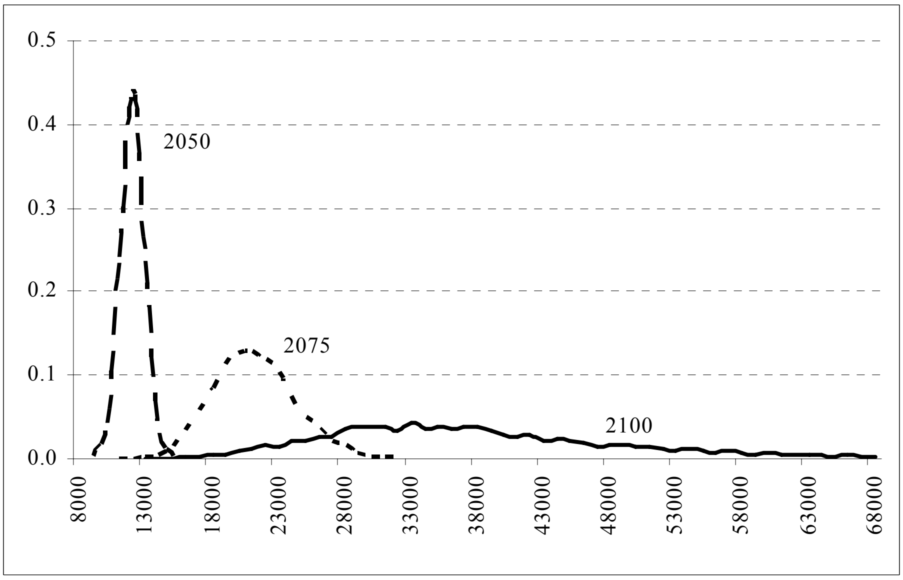


Figure 2: NPV (bln NOK) Predictive distribution



The expected value of the NPV increases regularly over time, from its current 3,074 billion NOK to 11,459 billion NOK in 2050 and 37,740 billion NOK in 2100. Our value for 2050 is very close to the one predicted by the Pension Commission: 11,554 billion NOK (see Table 3). The expected values for 2010 and 2025 are slightly lower than those of the commission. (The Pension Commission did not give predictions beyond 2050.) The predictive distribution for the year 2100 is so flat that it is hardly informative. One should be aware of the horizontal scale, of course – by compressing that scale, one could make the curve for 2100 as peaked as one wishes. But compared to the curves for 2050 and 2075, it is clear that the predictive distribution for the year 2100 reflects enormous uncertainty. Expressed as a ratio of the median forecast, the 80 per cent prediction interval of the NPV-distribution in 2100 is 0.83 -- four times that of the distribution in 2050 (see also Table 4).

How does uncertainty in the NPV compare with uncertainty in the age structure? In the current analysis the uncertainty in the NPV in any year in the future is fully determined by that in the population age structure N_x^t -- in other words, by the variance in each age group and the covariances across ages. Equations (1) to (3) show that the NPV is a weighted sum of the stochastic population sizes of subsequent age groups, with deterministic weights equal to the age-specific pension liabilities per capita. Through the reduction factor v_x, young workers get relatively little weight because they have rather short work histories. Pensioners over 67 contribute little to the overall NPV because they have rather short remaining life spans. Can the relative width of the 80 per cent prediction interval of the *NPV* be approximated by the relative width of that interval for a *certain age group*? If this were the case, a detailed pension model would be unnecessary since we could obtain a first impression of how fast the uncertainty in the NPV increases as a result of growing population uncertainty, by only inspecting population uncertainty.

The question of which age group, if any, might give a reasonable approximation is an empirical one. We have investigated a few selected age groups, and the results are given in Table 5.

In 2004, half the total liabilities were concentrated in ages 47-67. Table 5 gives the relative width of the 80 per cent prediction interval for the NPV and that of the population aged 47-67 in selected years. Comparing rows 1 and 2, we note that the relative uncertainty in the NPV can be approximated quite well by that in the population aged 47-67 during the first half of the century. In the second half of the century, however, this is no longer the case, since the NPV is less uncertain, in relative terms, than the population aged 47-67. Uncertainty in the latter grows rapidly after, because the children and grandchildren of currently unborn generations enter the age group 47-67.

Neither the retirees (row 3) nor the population of labour force age (row 4) give an accurate description of uncertainty in the NPV. The uncertainty in population aged 17-66 increases much faster than that in the NPV, as a result of the accelerating uncertainty attached to subsequent generations. For the population aged 67 and over, the increase is much slower than that in the NPV.

After some experimentation (not all results are reported here) we concluded that it is unlikely that one single age group is able to display the same relative uncertainty as the NPV for the entire 21st century. The changes in the age structure, in mortality, and in the pension rights per capita, result in a complex propagation of the forecast error in the NPV, as a result of the error in the population forecast. The population aged 47 to 67 can be used for the first half of the century only. In fact, the relative prediction interval in total population (row 6) shows a development over time that is closely parallel to that in the NPV – but this may be a mere coincidence.

Table 5. Relative uncertainty (width of 80 per cent prediction interval as a ratio of the median value) in NPV (all ages) and in population of selected age groups

	2010	2025	2050	2075	2100
NPV	0.015	0.064	0.191	0.391	0.829
POP 47-67	0.010	0.052	0.185	0.471	1.018
POP 67+	0.045	0.142	0.341	0.408	0.627
POP 16-66	0.022	0.086	0.309	0.803	1.577
POP 16+	0.018	0.071	0.237	0.612	1.216
POP all ages	0.023	0.117	0.377	0.839	1.586

The results in this paper are based on a number of assumptions. General assumptions for demographic variables for the underlying pension calculations and for uncertainty parameters were presented earlier. But two important assumptions for the remaining life expectancy at each age (the variable e_x^t) have not yet been made explicit. First, these life expectancies are based on period life tables instead of cohort life tables. Second, they are deterministic, not stochastic.

1. For the present calculations, we took the values for e_x^t from the period life tables that correspond to future age-specific mortality as assumed by Brunborg and Texmon in their long-range demographic projections. For instance, the assumed remaining life expectancy for a person aged 67 in the year 2010 is 16.8 years. This value is based on a period life table, i.e. the death rates assumed for the year 2010. However, mortality is assumed to fall after 2010. For instance, in the year 2050, when none of the persons who were aged 67 in 2010 are alive any longer, the remaining life expectancy at age 67 is assumed to be 22.3 years. When, however we inspect the remaining life expectancy at age 67 in 2010 based on a *cohort* life table (in other words for persons born in 1942) we find 18.1 years. In general, because mortality is falling at all ages, the use of period life tables implies underestimating the remaining life expectancy at all ages and thus also the NPV.
2. Remaining life expectancies for future years are stochastic, with uncertainty increasing with forecast horizon. For instance, the relative width of the 80 per cent prediction interval for remaining life expectancy of persons born in 1942 is 0.21, or one-fifth of the median value of 18.1 years. For birth cohort 1982 the corresponding number is 0.36, i.e. one-third the median value of 22.5 years. Remaining life expectancy is positively correlated with population numbers, and thus the NPV-intervals given above are too narrow.

Conclusion

In this paper we have analysed the uncertainty in the Net Present Value (NPV) of future public old age pension liabilities in Norway, as a result of growing uncertainty about the future Norwegian population. Under the current pension system, the liabilities are likely to grow by a factor ten towards the end of the century. A demographic driving force, life expectancy, is assumed to increase by some 13-16 years over the next 95 years, which is in accordance with long-term demographic projections of Statistics Norway, carried out by Brunborg and Texmon. Total fertility and net migration are assumed to remain constant in these projections. Demographic uncertainty is in accordance with that in the probabilistic population forecast for Norway computed in the framework of the UPE ("Uncertain Population of Europe") project. The UPE-calculations apply to the period 2003-2050, and we have extrapolated uncertainty parameters to 2100. The results show an increase not only in the expected value of the NPV, but also in the uncertainty surrounding central values. For instance, the 80 per cent prediction interval for the NPV is less than two per cent of its median value in 2010, but it grows rapidly to six per cent of the median in 2025, 19 per cent in 2050, 39 per cent in 2075 and to over 80 per cent of the median NPV-value in 2100. Thus, although our best guess for the NPV in 2050 is in the order of 11 500 billion Norwegian Crowns, the odds are one against four that the NPV that year will be higher than 12 600 billion, or lower than 10 400 billion crowns. Although the uncertainty in the NPV-prediction for 2050 is certainly non-negligible, it is much less than that in the population in 2050. Population size is expected to be 5.75 million in 2050, with a median equal to 5.63 million. The 80 per cent prediction interval stretches from 4.75 to 6.87 million – in other words, its width is 38 per cent of the median value. Thus the relative uncertainty in population size in 2050 is twice that of the NPV. We found that also in other years in the period to 2100 relative uncertainty in population size is approximately twice as large as relative uncertainty in NPV.

Although the results in this paper give a realistic impression of the prediction intervals around future public old age pension liabilities, they are no more than a first impression. In future work we need to take account of cohort mortality, instead of the period-based mortality parameters used in this paper. This will result in somewhat higher estimates for the NPV. A further point is that the prediction intervals for the NPV in this paper are somewhat too narrow, because we considered remaining life expectancies in the discount formula as deterministic, not stochastic.

Notes

1 For an English summary of the Pension Commission's proposal, see http://www.pensjonsreform.no/english.asp

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Application of a Probabilistic Framework to New Zealand's Official National Population Projections

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Abstract

This paper reports on the application of a probabilistic forecasting framework to Statistics New Zealand's 2004-based national population projections. The assumptions of the Series 5 projections (the middle series) were set as the medians of the fertility, mortality and net migration predictive distributions, and a combination of time series models and judgement was used to generate the distributions. Particular attention was paid to the forecasting of international migration. A model was designed that made use of the official total net migration assumption but provided separate age-sex-specific immigration and emigration inputs to the cohort-component model, thus overcoming a number of theoretical and practical limitations of forecasting with age-sex-specific net migration. The resulting probabilistic population forecasts suggest that New Zealand's demographic future is considerably uncertain. The forecasts indicate an 80 per cent probability that the population will lie between 4.41 and 5.07 million by 2026 and between 4.48 and 5.88 million by mid-century.

The demographic future cannot be precisely forecast. Migration, mortality and fertility trajectories tend to move in ways which are difficult to predict more than just a few years ahead. Migration in particular frequently includes sizeable annual and cyclical fluctuations around its general level, and despite the insights generated by a voluminous literature on migration modelling, migration forecast accuracy remains disappointing (Adam 1992; Shaw 1994). The traditional method of illustrating the uncertainty of population forecasts is to produce a number of variants which incorporate different assumptions about the future trajectories of fertility, mortality and migration. It is increasingly being

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recognised, however, that such an "'uncertainty variants" approach contains a number of shortcomings.

An obvious problem is the question of how the various fertility, mortality and migration assumptions should be combined into variant projections, and indeed how many variants should be produced. Table 1 shows the choices made by Statistics New Zealand in its 2004-based set of national projections. The Australian Bureau of Statistics recently produced 54 variants, though most attention was focused on just three (Australian Bureau of Statistics 2003). The United Nations, in its 2004 revision World projections, prepared six variants: high, medium, low, constant fertility, constant mortality and zero migration (UN 2005). Only the fertility assumption was varied between the high, medium and low variants.

Table 1: The combinations of assumptions in Statistics New Zealand's 2001-based population projection variants

e_0	Long-run TFR	Long-run annual net international migration		
		5,000	10,000	15,000
	1.60	Series 1		
Low	1.85		Series 3	
	2.10			
	1.60		Series 2	
Medium	1.85	Series 4	Series 5	Series 6
	2.10		Series 8	
	1.60			
High	1.85		Series 7	
	2.10			Series 9

Source: Statistics New Zealand

A related issue concerns the meaning of the variant projections. Producers of the projections usually state something like "the variants illustrate the uncertainty of the demographic future" but give no indication of the likelihood of any particular variant (Lutz and Scherbov 1998). Is variant X quite probable or highly unlikely? An estimate of the probability of any specific variant would be useful. But assigning probabilities to deterministic uncertainty variants is fraught with problems. How would it be done?

Perhaps an expert committee could examine a set of projection variants and declare the highest and lowest to cover a certain predictive interval. Yet how would they decide whether the high-low interval should cover 80 per cent, 90 per cent or 95 per cent of possible outcomes? Even if this challenge could somehow be overcome a fundamental problem would remain: uncertainty variants are probabilistically inconsistent (Lee 1999). Say, for example, that a high-low range for total population for a particular year in the future was chosen by experts to represent a 95 per cent predictive interval. It would be almost certainly be the case that the high-low range for other years, and the high-low ranges of other variables could not cover the same 95 per cent interval. For example, the latest United Nations projections for the world population in 2050 have a high-low range of 10.65-7.68 billion (United Nations 2005). Assume that this was (somehow) accorded a 95 per cent predictive interval. For the 65+ population the UN high-low range is 1.464939-1.464936 billion, clearly not a plausible 95 per cent range for 45 years' time.

The unrealistic paths that fertility, mortality and migration are assumed to take are a further shortcoming of uncertainty variant projections. Projected TFR and migration trajectories often consist of a constant long-run value preceded by a 'run-in' period of a few years in which the values are interpolated from recent observations. Life expectancy at birth paths are frequently assumed to be smooth curves where recent life expectancy gains gradually decelerate. Random fluctuations and cyclical patterns are all implicitly given zero probability (Lee 1999). The fixed relationships that exist between fertility, mortality and migration throughout the forecast horizon are another problematic feature of these assumptions. Such perfect correlation between the demographic components of change does not represent demographic reality.

Furthermore, embarrassing situations may arise from a set of variant projections because of the gradual trending in of long-run fixed values over several years (Bryant 2003; Lee 1999). For a hypothetical example, let the most recent TFR for a country be 1.8 and projected long-run high, medium and low TFR values be set at 1.9, 1.7 and 1.5. These might be held constant from 10 years into the forecast horizon with linear interpolations from the starting value covering the first 10 years. In the second year of the projections the three TFR assumptions would be 1.74, 1.78 and 1.82. If, for example, the TFR actually increased slightly to 1.84 by this time it would lie outside the high-low range, and rather unfairly make the producers of the projections look incompetent. This is particularly unfortunate if it occurs even before the projections are published. As illustrated later in the paper more realistic representations of uncertainty show that predictive intervals open up quite rapidly in the first few years of a forecast and more slowly thereafter.

The solution to these shortcomings is to produce probabilistic population forecasts. A literature on probabilistic population modelling has emerged over the last decade or so and forecasts have now been produced for a number of countries, including Australia (Wilson and Bell 2004), Austria (Lutz and Scherbov 1998), Finland (Alho 2002), Lithuania (Alho 2003), the Netherlands (de Beer and Alders 1999), Norway (Keilman *et al.* 2001), the United States (Lee and Tuljapurkar 1994) and for a number of world regions (Lutz and Scherbov 1999; Lutz *et al.* 2001; Lutz and Scherbov 2003). A set of probabilistic population forecasts have, in fact, already been produced for New Zealand as part of work on future government social expenditure (Creedy and Scobie 2002). The methods used by Creedy and Scobie differ considerably from other probabilistic applications, with each age-specific rate/flow being forecast separately and independence between variables being assumed across age groups and over time. The forecast population pyramids presented by the authors possess extremely narrow 95 per cent confidence intervals. This paper employs methods more in line with the main body of work in probabilistic population forecasting and applies a probabilistic framework to the 2004-based national population projections prepared by Statistics New Zealand (Statistics New Zealand 2005).

The plan of the paper is as follows. The next section provides details of the methods and assumptions. The importance of using immigration and emigration flows rather than net migration in the age-sex-specific calculations of the cohort component model is stressed. A simple method for forecasting the two international migration flows is proposed which permits wide predictive distributions for immigration and emigration whilst maintaining a correspondence between their two levels and thus a plausible predictive distribution for net migration. The next section presents the results, focusing specifically on the predictive distributions for total population, the demographic components of change and the age-sex structure. This section includes a comparison with the uncertainty variants of the latest Statistics New Zealand projections.

Methods and assumptions

Overview

The probabilistic population forecasts were produced by running a cohort component model 10,000 times with different fertility, mortality and migration rates/flows in each simulation. There were four main steps in the creation of the forecasts.

Step 1. Summary indicators of demographic change were selected. These were: the TFR, male e_0, female e_0, total immigration numbers and total emigration numbers. The emigration trajectories, however, were calculated indirectly as total immigration minus total net migration. This approach represents a simple way of ensuring a realistic correlation between immigration and emigration and, in addition, links well with the Statistics New Zealand practice of setting net migration assumptions. The reasons for not using age-sex-specific net migration directly in the calculations of the forecasts are given later. International migration is defined here as permanent plus long-term migration which corresponds with the common international migration definition in which migrant status is assigned to those resident in a country for one year or more.

Step 2. The time series models used to generate the sample paths for each of the summary indicators were fitted to past data. These are described in the sub-sections below.

Step 3. The models were used to provide forecasts for the 2004-51 forecast horizon. For each of the summary indicators 10,000 sample paths were generated. The 'raw' output of these models was adjusted slightly as it was generated. First, the whole distribution of each summary indicator was shifted so that the median was brought in line with Statistics New Zealand's series 5 assumptions (the middle variant). Second, the immigration and net migration predictive distributions were constrained to prevent them becoming too wide (so that negative emigration numbers were avoided, for example). This was achieved using the method of Keilman *et al.* (2001). Ceiling and floor limits were set for immigration and net migration. If during any simulation the value of the summary indicator wandered outside the set limits the sample path for the whole forecast horizon was rejected and another generated. About 3,000 immigration and net trajectories were rejected in total.

Step 4. Using the sample paths of each of the summary indicators 10,000 simulations of New Zealand's demographic future to 2051 were created by a cohort component model. The required age-specific rates for fertility, mortality and emigration and age-specific proportions for immigration were generated during the execution of the forecasting program. Age-specific fertility rates were produced by multiplying the TFR by a set of fertility rates summed to 1.0 over all age groups. A similar approach was used to obtain age-sex-specific immigration numbers: total immigration was multiplied by a set of age-sex proportions which summed to 1.0 over all ages and both sexes. Age-sex-specific mortality rates were obtained via a look-up procedure which picked out a schedule of mortality rates associated with a specific e_0 value. For emigration, age-sex-specific emigration numbers were calculated by applying a set of base year emigration rates to the population at risk and then scaling the preliminary emigration numbers to the emigration totals created in step 3. By using this method rather than a fixed age schedule of emigration numbers, the age pattern of emigration was able to respond to the evolving age structure of the population at risk, thereby considerably reducing the likelihood of emigrating out more people than existed in a particular age group.

Details of the jump-off populations and the various models used to generate the predictive distributions for fertility, mortality and migration are now given.

Jump-Off Populations

Mid-2004 population estimates by sex and single years of age were obtained from Statistics New Zealand. Estimates for ages 90 to 110 were prepared by allocating the 90+ population according to the distribution available from the Human Mortality Database (2004) for 31st December 2003. The Human Mortality Database population numbers for the highest ages have been estimated using the extinct generation and survivor ratio methods (Wilmoth 2004) and tend to be more reliable than census-based population figures.

Fertility

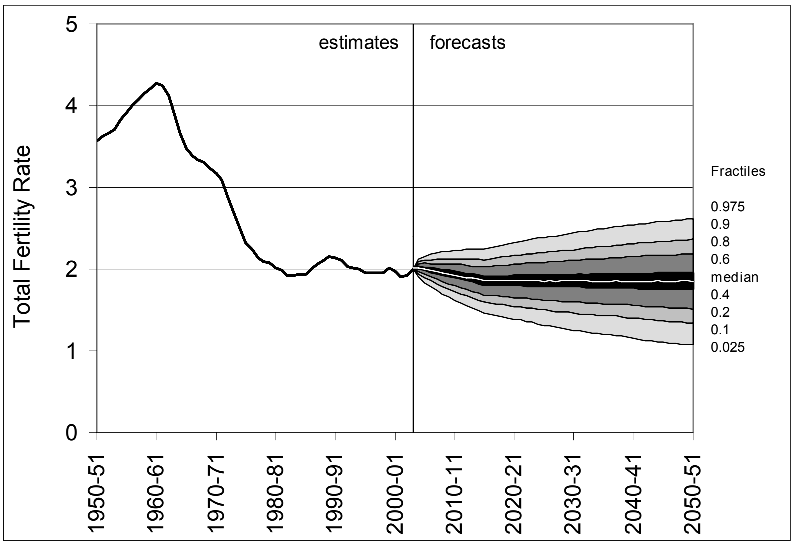
Initially, a time series model fitted to annual TFR data for the period 1921 (the first year for which statistics are available) to 2004 suggested an ARIMA(1,1,0) process was appropriate for modelling the New Zealand TFR. However, use of the model in forecasting resulted in the 95 per cent predictive range expanding rapidly and becoming implausibly wide after a couple of decades, even expanding to incorporate nonsensical negative TFRs. Other researchers have also encountered this problem. Proposed solutions include setting ceiling and floor limits and rejecting any sample paths which breach the limits (Keilman *et al.* 2001), using a logit transformation of the TFR (Lee and Tuljapurkar 1994), or by employing a different type of time series model. An example of the latter is the Autoregressive Conditionally Heteroscedastic (ARCH) class of time series models. Keilman and Pham (2004) have found these give predictive intervals for the TFR which accord well with past errors and naïve forecasting approaches.

A slightly different, and simpler, solution was adopted here. The Box-Jenkins time series model-fitting approach was still used, but only on TFR data from 1975-2004. This corresponds to a period of approximately replacement or below-replacement fertility in New Zealand, and a period in which the social and economic context of childbearing has been quite different to that of earlier decades. It seems appropriate therefore to restrict the model fitting to the most recent 30 years of data. The most appropriate model turned out to be a simple random walk process:

$$TFR(T) = TFR(T-1) + \varepsilon_{TFR}(T) + drift_{TFR}(T) \quad (1)$$

where T denotes a one year forecast interval, ε_{TFR} are random errors sampled from a normal distribution with a standard deviation of 0.0586 and a mean of zero, and $drift_{TFR}$ shifts the median of the predictive distribution to follow Statistics New Zealand's middle TFR assumption. This assumption sets the TFR on a gradual decline over the next few years until it reaches its long-run value of 1.85. The resulting TFR predictive distribution is shown in Figure 1.

Figure 1: Observed TFR and predictive distribution, 1950-51 to 2050-51



Source: Statistics New Zealand; author's calculations
Note: Years shown are mid-year to mid-year periods.

Mortality

Annual life expectancy at birth data by sex were obtained from the Human Mortality Database for the period 1937-2003 (Human Mortality Database 2004). However, because of very big year to year fluctuations for the first few years of this time series the model identification process was based on data from 1942 onwards. This process revealed that for male e_0 a simple random walk process was the most appropriate model, but for female e_0 an ARIMA(0,1,1) model proved to be the best option. Thus

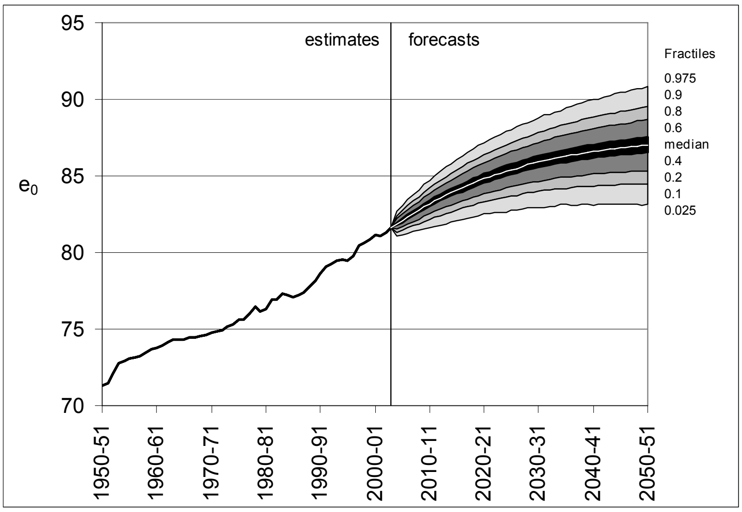
$$e_0(males,T) = e_0(males,T-1) + \varepsilon_{e_0}(males,T) + drift_{e_0}(males,T) \qquad (2)$$

$$\begin{aligned} e_0(females,T) = {} & e_0(females,T-1) + \varepsilon_{e_0}(females,T) \\ & - \theta_{e_0}\, \varepsilon_{e_0}(females,T-1) + drift_{e_0}(females,T) \end{aligned} \qquad (3)$$

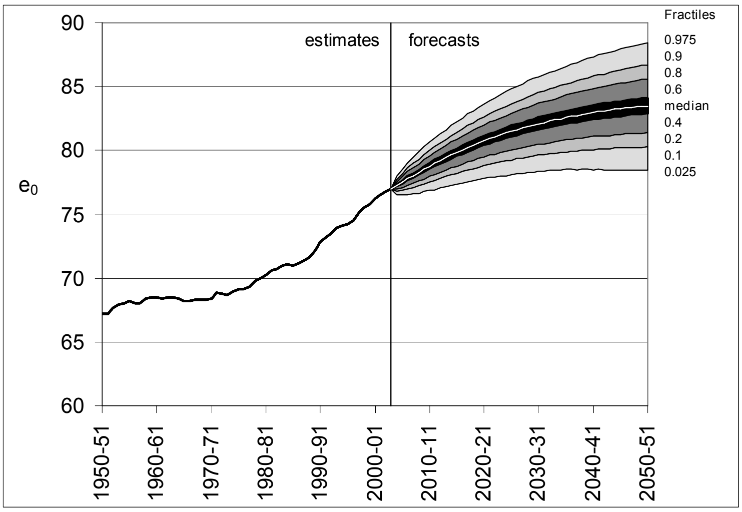
where ε_{e_0} is random error drawn from a normal distribution with a mean of zero and a standard deviation of 0.365 for males and 0.411 for females, θ_{e_0} is the moving average parameter (0.317), and $drift_{e_0}$ centers the predictive distribution on the Statistics New Zealand Series 5 assumptions. These assume that recent annual gains in life expectancy will gradually decline, giving mid-century e_0 values of 83.5 years for men and 87.0 years for women. The correlation between male and female random error was modelled by producing correlated random numbers via Cholesky decomposition of the variance-covariance matrix (Press *et al.* 2001: 89-91). The resulting male and female life expectancy at birth predictive distributions are displayed in Figure 2.

Figure 2: Observed life expectancy at birth and predictive distributions, 1950-51 to 2050-51

(a) Females



(b) Males



Source: Human Mortality Database (2004); author's calculations

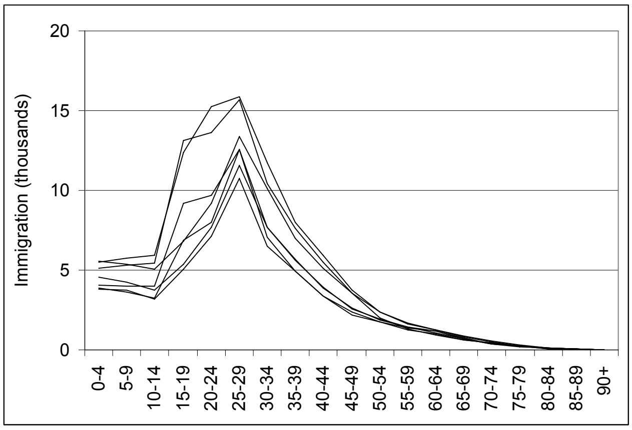
International Migration

International migration was modelled as age-sex-specific immigration and emigration flows rather than net migration. Whilst the use of age-sex-specific net migration is appealing because of limited data requirements (past net migration may be estimated as population change minus natural increase) and immigration-emigration relationships do not have to be considered, it is problematic for a number of reasons.

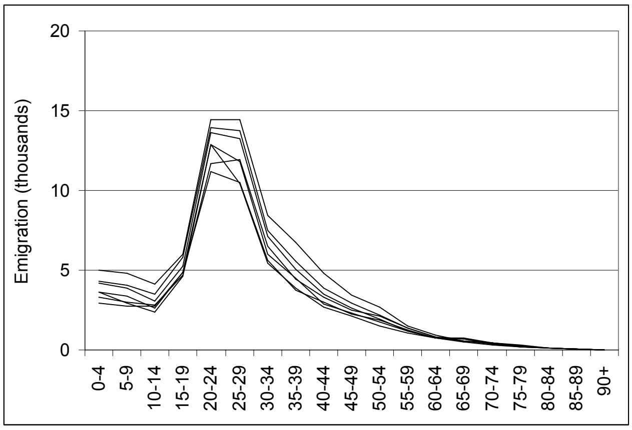
1. First, when net migration is negative there is the danger of "migrating out" more people in certain age groups than exist in the population to start with, resulting in the embarrassment of negative populations! This is more of a risk in the case of probabilistic than deterministic forecasting because some net migration sample paths near the lower end of the predictive distribution may be severely negative for the whole forecast horizon, and such low probability trajectories are unlikely to be chosen for deterministic variant projections. To test this risk for New Zealand a net migration model with a fixed net age profile was incorporated into the probabilistic forecasting program designed for this paper. Negative populations were generated before the end of the forecast horizon.
2. Secondly, many forecasting models which specify total numbers of net migration also use fixed age-sex schedules of net migration. Whilst immigration and emigration age profiles exhibit considerable temporal stability, the same cannot be said for net migration. Even the same net migration totals may be associated with quite different age patterns due to different immigration and emigration levels. As an example, Figure 3 shows the immigration, emigration and net migration age profiles for New Zealand for the years 1996-97 to 2002-03. It can be seen that the immigration and, particularly, emigration age schedules are roughly similar over time. The differences in the immigration profiles arise partly from different *levels* of immigration rather than fundamentally different age *patterns*. In contrast, the graph clearly demonstrates how net migration experiences dramatic fluctuations in its distribution across the age groups. It is difficult therefore to defend the use of fixed net age schedules in forecasts when a wide range of immigration and emigration levels will be encountered.

Figure 3: Immigration, emigration and net migration age profiles 1996-97 to 2002-03

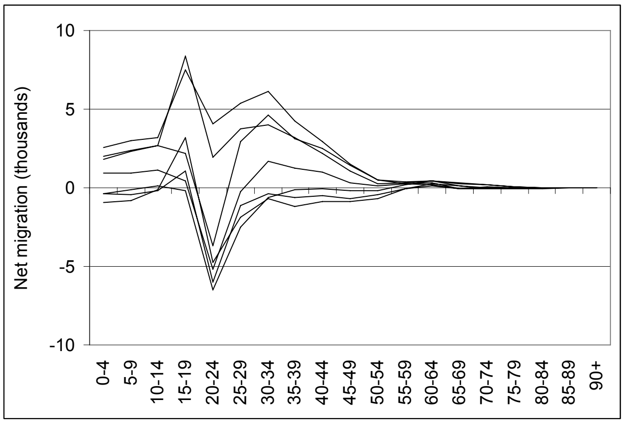
(a) Immigration



(b) Emigration



(c) Net migration



Source: Statistics New Zealand

3. Thirdly – and most importantly – net migration is a statistical quantity and not a demographic process, so from a conceptual point of view it is less satisfactory than modelling gross migration flows. As Rogers (1990) has pointed out there is no such thing as a net migrant, just people moving from one place to another. From a theoretical viewpoint the modelling of net migration rather than gross migration flows is akin to directly modelling natural change rather than births and deaths as separate processes.

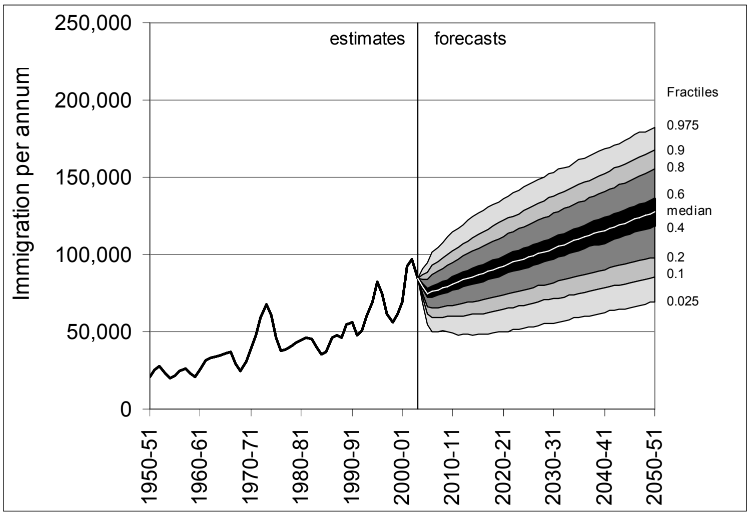
In order to determine what type of immigration and emigration models would be appropriate the time series of these two international migration streams were examined. Data were available from 1950 onwards. Over the last 50 years the long-run trend in both immigration to and emigration from New Zealand has been one of substantial increase, but with considerable annual and cyclical variations from this overall trajectory (Figures 4 and 6). But whilst the broad long-run average levels of immigration and emigration are closely related, this is not the case for the annual fluctuations. The year on year changes (or first differences) in immigration and emigration are weakly correlated, the strongest relationship being for emigration year on year differences lagged five or six years behind immigration, for which the correlation coefficients are about 0.5. The low level of covariance is evident in the large annual fluctuations in net international migration (Figure 5). If the immigration and emigration year on year differences showed a greater tendency to co vary – in other words if an increase (decrease) in immigration tended to be matched by an increase (decrease) in emigration – then the net migration time series would exhibit much less volatility. These characteristics suggested a migration model which permits large fluctuations in immigration and emigration but little difference between the long-run average trends of both streams. Furthermore, whilst it is reasonable to assume a continuing correspondence between these long-run trends of immigration and emigration, the future directions of these trends are quite uncertain.

With these issues in mind, it was decided that total immigration would be modelled directly but that total emigration would be forecast via total net migration. This provides a simple method of correlating the long-run trends in immigration and emigration and at the same time is closely related to the Statistics New Zealand practice of setting net migration assumptions. The appropriate model for immigration turned out to be an ARIMA(2,1,0) process,

$$I(T) = I(T-1) + \phi_{I,1}[I(T-1) - I(t-2)] + \phi_{I,2}[I(T-2) - I(t-3)] + \varepsilon_I(T) + drift_I(T) \quad (4)$$

where $\phi_{I,1}$ and $\phi_{I,2}$ are the autoregressive parameters with values 0.642 and -0.547 respectively, ε_I are random errors sampled from a normal distribution with a standard deviation of 5,594 and a mean of zero, and $drift_I$ aligns the median of the distribution with an extrapolated best-fit line through the historical data. The assumption of a long-run increase is in agreement with commentators who are predicting a rise in international migration through non-permanent (as opposed to permanent settler) migration (Bedford *et al.* 2002; Hugo 1999). Ceiling and floor limits of ±75,000 of the best-fit extrapolation were set to prevent nonsensical and implausible figures being forecast, whilst still permitting a wide predictive distribution indicating the considerable uncertainty of future migration levels. Figure 4 shows the immigration predictive distribution.

Figure 4: Observed permanent plus long-term immigration and predictive distribution, 1950-51 to 2050-51.



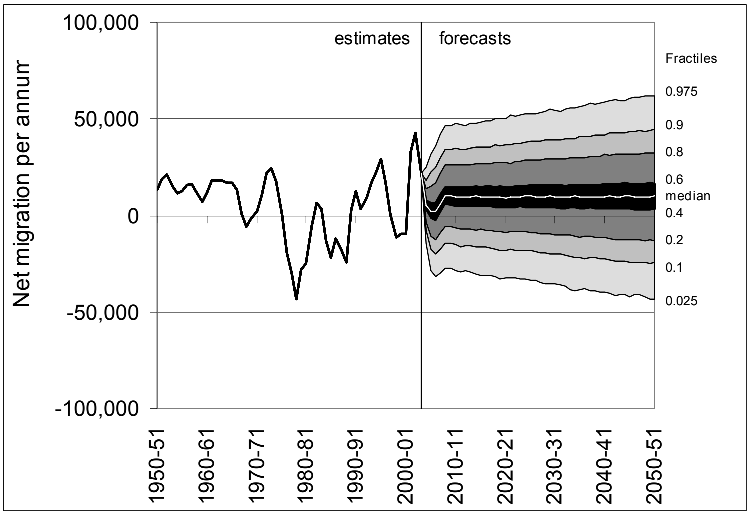
Source: Statistics New Zealand; author's calculations

For net migration, an ARIMA(1,0,1) model was fitted. Thus,

$$N(T) = \phi_N\, N(T-1) - \theta_N \varepsilon_N(T-1) + \varepsilon_N(T) + drift_N(T) \quad (5)$$

where ϕ_N is the autoregressive parameter (0.656), θ_N is the moving average parameter (-0.522), ε_N are random errors sampled from a normal distribution with a mean of zero and a standard error of 9,883 in the first year of the forecasts, gradually rising to 1½ times that by mid-century. This is admittedly arbitrary, but is incorporated to reflect the expected rise in net migration variation from non-permanent migration trends. Bedford *et al.* (2002: 58) predict that "Complex patterns of population circulation will cause even more volatility in annual arrival and departure figures, as people with internationally marketable skills increasingly develop transnational careers and multilocal lives". The $drift_N$ values ensure the median of the net migration distribution agrees with the Statistics New Zealand series 5 assumptions. The predictive distribution is shown in Figure 5.

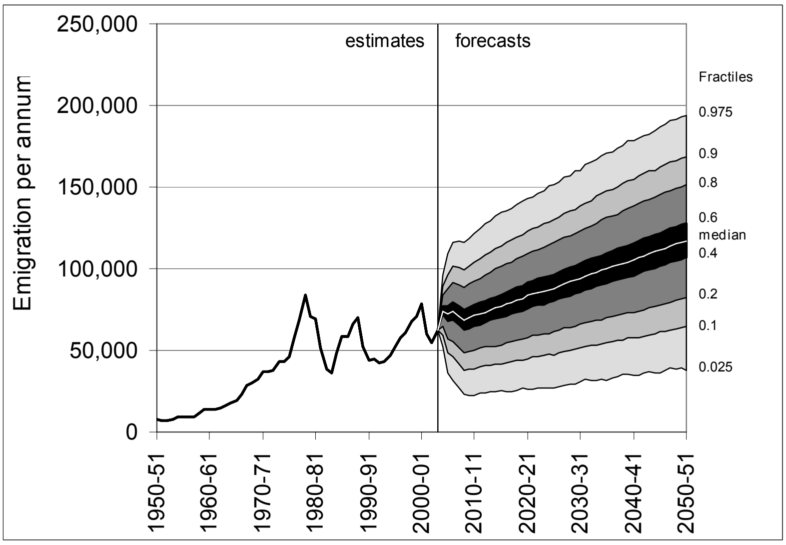
Figure 5: Observed permanent plus long-term net migration and predictive distribution, 1950-51 to 2050-51



Source: Statistics New Zealand; author's calculations

Total emigration was then forecast as immigration minus net migration. Both immigration and net migration were computed simultaneously so that where the immigration and net migration values implied negative emigration the sample paths could be rejected and replacement ones drawn. This occurred a few hundred times in the generation of 10,000 immigration and 10,000 net migration trajectories. Figure 6 illustrates the predictive distribution for emigration.

Figure 6: Observed permanent plus long-term emigration and predictive distribution, 1950-51 to 2050-51.



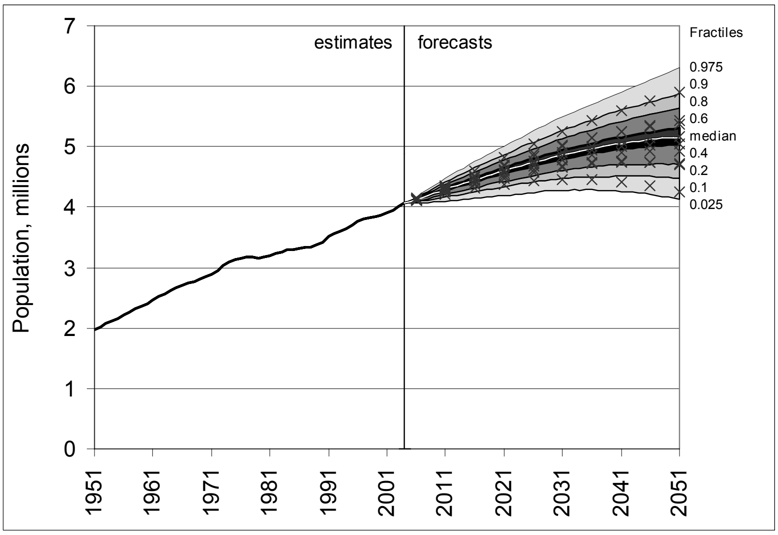
Source: Statistics New Zealand; author's calculations

Results

Total Populations

Figure 7 presents the predictive distribution for the total population of New Zealand for 2004-2051. The median population forecast for 2026 is 4.74 million, with an 80 per cent probability range covering 4.41 to 5.07 million. By 2051 this range has extended to 4.48 to 5.88 million, with the median of the distribution falling at 5.16 million. This figure is actually slightly higher than the Statistics New Zealand Series 5 projection of 5.05 million by 2051. Why is this the case given that the same TFR, life expectancy at birth and net migration assumptions were used? Primarily it is attributable to different methods of forecasting international migration. Statistics New Zealand uses constant net migration numbers in each age-sex group throughout the forecast horizon (except for the first few "run-in" years). The probabilistic model incorporates fixed immigration numbers, but the age profile of emigration is able to respond to the evolving age structure of the population, and hence the age pattern of net migration adjusts over the course of the forecast horizon. The result is slightly larger populations in the female childbearing age groups and therefore more births compared to the official projections.

Figure 7: Observed population and predictive distribution, 1951-2051



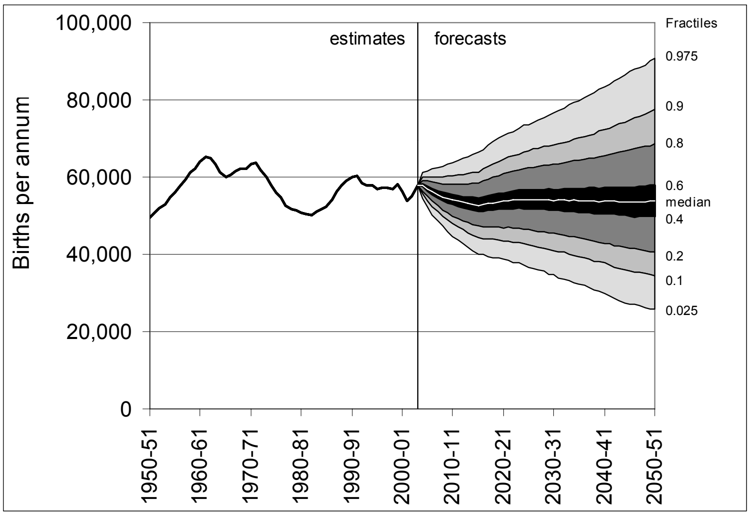
Notes: (1) The nine Statistics New Zealand projection variants are shown as the starred series
(2) In 1991 the population base was changed from a persons present to a "usually resident" definition

How do these forecasts compare with the official Statistics New Zealand projection variants? The nine series are marked in Figure 7 with crosses. Whilst these projection variants evidently cover a wide range of possible population outcomes, a close inspection of the graph reveals the range between the highest and lowest of these series opens up more slowly than the probabilistic forecasts. In 2011 all nine series fall between the 0.2 and 0.8 fractiles (in the 60 per cent predictive interval). By 2026 they fall within the 80 per cent interval (between fractiles 0.1 and 0.9), though by 2051 the trajectories plotted by series 1 and 9 are covered only by the 95 per cent probability range. This is one manifestation of the probabilistic inconsistency problem with uncertainty variants mentioned earlier: the probability between the highest and lowest of the deterministic series changes over time.

Births and deaths

Predictive distributions for the demographic components of change are displayed in Figures 8 and 9. The considerable uncertainty over the future numbers of births evident in Figure 8 stems from both uncertainty over the future TFR and, after about two decades, increasing uncertainty over the size of women in the childbearing age groups. After this time, some births are being born to women whose numbers are not known because they themselves were not born at the start of the forecast horizon.

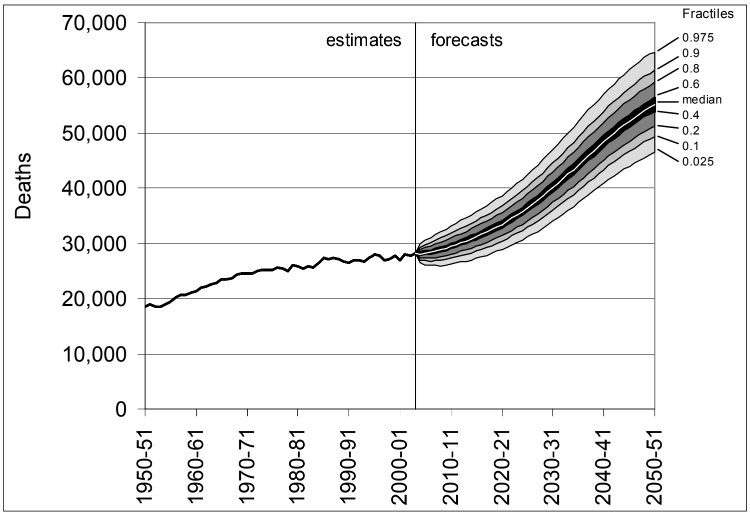
Figure 8: Observed births and predictive distribution, 1950-51 to 2050-51



Source: Statistics New Zealand; author's calculations

In contrast, much less uncertainty surrounds the future number of deaths: a substantial rise in the trend will be driven by the baby boom cohorts entering the high mortality ages, as shown by Figure 9. Even by the end of the forecast horizon all those in the high mortality ages were alive in 2004 (whether in New Zealand or not) so no uncertainty over births feeds into the predictive distribution. Some uncertainty over international migration has an impact, although with peak migration rates falling in the young adult ages it is only towards the end of the forecast horizon that these cohorts enter the high mortality age groups.

Figure 9: Observed deaths and predictive distribution, 1950-51 to 2050-51



Source: Statistics New Zealand; author's calculations

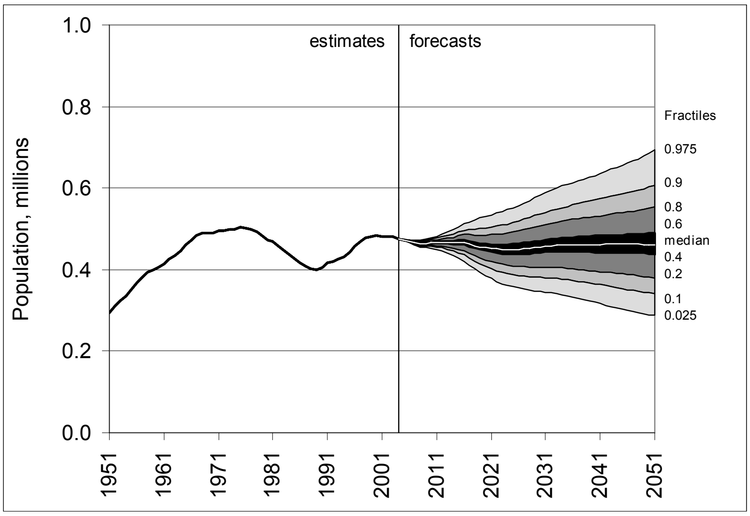
Age-sex structure

For many organisations the age composition of the population is more relevant than total numbers. Figures 10 to 13 show the estimated forecast uncertainty of several key age groups: the primary school ages (5-12), secondary school ages (13-17), the working age groups (approximated by ages 20-64) and the elderly (65+). Figure 10 suggests that the future size of the primary school age population is most likely to remain at roughly the level of recent years. However, five years into the forecast horizon the uncertainty over births begins to make an impact, indicating considerable declines or increases in this population are possible over the coming decades. The 80 per cent predictive intervals for this population cover 3.86 to 5.19 million by 2026 and 3.42 to 6.06 million by 2051. The future size of the secondary school age population is reasonably certain for the first 13 years whilst entries to this population are from those already alive in 2004 (Figure 11). Again, numbers in this age group are most likely to be similar to those of recent years. Once the uncertainty of births begins to make an impact, however, the predictive intervals follow much the same pattern as the primary school age population. The 80 per cent predictive intervals cover

2.71 to 3.30 million by 2026 and 2.43 to 3.84 million by 2051. The size of the working-age population is most likely to continue growing until the 2020s before levelling off at about 2.7 million, though the uncertainty surrounding migration contributes to the fairly wide predictive intervals for this age group. As with the two school age populations considerable growth or decline is within the bounds of possibility. The 80 per cent predictive intervals range between 2.46 and 2.89 million by 2026 and 2.32 to 3.16 million by 2051.

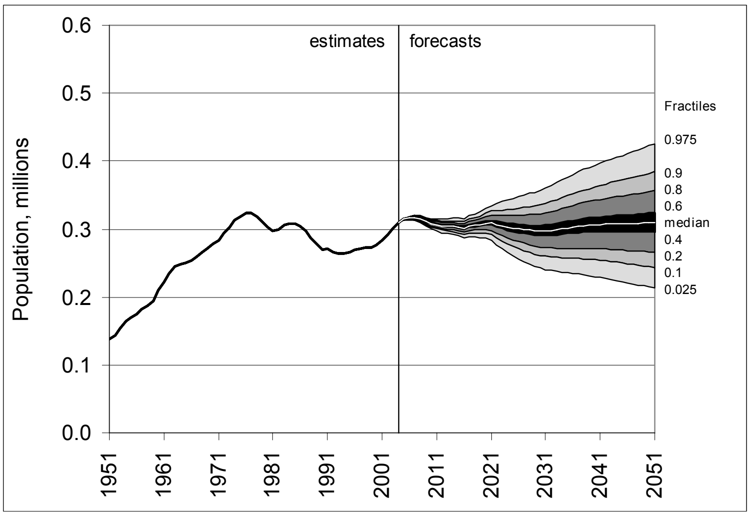
In contrast to the other age groups the population aged 65 and above will definitely increase in size, and by quite a substantial amount (Figure 13). The growth will be greatest during the second, third and fourth decades of the century when the baby boom cohorts reach their 65th birthdays. The figures suggest an 80 per cent probability that this population will reach one million people between 2028 and 2033. By 2051 the median forecast is 1.27 million with the 80 per cent predictive interval ranging from 1.13 to 1.41 million.

Figure 10: Observed population aged 5-12 and predictive distribution, 1951 to 2051



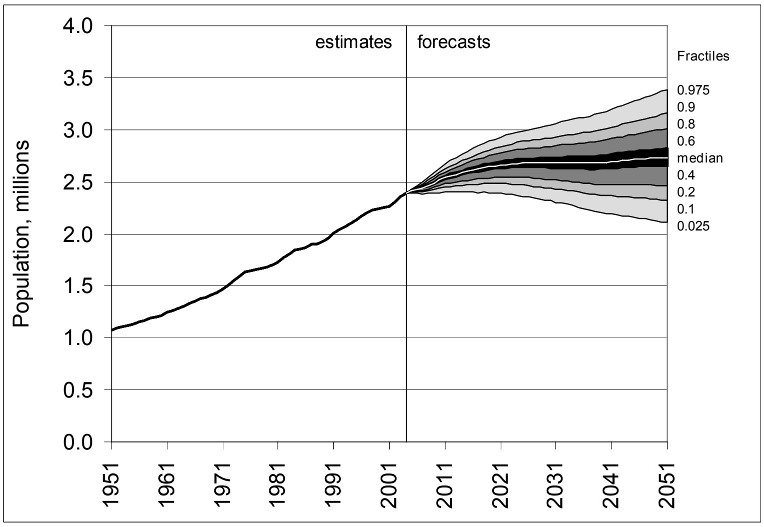
Source: Statistics New Zealand; author's calculations

Figure 11: Observed population aged 13-17 and predictive distribution, 1951 to 2051



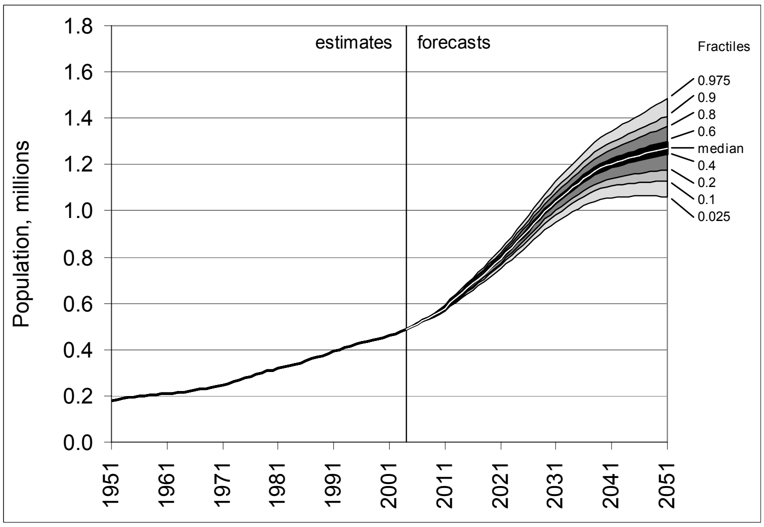
Source: Statistics New Zealand; author's calculations

Figure 12: Observed population aged 20-64 and predictive distribution, 1951 to 2051



Source: Statistics New Zealand; author's calculations

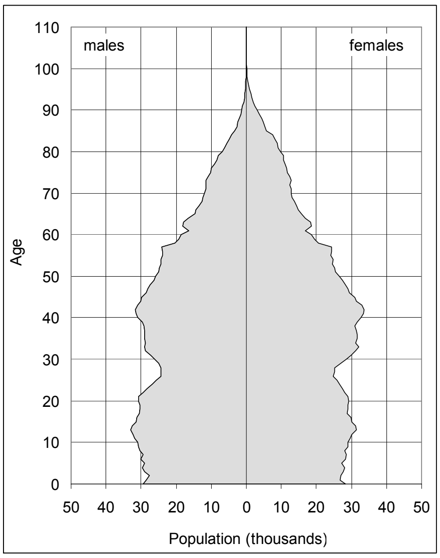
Figure 13: Observed population aged 65+ and predictive distribution, 1951 to 2051



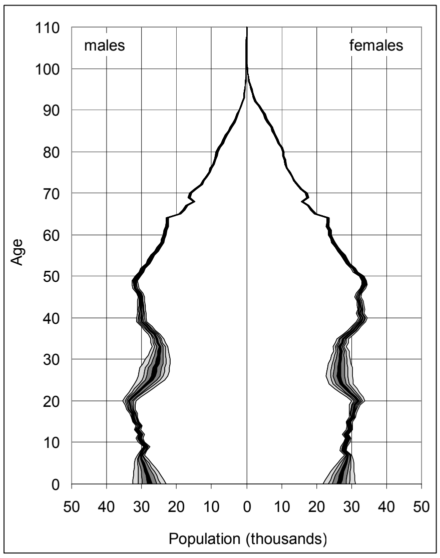
Source: Statistics New Zealand; author's calculations

A picture of how the uncertainty of New Zealand's future age structure unfolds across all ages is given in the population pyramids in Figure 14. Histogram (b) shows that in the early years of the forecast horizon the greatest uncertainty surrounds the numbers in the very youngest and early working age groups, reflecting respectively the uncertainty over births and international migration. Greater certainty surrounds the numbers of teenagers and older adults in 2011. The teenagers of 2011 were already born at the start of the forecast horizon and their migration rates are lower than many other age groups (Figure 3). The numbers in the older adult ages have been affected by very little migration uncertainty by this time. Twenty years into the forecasts (histogram (c)) fertility and international migration uncertainty combine; the numbers in the elderly ages remain influenced primarily by mortality uncertainty. By 2031 (histogram (d)) there is roughly the same uncertainty over the size of all age groups in the bottom half of the pyramid, and the sizes of the elderly age groups start to become more uncertain. After this date the predictive intervals become slightly wider but follow roughly the same pattern as shown for 2031.

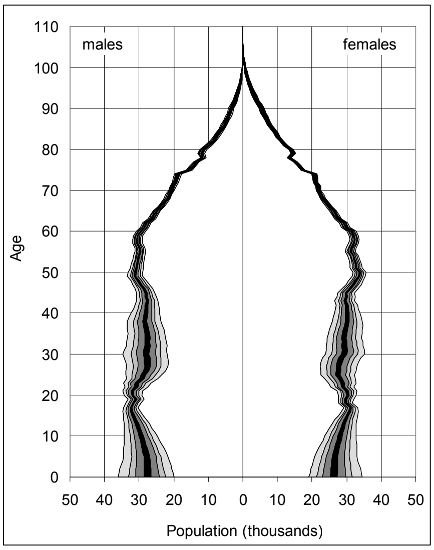
Figure 14: Observed and predictive distributions of New Zealand's age-sex structure, selected years.



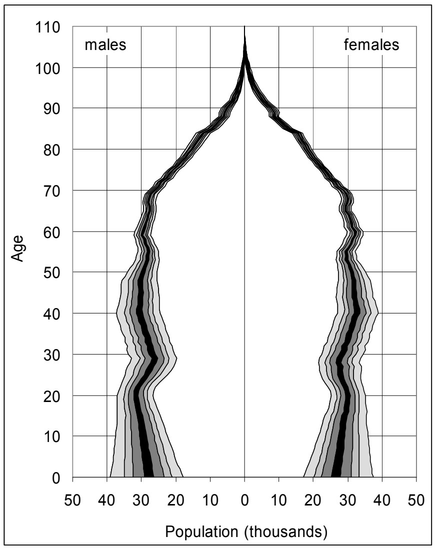
(a) 2004



(b) 2011



(c) 2021



(d) 2031

Note: Fractiles shown are: 0.0975, 0.9, 0.8, 0.6, 0.4, 0.2, 0.1 and 0.025
Source: Statistics New Zealand; author's calculations

Conclusion

This paper has applied a probabilistic forecasting model to the central projection variant of Statistics New Zealand's 2004-based national population projections. A method of modelling migration was proposed which incorporates three major features of New Zealand's immigration and emigration time series, namely the considerable fluctuations in both migration streams over time, the limited covariance between year on year changes in immigration and emigration numbers which translates to a sizeable net migration distribution, and the similarity in the long-run average levels of the two migration flows. The resulting forecasts demonstrate that much uncertainty exists over New Zealand's demographic future. The 80 per cent confidence interval for the population in 2026, for example, covers 4.41 to 5.07 million, whilst by 2051 it spans 4.48 to 5.88 million.

For users, probabilistic population forecasts offer a number of important advantages over deterministic "uncertainty variants". They are not offered an array of variants from which to choose with no information on their likelihood, a choice which is particularly difficult if there is an even number with no designated principal variant. Instead they can be provided with the upper and lower figures of a range together with an estimate of the probability that the future demographic trend will lie within that range. These predictive intervals also allow users to decide at what point in the future the intervals become too wide for the forecasts to be useful (Lee 1999). For example, governments planning the provision of primary school teachers and the number of primary schools will be able to see that even in 10 to 15 years' time there is quite a lot of uncertainty over the size of the primary school age population. Providers of goods and services directed at the 65+ population, however, can plan much further ahead as relatively little uncertainty exists for the next two to three decades. It should be added, of course, that what constitutes "relatively little uncertainty" will vary from one user to another depending on the costs of population forecasts being wrong. For example, it might be that population forecasts of the 65+ population which are 20 per cent too low may prove serious for a private health fund, but be tolerable for a publisher of large print books.

For the producers of population forecasts, probabilistic methods dispense with the need to produce many different variants and the decisions on what fertility, mortality and migration trajectories should be combined in each variant. After 15 years or so of improvement these forecasting methods are now sufficiently well-developed to be applied to national population forecasts. Furthermore, modern computing technology enables them to be produced easily and quickly.

However, as Lutz *et al.* (1996) point out, it is important to remember that the predictive intervals in probabilistic forecasts remain *estimates* of future uncertainty. These intervals are frequently based on time series models, past forecast errors and judgement about the future. In the forecasts presented here the judgement of Statistics New Zealand was incorporated by setting the Series 5 assumptions as the medians of the forecast distributions. Other assumptions about the medians of the distributions are, of course, possible, but it is sensible to use those of Statistics New Zealand as they possess the greatest expertise and experience in forecasting New Zealand's population. Probabilistic forecasting methods are not therefore a panacea for all the shortcomings of deterministic approaches. But it is preferable to have population forecasts generated by models which incorporate the randomness of population dynamics and which produce quantitative and consistent estimates of future uncertainty rather than deterministic variants and all their shortcomings.

Acknowledgments

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Special Issue, New Zealand Population Review, 31(1):77-124.

Biographic Forecasting: Bridging the Micro-Macro Gap in Population Forecasting

FRANS WILLEKENS*

Abstract

The paper outlines a new model for demographic projections by detailed population categories that are required in the development of sustainable (elderly) health care systems and pension systems.

The methodology consists of a macro-model (MAC) that models demographic changes at the population level and a micro-model (MIC) that models demographic events at the individual level. Both models are multistate models that rely on rates of transition between states of existence or stages of life. MAC focuses on transitions among functional states by age and sex. The transitions determine the distribution of cohort members among functional states. The output of MAC consists of ***cohort biographies***. MIC addresses demographic events and other life transitions at the individual level. It is a micro-simulation model that produces ***individual biographies***. This paper describes approaches to functional population projection and provides a detailed description of the multistate model. It also contains an overview of the MicMac project.

Demographic projections are usually confined to populations disaggregated by age, sex and sometimes race/ethnicity. The general methodology, the cohort-component method, is well-established. The basic approach is to distinguish birth cohorts, to determine the number of survivors in the base year and to determine *for each cohort* and for each future year the number of persons by age and sex that (1) enter a population through birth or migration and (2) leave a population due to death or emigration. The number of entries and exits are based on *rates* of birth, death and emigration by age and sex, and number of immigrants by age and sex. The estimation of empirical rates from data (often incomplete

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or defective data) and the prediction of future rates involve important methodological issues.

The projected population by age and sex serves as an input in functional population projections, which are related to particular functions or activities in society. They include projections of the population by functional status such as labour force status, educational status, health status and status in the household. These projections are made to determine the projected need for some "function" – a product, a service, an allowance, an activity or a facility (Kono 1993). Examples include:

- The future size of the labour force to determine the supply of labour and the demand for jobs.
- The future size of the population retired from the labour force to determine the demand for pensions.
- The future size of school enrolments to determine the demand for teachers and buildings and to determine the population composition by level of education and hence the human capital.
- The future size of the population by health status and/or disability status to determine the demand for health care including the number of physicians and hospital beds.
- The future number of households by size and type to determine the demand for housing and durable consumer goods.
- The future number of people eligible for assistance of different type. Eligibility criteria frequently include age, sex and functional status (eg. level of income, health status).
- The future size of vulnerable groups in society.

Despite the wide variety of functions, from a methodological viewpoint traditional functional projections differ from each other only in minor detail. Traditionally, people of a given age and sex are allocated to functional states using a set of prevalence rates, a distribution function or another allocation mechanism. The method is referred to as distribution method. In the forecasting literature the method is also known as *static* as opposed to methods that are based on transition rates (or incidence rates) and that are *dynamic* (such as the multistate model) (eg. Zeng Yi *et al.* 1997). Examples of the static method based on distributions are the headship rate method for household projections, labour force projections based on labour force participation rates, educational projections based on enrolment rates, the ratio method of sub national population projection, and health status projections based on prevalence rates ('Sullivan method'). The distribution function may change over time to capture real or assumed shifts in behaviour or conditions. For illustrations of the static method in functional population projections, see Bogue *et al.* (1993:Chapter 18).

In the dynamic method, the distribution of people among functional states is not imposed by a distribution function but is the outcome of transitions people make in life. People move between functional states and as a consequence, the structure of the population changes. The rates of transition determine the population dynamics and the rates may change in time and may vary between subpopulations. In the dynamic method, several states of existence are distinguished and the transitions between the states are considered. The method is known as the multistate method. Because of the pivotal role of transitions, multistate models picture more closely the *mechanism of demographic change* taking place in the real world. As a result, they are better suited for integrated population projections in which functional states and interactions between functional states play a crucial role. In addition, the transitions provide a way to assess the impact on population dynamics of behavioural changes brought about by technological, economic or cultural change, or policies. The multistate method has become the standard methodology among demographers (Rogers 1975, 1995; Willekens and Drewe 1984; Keyfitz 1985; Ahlburg *et al.* 1999; Van Imhoff and Keilman 1991; Zeng Yi 1991). It has been applied for projecting regional populations, and projections by educational status, household status, labour force participation and health/disability status. The multistate model is currently receiving much interest in epidemiology and public health (for a review, see Commenges 1999; Hougaard 1999, 2000). A major difference between multistate models in demography and epidemiology is that in demography age is a key variable, whereas in epidemiology it is not (yet).

The choice of static versus dynamic method has been the subject of long debates in demographic analysis and forecasting. In labour force projections, the debate was most intensive in the early 1980s after the publication in 1982 by the Bureau of Labor Statistics of multistate tables of working life (Smith 1982). In health status projections, the debate is of a more recent date (eg. Crimmins *et al.* 1994; Mathers and Robine 1997). Some authors attempted to reconcile the two approaches (eg. Newman 1988). In his review of functional population projections, Kono asserts that "Because of complex and precise data demands, however, almost no multistate models which could be used reliably in official national projections, beyond regional projections, have been developed" (Kono 1993:18.2). In this paper, we aim to show that multistate models represent an adequate basis for the specification of functional population projection models despite data demands.

Forecasting involves dealing with uncertainty since the future is inherently uncertain. Two basic issues arise. The first is to *quantify* the uncertainty, ie. to indicate the degree of precision of the projected figures. The precision is high when a predicted figure is likely to be true. The second is to *reduce* the uncertainty, i.e. to increase the predictive performance of forecasts. The quantification of uncertainty has received much attention in the scholarly literature. The traditional approach is to specify a few sets of vital rates and migration rates that represent possible futures (scenarios). A more recent approach is to generate probabilistic projections that are based on the assumption that point forecasts are available for the relevant vital rates and migration rates, and the expected uncertainty of the forecast can be characterized in terms of variances and certain simple covariance structures for the error terms. The outcome is a predictive interval that specifies the probability that the future population will be between x and y million (eg. Alho and Spencer 1997; Lee 1998; Alho 2003). In order to determine the nature of the distribution characterizing vital rates and the width of the distribution, three alternative approaches have been proposed in the literature. One approach is based on statistical time series analysis, the second uses an extrapolation of errors observed in past projections, while the third derives uncertainty bands from expert judgement. A synthesizing approach that includes the key elements of all three approaches has been outlined by Lutz *et al.* (1997).

The reduction of uncertainty has been studied less systematically in the scholarly literature although it is a core issue in the production of more accurate and reliable forecasts. Strategies for reducing uncertainty include (1) a better understanding of the mechanisms that govern demographic change and (2) a better measurement of vital rates (demographic parameters) for subpopulations. The second strategy, which involves better data, received extensive coverage in the literature. The first strategy was much less the subject of systematic investigation. It involves a better use of scientific knowledge in demographic projections. Twenty years ago, Keyfitz asked the question "Can knowledge improve forecasts?". He stated that "For policy purposes, causal knowledge is essential; for forecasting it is desirable, of course, but the forecast is not necessarily a failure if the causal mechanisms remains undiscovered. Observed regularities serve perfectly well for forecasting as long as they continue to hold." (Keyfitz 1982:747). For many years, the search for regularities dominated the demographic forecasting literature. There is nothing wrong with that. As Keyfitz observed "Pending the discovery of a truly behavioral way of estimating the future, we cannot afford to be ashamed of extrapolating the observed regularities of the past" (Keyfitz 1982:747). About ten years ago and in the context of forecasting the health of the elderly population, Manton, Singer and Suzman are less at ease when they summarized the state of the art as follows:

> Current forecasting procedures are often based on empirical extrapolations and do not directly reflect physiological processes at the individual level or the mixture of individuals in a cohort. The failure to deal with individual aging trajectories, and their cohort mix, makes it difficult to use epidemiological and biomedical evidence on the impact of health changes on the organism in forecasts."(Manton *et al.* 1993:25).

The effective use of substantive knowledge on causal mechanisms remains a challenge. Most demographic projection models have limited scope for incorporating substantive knowledge on causal mechanisms. Multistate models have that scope.

Over the years, researchers tried to improve the *predictive performance* of the models they developed by incorporating substantive knowledge on biological and behavioural mechanisms underlying demographic change. When Keyfitz published his views, no generally accepted framework existed that encompassed the many factors affecting demographic processes in a dynamic way and allowed a causal analysis. Today that framework exists. During the past decades, the life course paradigm has become a "metatheoretical perspective" that integrates biological processes, past experiences (antecendents) and historical context (Giele and Elder 1998:21). It provides a way to combine biological processes, cognitive processes and social processes that shape the lives and behaviours of people. It also provides a logical framework to integrate risk factors (particular attributes) and exposure analysis (duration at risk of particular events and risk levels). In the behavioural and social sciences and in epidemiology, biological and behavioural mechanisms are increasingly being studied from a life-course perspective (eg. Giele and Elder 1998; Elder 1999; Kuh and Ben-Shlomo 1997; Barker 1998; Ben-Shlomo and Kuh 2002; Kuh and Hardy 2002; WHO, 2002; Halfon and Hochstein 2002). The concept of a life course refers to the way in which the countless aspects of our lives are interwoven and shaped by biological, technological, cultural and institutional influences and how their interaction results in an organic system that evolves in time. The factors affecting our lives include personal characteristics, individual histories, contextual factors and collective histories. Since the life course is embedded in a historical context, the effects of these factors are revealed more clearly if different cohorts (or generations) are considered. The life course paradigm continues to be a successful organizational principle for research. It has been proposed as a paradigm for demographic forecasting (Willekens 2002). It is gradually becoming a paradigm in policy making in the private and public sector. It is the dominant framework that underlies life planning, a subject that is receiving a growing interest as the population ages and the role of government in social support is being debated. Governments and financial institutions are providing tools for assessing lifetime financial and other consequences of life events such as marriage, divorce, childbirth, and retirement. New government policies are introduced that adopt a life course perspective (Rowe 2003). For example, health policies are increasingly targeting risk factors that affect health in later life (eg. smoking and obesity), and the provision of pensions is increasingly being discussed within the context of life planning extending over the entire life course.

This paper defends four complementary views:

1. *Functional population projections are essentially projections of cohort biographies.* Functional population projections pertain to different domains of life including work, family, health and residence. The aim of functional population projections is to project how many members of a real or synthetic cohort occupy the functional states at a given age and a given point in time. In other words, the aim of functional population projections is to project ***state occupancies***. The sequence of state occupancies by cohort members as they age describes a ***cohort biography.***[1] Consequently, functional population projections are essentially projections of cohort biographies (biographic projections).

2. *Whenever possible, functional population projections should utilize multistate models since they picture more closely the mechanisms of demographic change.* Static projection models rely on observed state occupancies (prevalence rates, ratio method). However, the state occupancies are the outcome of ***state transitions*** at earlier ages. The dynamic method derives state occupancies from transitions between functional states. The transitions are governed by transition rates (or incidence rates) and transition probabilities.
3. *The life course offers a logical framework for incorporating substantive knowledge in forecasts.* Knowledge on biological and behavioural mechanisms can indeed improve forecasts and the life course is the way to incorporate substantive knowledge. Techniques of event history or life history modeling permit causal analysis (Blossfeld and Rohwer 2002). They can be extended to forecasting.
4. *Functional population projections should evolve to projections of individual biographies.* Cohort members differ in personal attributes and living conditions (context). The best approach to account for these differences is to distinguish individuals and to characterize each individual by a bundle of attributes. These *virtual* or *synthetic* individuals bridge the micro-macro gap in population forecasting. The life courses of these individuals may be projected using techniques of micro-simulation. The aggregation of the individual biographies that result yields a bottom-up estimate of the cohort biography.

This paper suggests a shift from conventional population projection, with its emphasis on numbers of people, to a projection of the lives of people. It links macro-level models of population dynamics with micro-level models of the individual life course. The life course is viewed as a sequence of *states* (or stages) and *events* that involve transitions from one state to another. The advantages of such a shift are the following.

i. Population heterogeneity can be dealt with in a better way than when other approaches are adopted. Traditional projections assume that members of the same cohort have identical demographic behaviour. Within-cohort differences are introduced by stratifying the population into subpopulations on the basis of significant attributes such as sex, marital status, health status, and region of residence. Membership of a subpopulation is usually not fixed forever. During the life course, people move between subpopulations. They marry and divorce, change health status and migrate. Members of the same stratum or subpopulation are not homogeneous either; they may differ in many ways and the differences are likely to affect their chances for survival, the number of children they have, and other aspects of demographic behaviour. An investigation and representation of these differences at the population level becomes infeasible quickly. An approach that focuses on individual actors, their lifestyles and life courses, facilitates the implementation of heterogeneity.

ii. Population dynamics is the outcome of changes in the relative size of subpopulations (composition effect) and changes in the behaviour of members of a subpopulation (rate effect). Population forecasting involves the prediction of or hypotheses about changes at the individual level. Since demographic events are embedded in the life course, these predictions are difficult to make without a life course perspective. For instance, it has been stressed that mortality projections should use the growing insights in the physiological mechanisms underlying aging and their relation to mortality (Manton 1993:79). Considerable progress has been made. Yashin (2001) reviews mortality models that incorporate theories of aging. What applies to mortality, applies to fertility, migration, marital status change, and other demographic events.

iii. Life course projections provide information not available in regular functional population projections. Functional projections provide information on state occupancies and types and numbers of state transitions at some future time. Life course projections also provide sequences of states occupied (pathways) and estimates of expected sojourn times in the different states or episodes of life. The episodes may relate to unemployment, disease, dependency, or poverty. For instance, population projections generally include estimates of dependency ratios, but the expected duration of dependency remains unknown. Life course projections provide information on expected sojourn times in dependency. For instance, unemployment projections would be more relevant to policy making if durations of unemployment spells would be predicted in addition to the proportion unemployed.

iv. The projection of the lives of people has significance in its own right, independent of its contribution to improved population forecasts. The prediction of the probability of an event in a given period or a lifetime has significance beyond its meaning for changes at the population level. Examples include the prediction of the impact of risk factors on the incidence of a chronic disease, the likelihood of deviant or criminal behaviour, the probability that a marriage ends in a divorce, the probability of entry into relative poverty, etc.. The number of papers on these subjects is immense. There exists however a common modelling approach that is often used. It is the prediction of probabilities based on hazard functions estimated conditionally on risk factors and other covariates that affect the rate of occurrence, sometimes augmented by unobserved random effects. The incidence is often linked to events and experiences early in life (including foetal life and infancy). The term "programming" has been used to describe a process whereby a stimulus at a sensitive or critical period of development has lasting or lifelong significance (eg. Barker 1998:13). One of the best examples of the programming phenomenon is the permanent change that is induced by under-nutrition in early life.

The paper is organised as follows. Section 2 presents the approach that is adopted in biographic forecasting. Life is viewed as a sequence of states and events. They may pertain to one particular domain of life or to a combination of domains such as work and family. A sequence in one domain is referred to as a career. Life consists therefore of a set of interdependent careers (Elder 1985).

Section 3 presents the multistate model. The projection model is an extension of the cohort-component model and the model for functional population projections. The basic parameters are **transition rates** and **transition probabilities**. These rates and probabilities must be estimated from the data and consequently the model rates/probabilities are equal to empirical rates/probabilities. The core of the method is the multistate model and regression models that predict rates (or probabilities) of transition. In this paper, no distinction is made between the multistate life table model and the projection model. We make use of two perspectives on the life table. The first is a population perspective: the life table describes the characteristics of a stationary population. The second is a life history perspective: the life table describes the life history of members of a synthetic cohort, i.e. the cohort biography. In traditional projections, the first perspective dominates. The life table serves as the source of the parameters of the projection model. In this paper, the life history perspective is followed. Although that perspective has been around for decades and the multistate life table has been used to describe life histories (eg. Willekens and Rogers 1978), it has not caught on.

Section 4 discusses a generic approach to accommodate substantive knowledge and causal mechanisms in population forecasting. The approach relies on transition rate models and transition probability models and follows the perspective on causal analysis adopted by Blossfeld and Rohwer (2002).

The empirical base for demographic forecasting consists of data of various types. Two broad categories are distinguished: data on events and data on discrete-time transitions. The multistate life table contains methods for estimating transition probabilities from transition rates. Section 5 describes a method for estimating transition rates from probabilities. It is the inverse method, developed by Singer and Spilerman (1979).

The central position of transition rates in demographic analysis is also illustrated in Section 6. It is asserted that the transition rates are the logical parameters to integrate scenario-setting and various types of uncertainty in demographic forecasting. The view is held that probabilistic forecasting should concentrate on quantifying the uncertainty in transition rates and transition probabilities. The transition rates also constitute a bridge between the population level and the individual level. At the individual level of analysis, e.g. to predict individual biographies, use is made of transition rates that depend on individual attributes. At the population level, e.g. to forecast cohort biographies, expected values of transition rates across individuals are used. The micro-macro link is further described in Section 7.

Section 8 presents a brief description of the MicMac project funded by the European Commission and implemented by a consortium of research centres in Europe. An introduction to the software is also given. Section 9 concludes the paper.

The Approach: Forecasting Biographies/Life Histories

Generic models of the life course view an individual as a carrier of attributes and the life course as sequences of events and states/episodes. Sequences are defined in different domains of life and they co-exist, co-evolve and interact. A population consists of individuals and the population structure is the aggregate effect of individual life courses. For the purpose of analysis and projection, a population is stratified in birth cohorts. A cohort may be further stratified by functional state or state of existence. A cohort evolves because members make transitions between functional states and eventually die. Existing cohorts are replaced by new birth cohorts. Functional population projections are projections of state occupancies.

Multistate models describe the life course. Age is the main time scale used to position life events in time. In its simple form, the multistate model describes the collective life history or biography of a cohort and disregards intra-cohort variations. The description of the cohort biography is facilitated by the multistate life table and extensions of the life table. Multistate models have been used for population projection. Examples include LIPRO (Van Imhoff and Keilman 1991), MUDEA (Willekens and Drewe 1984), and PROFAMY (Zeng Yi *et al.* 1997). The models are designed to describe and project changes in the population composition at the macro level. They concentrate on the position individuals occupy in the collective biography at consecutive points in time and the population structure that results. They do not address the prognosis of events and episodes in the lives of people, which is the subject of life course projections. The link between the traditional macro-level models and the new micro-level models is the multistate life table, and more particularly the **occurrence-exposure rate**. Occurrence-exposure rates are also known as event rates, hazard rates and transition rates, depending on the field of study. The occurrence-exposure rate bridges the micro-macro gap in population forecasting. The occurrence-exposure rate may be used to describe the dynamics at the macro-level and the transitions at the micro-level. Observed differences between cohort members are considered in terms of risk factors and covariates and the risk ratios or relative risks associated with different levels of risk factors and covariates. Unobserved differences are described by mixture models and random effect models. Mixture models classify people in a finite number of categories. Random effect models assume a continuous distribution of individual differences.

The life table underlies both the dynamics at the population level and the individual life history. That is consistent with the population and the life history perspectives on the life table (see above). The multistate life table and the multistate projection model are adequately documented in the literature (eg. Roger, 1975; Schoen 1988; Manton and Stallard 1988). In this paper, no fundamental distinction is made between the life table and the projection model. The life table is viewed as a projection model.

The combination of a hazard model and a multistate life table constitutes the main ingredient of the proposed method for functional population projections and the prediction of the life course. The combination of regression models and life tables was introduced more than thirty years ago by Cox (1972) and, for multistate life tables, more than 10 years ago by Gill (1992). Both authors give a central position to occurrence-exposure rates or transition rates. Many models in demography and epidemiology rely on probabilities or on types of rates that differ from occurrence-exposure rates. The method that allocates a key position to occurrence-exposure rates is sometimes referred to as the person-years approach.

By way of illustration of biographic forecasting, we consider chronic diseases. The prognosis of a chronic disease involves the prognosis of the occurrence of the disease, the age at onset of the disease, and the number of years with the disease. It also involves the identification of the factors that increase or reduce likelihood of the disease. Risk factors are among them, but also the factors that influence the length of life. The prognosis of a disease cannot be separated from a prognosis of the length of life. Figures on lifetime risks that are often cited in the media or scholarly literature involve statements or assumptions on length of life. To clarify the interdependence, the occurrence-exposure is the key. To demonstrate the significance of this statement, which may be common knowledge in demography, a reference is made to recent discussions in the medical literature. Many studies that estimate the probability of an event during a period of a given length or the lifetime risk of an event overestimate the probability by an inadequate treatment of the competing risks. The matter is at the core of life-course forecasting. We consider a few examples.

The probability that a person in the Netherlands develops cancer is 45.1 per cent for males and 30.4 per cent for females, if the person survives to the age of 85. The probabilities are conditional on survival to the age of 85. If mortality before the age of 85 is taken into account the probabilities of developing cancer before the age of 85 is 33.2 per cent for males and 27.8 per cent for females (Schouten *et al.* 1994). The first type of probability is known as the cumulative incidence (CI), the second is the life table probability. As people live longer, the probability of developing cancer will increase, even when the age-specific cancer rates do not change. It is the composition effect, referred to in the introduction of this paper. More people survive to ages when the risk is high. Schouten *et al.* also estimate that the probability that women in the Netherlands develop breast cancer before the age of 85 is 9.4 per cent in the absence of mortality before 85 and 7.9 per cent in the presence of mortality. An often-cited figure in the United States is a probability of breast cancer of 12.8 per cent. The estimate is from the National Cancer Institute (NCI) and is the *lifetime* probability of breast cancer (e.g. National Cancer Institute 2001; Morris *et al.* 2001). It is based on the NCI's Surveillance Program (SEER) and cancer rates from 1995 through 1997, and it takes into account that not all women live to older ages, when breast cancer risk becomes the greatest (National Cancer Institute 2001). Cancers that develop at a higher age are more prevalent among population groups that live longer. For instance, the lifetime risk of prostate cancer is higher among Whites than Blacks because fewer Blacks reach the ages where prostate cancer develops rapidly (Wun *et al.* 1998:183). The lifetime risk of parkinsonism and Parkinson's disease is only slightly higher in men than in women because of the opposite effects of higher incidence and higher mortality in men (Elbaz *et al.* 2002). It is well-known that healthy life may increase the lifetime probability of chronic diseases that start at higher ages, such as cardiovascular disease and cancer. The greater longevity of women is the primary cause of their greater lifetime probabilities of congestive heart failure and stroke (Peeters *et al.* 2002). And when the disease occurs, women lose a greater number of years of life than men. A final illustration highlights the complex interrelation between smoking, cardiovascular disease and mortality. Although smoking is known to increase the risk of cardiovascular disease at each age, over a lifetime never-smokers have approximately the same risk of cardiovascular disease as always smokers, simply because they live longer (Mamun *et al.* 2002). Furthermore, if fewer smokers die from lung cancer, the lifetime risk of heart disease among former smokers may rise. It is the association between the risk factors and different chronic diseases that underlie the tempo distortions of mortality, identified by Bongaarts and Feeney (2002) and discussed by Vaupel (2002). It links the tempo distortions to heterogeneity and selection.

The cumulative incidence or cumulative risk is often used to determine the likelihood of a disease. It is the number of new cases during a given period (5 years, 10 years, or lifetime) divided by the initial population free of a disease (*event-free population*). The CI is generally not adjusted for the presence of competing risks, such as death. It is therefore free of the influence of mortality.[2] Formulated differently, it assumes that there is no competing risk of death. In the absence of death or another competing event, the amount of time at risk is the same for every member of the group and members are assumed to live for the entire lifespan. It is a conditional probability; conditional on survival. As a consequence, the CI or cumulative risk overestimates the risk of developing a disease. The effect of the competing risks is taken into account by constructing a multiple decrement life table. The life table risk or lifetime risk, as it is often called in epidemiology, is lower than the CI. For a discussion, see Schouten *et al.* (1994), Lloyd-Jones *et al.* (1999), Beiser *et al.* (2000:1499) and Elbaz *et al.* (2002). Beiser *et al.* (2000) distinguish an unadjusted cumulative incidence (UCI) and an adjusted cumulative incidence (ACI). The UCI overestimates the incidence of an event because not all people live till the maximum age. The ACI proposed by the authors account for the competing risk of death by calculating the CI using the multiple-decrement life table. In the absence of a mortality pattern of the study population, the authors suggest using the mortality experience of a "standard" population, leading to a standardised lifetime risk. This brief discussion of cumulative risks and lifetime risks or lifetable probabilities illustrate the importance of competing events in the estimation of probabilities. The use of occurrence-exposure rates as defined above, is a guarantee for the correct estimation of probabilities. In the field of epidemiology, the person-years analysis of incidence rates has been described by Breslow and Day (1987). For a detailed recent description in the context of the prediction of lifetime incidence, see Beiser *et al.* (2000). Occurrence-exposure rates are used throughout this paper.

The illustration demonstrates the types of issues that arise in biographic forecasting. Prediction or prognosis of events and experiences, e.g. episodes of poverty, unemployment, or impairment, is not common yet in demography, but is common in epidemiology, public health, and medical practice. In those fields, it is still considered "a complicated business" (De Backer and de Bacquer 1999). The probabilities that are estimated from data and projected in the future are used by physicians to determine the need for intervention or treatment. The probabilities are also used in public health to determine public health concerns and to assess the public health and financial consequences of the presence of risk factors.

Transition rates depend on risk factors and other determinants. A risk factor is defined as a factor that is causally related to an outcome. The concept originated in epidemiology, where the identification of the causal link is an important element of the etiology of a disease. In many cases, a causal link cannot be determined and the association between predictor and outcome is a statistical one. In the prediction of the life course, risk factors and other factors are evaluated in terms of their predictive performance and not their explanatory power. Two comments are warranted here. First, the link between a risk factor and the outcome is probabilistic. It means that the presence of a risk factor changes (usually increases) the *probability* of an event or the *expected* duration of an episode. The significance of an event lies in the consequences to the life history of an individual (Peeters *et al.* 2002). Second, several risk factors may change during the course of life. Modifiable risk factors are particularly relevant in the design of health policies and public health programmes. They should also be considered in forecasting since the health outcomes (and mortality) depends on the modifiable risk factors. For instance, when more people stop smoking and start eating healthy, the long-term consequences will be increased survival, possibly associated with longer periods of chronic disease.

The Multistate Model

In this section, we derive the multistate model for a sample of m individuals born at the same time (same year, say). We adopt a probabilistic perspective which has been introduced in multistate demographic modelling by Hoem and Jensen (1982), Namboodiri and Suchindran (1987) and others (eg. Chiang 1984).

State Occupancies

Let $Y_k(x)$ be a time-varying indicator variable representing the state occupied by individual k (k = {1, 2, …, m}) at age x. Individual k is not necessarily a specific person but a combination of attributes. Instead of age, we may use another time scale. In that case, x indicates the time elapsed since the reference event. The possible states are given by the state space **S** ={1, 2, 3, …, I}, with I the size of the state space. The state space includes all possible states. If death is considered, it includes the state of dead. Dead is an absorbing state and cohort members who die remain in that state. The polytomous random variable $Y_k(x)$ is a discrete variable that can take on as many non-zero values as there are states in the state space. $Y_k(x)$ is zero if individual k died before age x.

The number of individuals in state i (i = 1, 2, ..., I) at age x is denoted by $N_i(x)$. It is equal to

$$N_i(x) = \sum_{k=1}^{m} I_{Y_k(x)} = \sum_{k|Y_k(x)=i}^{m} \mathrm{I}$$

where m is the number of individuals in the birth cohort and $I_{Y_k(x)}$ is an indicator function which is 1 if $Y_k(x)$ is i and 0 otherwise. $N_i(x)$ is a random variable.

A second approach exists to denote the state occupied at a given age. It defines a binary random variable $Y_{ki}(x)$. It is equal to 1 if individual k is in state i at age x and 0 otherwise. The number of individuals in state i at x is

$$N_i(x) = \sum_{k=1}^{m} Y_{ki}(x)$$

The expected value of $Y_{ki}(x)$ is the probability that individual k is in state i at age x. It is the *state probability*. Two types of state probabilities are distinguished: unconditional and conditional. The unconditional state probability is the probability that cohort member k occupies state i at age x; it is denoted by ${}_k\ell_i(x)$ and

${}_k\ell_i(x) = E[Y_{ki}(x)] = \Pr\{Y_{ki}(x)=1\} = \Pr\{Y_k(x)=i\}$.

It is a composite probability that depends on survival. The conditional state probability is the probability that cohort member k occupies state i at age x, provided k is alive at x. It is denoted by ${}_k\pi_i(x)$. The relation between the two probabilities is: ${}_k\ell_i(x) = {}_k\ell_+(x) * {}_k\pi_i(x)$, where ${}_k\ell_+(x)$ is the probability that cohort member k is alive at age x. If all cohort members are identical, i.e. if the cohort is homogeneous, the state probabilities are the same for all individuals: ${}_k\ell_i(x) = {}_+\ell_i(x) = \ell_i(x)$ for all k and ${}_k\pi_i(x) = \pi_i(x)$ for all k. The traditional multistate cohort-component model relies on the homogeneity assumption. In the absence of intra-cohort variation, the expected number of cohort members in state i at age x is $K_i(x) = E[N_i(x)] = Q * \ell_i(x) = Q * \ell_+(x) * \pi_i(x)$, with Q the cohort size or radix. This expression is part of the traditional multistate life table and is implicit in the multistate cohort-component model (macro model). If individuals differ in a few characteristics only or if a few characteristics suffice to predict the state occupied at age x, then ${}_k\pi_i(x) = \pi_i(x,Z)$, where Z represents a specific combination of characteristics or covariates. The probability that individual k occupies state i at exact age x depends on the covariates only and individuals with the same covariates have the same state probability. Covariates will be introduced later.

In functional population projections, the state probabilities are estimated directly from the data (exogenous) if the static method is adopted and are generated by a multistate model (endogenous) if the dynamic method is used. Note that the prevalence rates and headship rates in static functional population projections are in fact state probabilities. We consider the estimation of state probabilities from sample data. Consider a sample of m individuals. We do not consider covariates, implying that all individuals are identical. Covariates are introduced below. In addition, age is omitted for convenience. The number of individuals observed in state i is

$$N_i = \sum_{k=1}^{m} Y_{ki}$$

The probability of observing n_1 individuals in state 1, n_2 in state 2, n_3 in state 3, etc., is given by the multinomial distribution

$$\Pr\{N_1 = n_1, N_2 = n_2, \ldots\} = \frac{m!}{\prod_{i=1}^{I} n_i!} \prod_{i=1}^{I} \pi_i^{n_i}$$

where n_i is the observed number of individuals in i. π_i is the probability that an individual is found in state i; it is the expected value of Y_i: $\pi_i = E[Y_i]$. The restrictions $\sum \pi_i = 1$ and $\sum N_i = \sum n_i = m$ apply. The most likely values of the parameters π_i, given the data, are obtained by maximizing the likelihood that the model predicts the data, which is the maximum likelihood method. The value of π_i (i = 1, 2, …, I) that maximizes the above multinomial distribution is $\hat{\pi}_i = \frac{n_i}{m}$. $\hat{\pi}_i$ is the estimate of the state probability $\hat{\pi}_i$.

The expected (predicted) number of individuals occupying state i is $E[N_i] = \hat{\pi}_i\, m$. The variance of N_i is $Var[N_i] = \pi_i(1-\pi_i)m$. It is estimated as $\hat{\pi}_i(1-\hat{\pi}_i)m$. The variance of Y_i is $Var[\pi_i] = Var[N_i/m] = Var[N_i]/m^2 = [\pi_i(1-\pi_i)]/m$. It is estimated as $\hat{\pi}_i(1-\hat{\pi}_i)/m$. The variance declines with increasing sample size.

The parameters used in demographic projections are frequently based on vital statistics or census data and not on sample surveys. For large m, the estimate of the state probability π_i has low variance, and estimation errors may be omitted. That is common practice in population projections. Other measurement errors should be considered, however.

State Transitions

In this section, we derive expressions for transition probabilities and transition rates. First we provide a logical link between state occupancies and state transitions. The link is useful since the static method of functional population projections focuses on state occupancies whereas the dynamic method focuses on state transitions and obtains state occupancies from the initial condition and a sequence of state transitions.

The state occupied at a given age generally depends on the states occupied at previous ages, in addition to personal attributes at the given age and prior experiences and conditions captured in the life history. Hence the probability of being in state j at age y depends on the states occupied at previous ages x_1, x_2, x_3 etc: $Pr\{Y(y) = j \mid Y(x_3), Y(x_2), Y(x_1); Z\}$ $y > x_i$ $i = 1, 2, 3$ where Z denotes contemporary and prior characteristics and experiences. It is often assumed that only the most recent state occupancy is relevant (denoted by x):

$$Pr\{Y(y) = j \mid Y(x_3), Y(x_2), Y(x_1); Z\} = Pr\{Y(y) = j \mid Y(x); Z\}$$

If the state occupied at x is i, then

$$\Pr\{Y(y) = j \mid Y(x) = i, Z\} = p_{ij}(x, y, Z)$$

$p_{ij}(x,y,Z)$ is the probability that an individual with characteristics Z, who occupies state i at x occupies state j at y. It is the discrete-time transition probability. The interval can be of any length but is generally one or five years.

Transitions may be measured in continuous time and in discrete time. The distinction is consistent with the traditional distinction between two approaches to microsimulation modeling: continuous-time modeling and discrete-time modeling (eg. Galler 1997; O'Donoghue n.d.:13). We first consider **continuous time**. Let ${}_kY_{ij}(x)$ be a time-varying indicator variable which takes on the value 1 if individual k makes a move from state i to state j at exact age x, i.e. in the infinitesimally small interval following x. It is zero otherwise. The interval is sufficiently small to exclude multiple transitions. During the interval, at most one transition may occur. The number of transitions by members of the birth cohort is

$$N_{ij}(x) = \sum_{k=1}^{m} {}_kY_{ij}(x)$$

The expected value of ${}_kY_{ij}(x)$ is the probability that individual k makes a transition from i to j at age x. It depends on being alive at x and being in i at that age. The conditional transition probability is the probability of a move from i to j provided individual k is alive and in state i at age x. It is the transition probability:

$$_k\mu_{ij}(x) = \lim_{(y-x)\to 0} \frac{\Pr\{Y_k(y) = j \mid Y_k(x) = i\}}{y-x} = \lim_{(y-x)\to 0} \frac{_k p_{ij}(x,y)}{y-x}$$

It is the transition probability per unit time for very small intervals. The probability that individual k who occupies i at exact age x moves to j at that age, $_k\mu_{ij}(x)$, is known as the instantaneous rate of transition or ***transition intensity.***[3]

The unconditional transition probability is $_k\ell_{ij}(x)$ which may be written as $_k\ell_{ij}(x) = {_k\ell_{i+}}(x) * {_k\mu_{ij}}(x) = {_k\ell_{+}}(x) * {_k\pi_{i}}(x) * {_k\mu_{ij}}(x)$ where the first term is the probability of surviving to age x, the second the conditional state probability and the third the transition intensity. It is the event rate during the infinitesimally small interval following exact age x.

If all cohort members are identical, the transition probabilities are the same for all individuals: $_k\ell_{ij}(x) = \ell_{ij}(x)$ for all k and $_k\mu_{ij}(x) = \mu_{ij}(x)$ for all k. The traditional multistate cohort-component model (macro model) relies on the homogeneity assumption. In the absence of intra-cohort variation, the expected number of cohort members making a transition at age x from state i to state j is $K_{ij}(x) = E[N_{ij}(x)] = Q * \ell_{ij}(x) = Q * \ell_{+}(x) * \pi_{i}(x) * \mu_{ij}(x)$ where Q is the cohort size or radix.

In some applications, such as migration, the transition intensity $\mu_{ij}(x)$ is decomposed into two components: a generation component and a distribution component. The generation component is intensity of leaving the state of origin (exit rate). The distribution component is the probability of a given destination, conditional on leaving the state of origin. The transition intensity may be written as $\mu_{ij}(x) = \mu_{i+}(x) * \xi_{ij}(x)$ with $\mu_{i+}(x)$ hte instantaneous rate of leaving state i and $\xi_{ij}(x)$ the probability that an individual who leaves state i selects j as the destination. It is the conditional probability of a *direct transition* from i to j. Direct transition differ from discrete-time transitions discussed later in this paper. Direct transitions are events while discrete-time transitions refer to states occupancies at two points in time. Within an interval, several direct transitions may occur. In migration analysis and multiregional demography, direct transitions are generally referred to as *moves* (Rogers *et al.* 2002). Probabilities of a direct transition are estimated in LIFEHIST, a packaged developed by Rajulton at the University of Western Ontario. Note that $\xi_{ij}(x) = \dfrac{\mu_{ij}(x)}{\mu_{i+}(x)}$. Note also that the above expression is that of a competing risk model or a transition rate model with multiple destinations (Blossfeld and Rohwer 2002). In the terminology of competing risks, the first term is the rate of event and the second term (destination) indicates the type of event. The separation of the transition intensity into two parts is particularly useful when the factors that affect the occurrence of an event (movement out of a state of existence) differ from the factors that affect the type of event (direction of change or destination after the event). In that case the event occurrence and the direction of change are two distinct causal processes and $\mu_{i+}(x)$ and $\xi_{ij}(x)$ can be estimated independently (Hachen 1988:29; Sen and Smith 1995:372). The transition rate is studied using a rate model whereas the destination probability is studied using a logit or logistic regression model.

Transitions may also be measured in **discrete time** by comparing the states occupied at two consecutive ages. Consider the interval between ages x and y. Let ${}_kY_{ij}(x,y)$ be a time-varying indicator variable which takes on the value 1 if individual k occupies state i at exact age x and state j at exact age y. It is zero otherwise. State j may be the state of "dead" which is absorbing. Note that k refers to any cohort member and is not restricted to cohort members occupying state i at x. Below we consider the sub cohort of occupants of i at x.

The number of discrete-time transitions between origin state i and destination state j during the interval from x to y is equal to the (initial) number of cohort members (cohort size m) in state i at exact age x and state j at exact age y. It is denoted by $N_{ij}(x,y)$. It is

$$N_{ij}(x,y) = \sum_{k=1}^{m} {}_kY_{ij}(x,y)$$

${}_kY_{ij}(x,y)$ and $N_{ij}(x,y)$ are random variables. Let ${}_ky_{ij}(x,y)$ be an observation on ${}_kY_{ij}(x,y)$ and let $n_{ij}(x,y)$ denote the observed number of individuals in state i at age x and state j at age y:

$$n_{ij}(x,y) = \sum_{k=1}^{m} {}_ky_{ij}(x,y) = \sum_{k=1}^{m} {}_ky_i(x)\; {}_ky_j(y)$$

where ${}_ky_i(x)$ is 1 if individual k is observed to occupy state i at exact age x and 0 otherwise. The probability of observing $n_{ij}(x,y)$ cohort members occupying state i at exact age x and state j at exact age y for various i and j is given by the multinomial distribution provided the transitions are independent:

$$\Pr\{N_{12}(x,y)=n_{12}(x,y), N_{13}(x,y)=n_{13}(x,y),\ldots\}=\frac{m!}{\prod_{i=1}^{I}\prod_{j=1}^{J} n_{ij}(x,y)!}\prod_{i=1}^{I}\prod_{j=1}^{J}\ell_{ij}(x,y)^{n_{ij}(x,y)}$$

where $\ell_{ij}(x,y)$ is the probability that cohort member occupies i at x and j at y with $\sum_i\sum_j \ell_{ij}(x,y)=1$. $n_{ij}(x,y)$ is the observed number of individuals (among the original cohort of m individuals) occupying i at age x and j at age y with $\sum_i\sum_j N_{ij}(x,y)=\sum_i\sum_j n_{ij}(x,y)=m$. The most likely values of the parameters $\ell_{ij}(x,y)$, given the data, are obtained by maximizing the likelihood that the model predicts the data. It is the maximum likelihood method. The likelihood function is

$$\prod_{i=1}^{I}\prod_{j=1}^{J}\ell_{ij}(x,y)^{n_{ij}(x,y)}$$

The values of ℓ_{ij} (i,j = 1, 2, …, I) that maximize the above multinomial distribution is $\hat{\ell}_{ij}(x,y)=\frac{n_{ij}(x,y)}{m}$. The quantity $\hat{\ell}_{ij}(x,y)$ is the estimate of the probability that a cohort member occupies state i at age x and state j at age y, which is the expected value of $Y_{ij}(x,y)$: $\ell_{ij}(x,y) = E[Y_{ij}(x,y)]$. Note that $\ell_{ij}(x,y)$ is an unconditional probability since it relates to an initial cohort member.

The population is usually stratified by age and the base population is the number of cohort members surviving to exact age x. In that case, m is replaced by m(x) and the transition probability is the (conditional) probability that a cohort member *surviving at age x* occupies state i at age x and state j at age y. It is the probability that any person of age x occupies state j at age y, irrespective of the state occupied at x. In multistate demography, this is known as a population-based life-table measure (Willekens 1987:136ff). The transitions may be conditioned, not only on survival, but also on the state occupied at age x. It is a status-based life-table measure and is denoted by $\pi_{j|i}(x,y)$ and it is the probability that a cohort member of age x (i.e. surviving at age x) and occupying state i, will be in j at age y. The probability will be denoted by $p_{ij}(x,y)$. The probability of a given observed set of transitions is

$$\Pr\{N_{i1}(x,y)=n_{i1}(x,y), N_{i2}(x,y)=n_{i2}(x,y),\ldots|\, Y_i(x)=1\}=\frac{m_i(x)!}{\prod_{j=1}^{J} n_{ij}(x,y)!}\prod_{j=1}^{J} p_{ij}(x,y)^{n_{ij}(x,y)}$$

The above equation represents the competing risks model or multiple destination model (eg. Blossfeld and Rohwer 2002).

Transition Intensities, Rates and Probabilities

The probability that individual k in i transfers to j during an infinitesimally small interval following x is the instantaneous rate of transition:

$${}_k\mu_{ij}(x) = \lim_{(y-x)\to 0} \frac{\Pr\{Y_k(y) = j \mid Y_k(x) = i\}}{y-x} = \lim_{(y-x)\to 0} \frac{{}_k p_{ij}(x,y)}{y-x} \qquad \text{for i not equal to j.}$$

In this section, we assume that all cohort members are identical. Within-cohort variation is absent. The instantaneous rate of transition is also known as the transition intensity and the force of transition. The term $\mu_{ii}(x)$ is defined such that $\sum_j \mu_{ij}(x) = 0$

Hence

$$-\mu_{ii}(x) = -\sum_{j \neq i} \mu_{ij}(x) = \lim_{(y-x)\to 0} \frac{p_{ij}(x) - 1}{y-x}$$

The quantity $\mu_{ii}(x)$ is non-negative. The quantity $\mu_{ii}(x)$ is sometimes referred to as the intensity of passage because it relates to the transition from i to any other state different from i (eg. Namboodiri and Suchindran 1987:38). Schoen (1988:65) refers to it as the "force of retention.

The intensities are the basic parameters of a continuous-time multistate process. Under the restrictive Markov assumption, the probability that an individual leaves a state depends only on the state. It is independent of other characteristics. In this paper, the transition probability also depends on age.

The matrix of instantaneous rates with off-diagonal elements $-\mu_{ij}(x)$ and with $\mu_{ii}(x)$ on the diagonal is known as the generator of the stochastic process $\{Y_k(x);\ x \geq 0\}$ (Çinlar 1975:256). The matrix is denoted by $\boldsymbol{\mu}(x)$. It has the following configuration:

$$\boldsymbol{\mu}(x) = \begin{bmatrix} \mu_{11}(x) & -\mu_{21}(x) & . & . & -\mu_{I1}(x) \\ -\mu_{12}(x) & \mu_{22}(x) & . & . & -\mu_{I2}(x) \\ . & . & . & . & . \\ . & . & . & . & . \\ -\mu_{1I}(x) & -\mu_{2I}(x) & . & . & \mu_{II}(x) \end{bmatrix}$$

In multistate demographic models, the diagonal also includes death rates and emigration rates:

$$\mu_{ii}(x) = \mu_{id}(x) + \mu_{io}(x) + \sum_{j \neq i}^{J} \mu_{ij}(x)$$

where $\mu_{id}(x)$ is the mortality rate at age x in state i, and $\mu_{io}(x)$ the instantaneous rate of leaving state i to outside of the system.

Note that

$$\lim_{(y-x)\to 0} \frac{\mathbf{P}(x,y) - \mathbf{I}}{y-x} = -\boldsymbol{\mu}(x)$$

The matrix of discrete-time transition probabilities is:

$$\mathbf{P}(\mathrm{x,\,y}) = \begin{bmatrix} p_{11}(x,y) & p_{21}(x,y) & . & . & p_{N1}(x,y) \\ p_{12}(x,y) & p_{22}(x,y) & . & . & p_{N2}(x,y) \\ . & . & . & . & . \\ . & . & . & . & . \\ p_{1N}(x,y) & p_{2N}(x,y) & . & . & p_{NN}(x,y) \end{bmatrix}$$

and $\mathbf{P}(x,x) = \mathbf{I}$.

An element of $\mathbf{P}(x,y)$, $p_{ij}(x,y)$, denotes the (conditional) probability that an individual who is in state i at exact age x is in state j at exact age y. The Markovian assumption implies the following relationship between $\mathbf{P}(x,x+\nu)$ and $\mathbf{P}(x+\nu,y)$:

$$\mathbf{P}(x,y) = \mathbf{P}(x,x+\nu) * \mathbf{P}(x+\nu,y) \qquad x < x + \nu < y$$

Subtraction of $\mathbf{P}(x+\nu,y)$ from both sides of the equation yields

$$\frac{\mathbf{P}(x,y) - \mathbf{P}(x+\nu,y)}{\nu} = \frac{[\mathbf{P}(x,x+\nu) - \mathbf{I}]\mathbf{P}(x+\nu,y)}{\nu}$$

and

$$\lim_{\nu\to 0} \frac{\mathbf{P}(x,y) - \mathbf{P}(x+\nu,y)}{\nu} = \lim_{\nu\to 0} \frac{[\mathbf{P}(x,x+\nu) - \mathbf{I}]\,\mathbf{P}(x+\nu,y)}{\nu}$$

or

$$\frac{d\mathbf{P}(x,y)}{dx} = -\boldsymbol{\mu}(x)\mathbf{P}(x,y)$$

Recall

$$\lim_{(y-x)\to 0} \frac{\mathbf{P}(x,y) - \mathbf{I}}{y-x} = -\boldsymbol{\mu}(x)$$

Multiplying both sides with the vector of state probabilities at age x, $\mathbf{P}(x)$, leads to:

$$\frac{d\mathbf{P}(x)}{dx} = -\boldsymbol{\mu}(x)\mathbf{P}(x)$$

The model is a system of differential equations. In multistate demography, two avenues are followed to solve the system. Both introduce age intervals (Rogers and Willekens 1986:370ff). The first avenue postulates a piecewise constant intensity function, $\boldsymbol{\mu}(t) = \boldsymbol{\mu}(x)$ in the interval from x to y ($x \leq t < y$). This implies an exponential distribution of demographic events within each age interval. The model that results is referred to as the exponential model. The second avenue postulates a piecewise linear survival function. A piecewise linear survival function is obtained when demographic events are uniformly distributed within the age intervals. The model that results is referred to as the linear model. The first avenue is followed by Van Imhoff (1990) and Van Imhoff and Keilman (1991) among others; the second by Willekens and Drewe (1984) among others. The state occupancies and the sojourn times must be estimated simultaneously from the population at the beginning of the interval and the events during the interval.

To solve the system of differential equations, it may be replaced by a system of integral equations:

$$\mathbf{P}(x,y) = \mathbf{I} - \int_0^{y-x} \boldsymbol{\mu}(x+t)\,\mathbf{P}(x,x+t)\,dt$$

To derive an expression involving transition rates, we write

$$\mathbf{P}(x,y) = \mathbf{I} - \left[\int_0^{y-x} \boldsymbol{\mu}(x+t)\,\mathbf{P}(x,x+t)\,dt\right]\left[\int_0^{y-x} \mathbf{P}(x,x+t)\,dt\right]^{-1}\left[\int_0^{y-x} \mathbf{P}(x,x+t)\,dt\right]$$

$$\mathbf{P}(x,y) = \mathbf{I} - \mathbf{M}(x,y)\,\mathbf{L}(x,y) \qquad (1)$$

where $\mathbf{M}(x,y)$ is the matrix, with elements $m_{ij}(x,y)$, of average transition rates during the interval from x to y and $\mathbf{L}(x,y) = \int_0^{y-x} \mathbf{P}(x,x+t)\,dt$ is the sojourn time spent in each state between ages x and y per person in each state at age x.

i. *Exponential model*

The transition intensities $\boldsymbol{\mu}(x)$ are assumed to remain constant during the age interval from x to y and to be equal to the model transition rates $\mathbf{M}(x,y)$. It is furthermore assumed that they can be estimated by empirical occurrence-exposure rates for that age interval. This assumption is consistent with the general assumption in demography that life-table rates are equal to empirical rates. In this paper no separate notation is used for model rates and empirical rates. The matrix of transition probabilities between x and y is

$$\mathbf{P}(x,y) = \exp\left[-(y-x)\mathbf{M}(x,y)\right]$$

where $\mathbf{M}$(x,y) is the matrix of empirical occurrence-exposure rates or transition rates for the age interval from x to y and $\mu_{ij}(t) = m_{ij}(x,y)$ for $x \leq t < y$ and $\mu(t) = \mathbf{M}(x,y)$ for $x \leq t < y$.

A number of methods exists to determine the value of exp[-$\mathbf{M}$] (eg. Director and Rohrer 1972:431ff; Aoki 1976:387; Strang 1980:206). We use the Taylor series expansion. Note that for matrix $\mathbf{A}$, exp($\mathbf{A}$) may be written as a Taylor series expansion

$$\exp(\mathbf{A}) = \mathbf{I} + \mathbf{A} + \frac{1}{2!}\mathbf{A}^2 + \frac{1}{3!}\mathbf{A}^3 + \ldots$$

Hence

$$\exp[-(y-x)\mathbf{M}(x,y)] = \mathbf{I} - (y-x)\mathbf{M}(x,y) + \frac{(y-x)^2}{2!}[\mathbf{M}(x,y)]^2 - \frac{(y-x)^3}{3!}[\mathbf{M}(x,y)]^3 + \ldots$$

(see also Schoen 1988:72).

The transition rates $\mathbf{M}$(x,y) are estimated from the data. The transition rate $m_{ij}(x,y)$ is equal to the ratio of the number of moves or direct transitions from i to j during the interval from x to y, and the duration of exposure spent in the state of origin i:

$$m_{ij}(x,y) = \frac{n_{ij}(x,y)}{L_i(x,y)}$$

where $n_{ij}(x,y)$ is the observed number of moves from i to j during the interval and $L_i(x,y)$ is the duration in i exposed to the risk of moving to j. It is the sojourn time in i during the (x,y) interval. Exposure is measured in person-months or person-years. In case of two states, the rate equation may be written as follows:

$$\begin{bmatrix} m_{11}(x,y) & -m_{21}(x,y) \\ -m_{12}(x,y) & m_{22}(x,y) \end{bmatrix} = \begin{bmatrix} n_{11}(x,y) & -n_{21}(x,y) \\ -n_{12}(x,y) & n_{22}(x,y) \end{bmatrix} \begin{bmatrix} L_1(x,y) & 0 \\ 0 & L_2(x,y) \end{bmatrix}^{-1}$$

where $m_{11}(x,y) = m_{12}(x,y)$ and $m_{22}(x,y)=m_{21}(x,y)$. In multistate demography, the state of dead is generally not treated as a separate state and the death rate is included in the diagional elements, e.g. $n_{11}(x,y) = n_{12}(x,y)+n_{1d}(x,y)$ where $n_{1d}(x,y)$ is the number of deaths among cohort members occupying state 1 and aged x to y.

In matrix notation: $\mathbf{M}(x,y) = \mathbf{n}(x,y)\left[\mathbf{L}(x,y)\right]^{-1}$

Let $\overline{\mathbf{L}}(x,y)$ be the vector of sojourn times containing the diagonal elements of $\mathbf{L}$(x,y) and let $\mathbf{K}$(x) be a vector with the state occupancies at age x by surviving cohort members as its elements:

$$\mathbf{K}(x) = \begin{bmatrix} K_1(x) \\ K_2(x) \end{bmatrix}$$

with $K_i(x)$ the number of cohort members in state i at exact age x. The vector of sojourn times by all cohort members in the various positions is obtained by the following equation:

$$\overline{\mathbf{L}}(x,y) = \left[\int_0^{y-x} \mathbf{P}(x,x+t)\,dt\right]\mathbf{K}(x)$$

Since the transition intensities are constant in the interval from x to y, the equation may be written as follows:

$$\overline{\mathbf{L}}(x,y) = \left[\int_0^{y-x} \exp(-t\,\mathbf{M}(x,y)\,dt\right]\mathbf{K}(x)$$

Integration yields

$-\left[\mathbf{M}(x,y)\right]^{-1}\left|\exp\left[-t\,\mathbf{M}(x,y)\right]\right|_0^{y-x}$ which is equal to

$$\left[\mathbf{M}(x,y)\right]^{-1}\left[\mathbf{I} - \exp\left[-(y-x)\,\mathbf{M}(x,y)\right]\right]$$

Hence the sojourn times in the various states during the (x,y)-interval are given by:

$$\overline{\mathbf{L}}(x,y) = \left[\mathbf{M}(x,y)\right]^{-1}\left[\mathbf{I} - \exp\left[-(y-x)\,\mathbf{M}(x,y)\right]\right]\mathbf{K}(x)$$

ii. *Linear model*

To solve equation (1), one may introduce an approximation of $\mathbf{L}$(x,y). A simple approximation is that $\mathbf{P}$(x,x+t) is linear on the interval x ≤ x+t < y. Hence $\mathbf{L}(x,y) = \int_0^{y-x} \mathbf{P}(x,x+t)\,dt$ may be approximated by a linear integration:

$$\mathbf{L}(x,y) = \frac{y-x}{2}\left[\mathbf{I} + \mathbf{P}(x,y)\right]$$

Introducing this expression in equation (1) gives

$$\mathbf{P}(x,y) = \mathbf{I} - \frac{y-x}{2}\mathbf{M}(x,y)\left[\mathbf{I} + \mathbf{P}(x,y)\right]$$

$$\mathbf{P}(x,y) = \mathbf{I} - \frac{y-x}{2}\mathbf{M}(x,y)\,\mathbf{I} + \frac{y-x}{2}\mathbf{M}(x,y)\,\mathbf{P}(x,y)$$

$$\mathbf{P}(x,y) + \frac{y-x}{2}\mathbf{M}(x,y)\,\mathbf{P}(x,y) = \mathbf{I} - \frac{y-x}{2}\mathbf{M}(x,y)\,\mathbf{P}(x,y)$$

$$\mathbf{P}(x,y) = \left[\mathbf{I} + \frac{y-x}{2}\mathbf{M}(x,y)\right]^{-1}\left[\mathbf{I} - \frac{y-x}{2}\mathbf{M}(x,y)\right]$$

The linear approximation implying the assumption that the events are uniformly distributed over the interval is adequate when the transition rates are small or the interval is short. It can be shown that the linear model is an approximation to the exponential model that retains the first three terms of the Taylor series expansion (Annex I).

In the previous section we described the separation of the origin-destination specific transition rate into two components, a generation component and a distribution component. The discrete-time transition probabilities are related to the probabilities of direct transition in an interesting way. The off-diagonal elements of **M**(x,y) may be replaced by $-m_{i+}(x,y)\ \xi_{ij}(x,y)$ where $m_{i+}(x,y)$ is the rate of leaving i (exit rate), which is assumed to be constant in the interval from x to y. The diagonal elements are $m_{i+}(x,y)$. The $\boldsymbol{\mu}$-matrix may be written as

$$\begin{bmatrix} \mu_{11}(x,y) & -\mu_{21}(x,y) & . & . & -\mu_{I1}(x,y) \\ -\mu_{12}(x,y) & \mu_{22}(x,y) & . & . & -\mu_{I2}(x,y) \\ . & . & . & . & . \\ . & . & . & . & . \\ -\mu_{1I}(x,y) & -\mu_{2I}(x,y) & . & . & \mu_{II}(x,y) \end{bmatrix} = \begin{bmatrix} \xi_{11}(x,y) & -\xi_{21}(x,y) & . & . & -\xi_{I1}(x,y) \\ -\xi_{12}(x,y) & \xi_{22}(x,y) & . & . & -\xi_{I2}(x,y) \\ . & . & . & . & . \\ . & . & . & . & . \\ -\xi_{1I}(x,y) & -\xi_{2I}(x,y) & . & . & \xi_{II}(x,y) \end{bmatrix} \begin{bmatrix} \mu_{1+}(x,y) & 0 & . & . & 0 \\ 0 & \mu_{2+}(x,y) & . & . & 0 \\ . & . & . & . & . \\ . & . & . & . & . \\ 0 & 0 & . & . & \mu_{I+}(x,y) \end{bmatrix}$$

with $\xi(x,y)$ the probability of at least one direct transition from i to j during the interval from x to y.

$$\mathbf{P}(x,y) = \begin{bmatrix} p_{11}(x,y) & p_{21}(x,y) & . & . & p_{N1}(x,y) \\ p_{12}(x,y) & p_{22}(x,y) & . & . & p_{N2}(x,y) \\ . & . & . & . & . \\ . & . & . & . & . \\ p_{1N}(x,y) & p_{2N}(x,y) & . & . & p_{NN}(x,y) \end{bmatrix}$$

$$= \exp\left[-(y-x)\begin{bmatrix} \xi_{11}(x) & -\xi_{21}(x) & . & . & -\xi_{I1}(x) \\ -\xi_{12}(x) & \xi_{22}(x) & . & . & -\xi_{I2}(x) \\ . & . & . & . & . \\ . & . & . & . & . \\ -\xi_{1I}(x) & -\xi_{2I}(x) & . & . & \xi_{II}(x) \end{bmatrix} \begin{bmatrix} \mu_{1+}(x) & 0 & . & . & 0 \\ 0 & \mu_{2+}(x) & . & . & 0 \\ . & . & . & . & . \\ . & . & . & . & . \\ 0 & 0 & . & . & \mu_{I+}(x) \end{bmatrix}\right]$$

Population Projection

The distribution of a population of a given age at a given point in time is represented by the vector of *state occupancies* K(x,t)

$$\mathbf{K}(x,t) = \begin{bmatrix} K_1(x,t) \\ K_2(x,t \\ \ldots \\ K_N(x,t) \end{bmatrix}$$

where $K_i(x,t)$ is the number of persons of age x in state i at time t.

In this section we consider a projection model that allows for international migration. The number of people at a given age above 0 depends on an initial condition, deaths, interstate transitions, emigrations during an interval and immigrants during an interval.

i. *Exponential model*

The exponential model of multistate population growth is derived from a system of differential equations

$$\frac{d\,\mathbf{K}(t)}{d\,t} = -\mathbf{M}(t)\,\mathbf{K}(t) + \mathbf{F}(t)\,\mathbf{I}_m(t)$$

where **K**(t) is a vector of state occupancies, i.e. the number of individuals in the various states, $\mathbf{I}_m(t)$ is the vector of immigrants at time t by state of existence, and **M**(t) and **F**(t) are coefficient matrices. We consider the age interval from x to y and introduce piecewise constant rates **M**(x,y). The projection model expresses the state occupancies of the cohort members at age y in terms of the state occupancies at age x and the transition rates during the interval from x to y. The solution to the system of differential equations is

$$\mathbf{K}(y) = \exp[-(y-x)\mathbf{M}(x,y)]\mathbf{K}(x) + \int_0^{y-x} \exp[-(y-t)\mathbf{M}(x,y)]\mathbf{I}_m(t)\,dt$$

Since the instantaneous rates are assumed constant in the interval (x,y) and if immigration $\mathbf{I}_m$ is uniformly distributed then

$$\mathbf{K}(y) = \exp[-(y-x)\mathbf{M}(x,y)]\mathbf{K}(x) + \int_0^{y-x} \exp[-(y-t)\mathbf{M}(x,y)\,dt]\mathbf{I}_m \text{ and}$$

$$\mathbf{K}(y) = \exp[-(y-x)\mathbf{M}(x,y)]\mathbf{K}(x) + [\mathbf{M}(x,y)]^{-1}[\mathbf{I} - \exp[-(y-x)\mathbf{M}(x,y)]]\mathbf{I}_m$$

$$= \mathbf{G}(x,y)\mathbf{K}(x) + \mathbf{F}(x,y)\mathbf{I}_m$$

G(x,y) represents the contribution of cohort members present at age x to the population at age y and **F**(x,y) represents the contribution of immigrants aged x to y.

ii. *Linear model*

The multistate projection model predicts the state occupancies from information on state occupancies at a previous point in time and immigration:

$$\mathbf{K}(y) = \mathbf{P}(x,y)\,\mathbf{K}(x) + \mathbf{F}(x,y)\,\mathbf{I}_m$$

where **P**(x,t) is the matrix of transition probabilities for persons aged x, and $\mathbf{I}_m$ is a vector representing the number of immigrants during a unit interval. **F**(x,y) is the coefficient matrix that denotes the contribution of immigrants during a given period to the population at the end of the period. The coefficient matrices are related to the transition rates (Willekens 1998):

$$\mathbf{P}(x,y) = \left[\mathbf{I} + \frac{y-x}{2}\mathbf{M}(x,y)\right]^{-1}\left[\mathbf{I} - \frac{y-x}{2}\mathbf{M}(x,y)\right]$$

and

$$\mathbf{F}(x,y) = \left[\mathbf{I} + \frac{y-x}{2}\mathbf{M}(x,y)\right]^{-1}$$

Transition Probability Models and Transition Rate Models in Population Forecasting

Now we introduce covariates, including contextual variables. Covariates may be introduced in two ways: by stratifying the population by the relevant covariate(s), provided the covariates are discrete variables, or by a regression equation. In population projections, stratification is generally used. For instance, a population is usually stratified by sex and birth cohort (age) and demographic parameters are sex- and birth cohort-specific. Regression models are more economic at a cost of precision. Stratification involves as many parameters as there are cells in the cross-classification of covariates. The same is true only in a saturated regression model, which is a model that has as many independent parameters as there are unknowns (cells in the cross-classification). A saturated regression model involves several interaction effects, which may be redundant in most practical applications.

In the regression model, the covariates are denoted by **Z** (**Z** = {Z_1, Z_2, Z_3, …}). A covariate Z_p may represent a single attribute or a combination of attributes (to denote interaction effects). In addition to covariates one may include time (when the rates are time-varying) and/or cohort (when rates are estimated for different cohorts) among the explanatory variables or predictors. Furthermore, the transition rates may depend on the entire previous life course: **M**(x,Θ[0,x]) where Θ [0,x] represents the life course from birth to age x. We consider state probabilities and transition rates. State probabilities are related to covariates using a logit model or logistic regression. Transition rates are related to covariates using transition rate models that are related to the family of Poisson regression models. Logit models are also applied to link transition probabilities to covariates.

iii. *State probabilities*

The **state probability** at age x, $\pi_i(x,\mathbf{Z})$, is the probability that an individual of age x and with covariates **Z** occupies state i. The logit equation relates the state probabilities to covariates.

$$logit[\pi_i(x,\mathbf{Z})] = \ln\frac{\pi_i(x,\mathbf{Z})}{\pi_r(x,\mathbf{Z})} = \eta_i(x,\mathbf{Z}) = \beta_{i0}(x) + \beta_{i1}(x)Z_1(x) + \beta_{i2}(x)Z_2(x) + \beta_{i3}(x)Z_3(x) + ...$$

where $\dfrac{\pi_i(x,\mathbf{Z})}{\pi_r(x,\mathbf{Z})}$ is the odds that a cohort member of age x occupies state i rather than the reference state r (reference category). The logit transformation assures that the state probabilities lie between 0 and 1, and that their sum is equal to one. The value of η_i may range from -∞ to +∞, but the value of π_i stays within 0 and 1. To obtain the probabilities, the logit scale is converted into the probability scale:

$$\pi_i(x,\mathbf{Z}) = \frac{\exp[\eta_i(x,\mathbf{Z})]}{\exp[\eta_1(x,\mathbf{Z})] + \exp[\eta_2(x,\mathbf{Z})] + ...} = \frac{\exp[\eta_i(x,\mathbf{Z})]}{\sum_{j=1}^{I}\exp[\eta_j(x,\mathbf{Z})]}$$

where one category is the reference category. The model is the multinomial logistic regression model.

iv. Transition rates

The **transition rates** may depend on time [$\mu_{ij}(x,t)$] and may also depend on personal characteristics. For instance **M**(x,**Z**) is the matrix of transition rates for individuals of age x and the vector of background variables **Z** (**Z** = {Z_1, Z_2, Z_3, …}). The dependence of transition rates on personal attributes and other explanatory variables is described by transition rate models, better known as hazard models (Tuma and Hannan 1984; Blossfeld and Rohwer 2002). These models are Poisson regression models. Transition rate models include the basic (exponential) transition rate model, the piecewise constant rate model, and the Cox regression model. Transition rate models also include parametric models of time- (or age-)dependence such as the Gompertz model, the Weibull model, the Coale-McNeil model (for fertility and nuptiality), the Heligman-Pollard model (for mortality) and the Rogers-Castro model (for migration). Transition rate models are estimated from empirical data. The data may be vital statistics, census data or surveys. The estimation of transition rates from survey data requires recently developed theories of statistical inference.

The basic parameters of the multistate model are the transition rates $m_{ij}(x,y)$. As described in a previous section, the transition rate may be written as the product of an exit rate $m_i(x,y)$ and a conditional transition probability. The exit rate is modeled using a transition rate model for a single event (leaving the state of origin). The elementary transition rate model is the basic exponential model, with the rate being independent of age (Blossfeld and Rohwer 2002). The regression model linking an exit rate to covariates is

$$m_i = \exp[\beta_{i0} + \beta_{i1}Z_1 + \beta_{i2}Z_2 + \ldots]$$

and a regression model linking transition rates to covariates is

$$m_{ij} = \exp[\beta_{ij0} + \beta_{ij1}Z_1 + \beta_{ij2}Z_2 + \ldots]$$

The models may be written as log-linear models

$$\ln m_i = \beta_{i0} + \beta_{i1}Z_1 + \beta_{i2}Z_2 + \ldots$$

$$\ln m_{ij} = \beta_{ij0} + \beta_{ij1}Z_1 + \beta_{ij2}Z_2 + \ldots$$

The transition rate is the ratio of number of events over total exposure time. These two components may be studied separately, as is done in the log-rate model (eg. Yamaguchi 1991:Chapter 4). It that model, it is assumed that changes in the number and timing of direct transitions (events) do not significantly affect the total exposure time. The assumption is realistic when exposure time is large compared to the number of transitions. If a variation in number or timing of transitions does not affect total exposure, the latter component may be considered fixed and may be treated as an *offset* in probability models including regression models. The problem of modeling transitions reduces to the prediction of the number of events (counts) which is the numerator of the transition rate. The number of direct transitions that occur during a unit interval is often represented by a Poisson random variable. The number of events that may occur during the interval is not restricted in any way. Subjects in a (sample) population may experience more than one event during the unit interval. The Poisson model is

$$\Pr\{N_{ij} = n_{ij}\} = \frac{\lambda_{ij}^{n_{ij}}}{n_{ij}!} \exp[-\lambda_{ij}]$$

where N_{ij} denotes the number of transitions from i to j, n_{ij} is the observed number of transitions, and λ_{ij} is the expected number of transitions. The latter is the parameter of the Poisson model. It is assumed that the transitions are independent. The parameter may be made dependent on covariates:

$$E\lfloor N_{ij} \rfloor = \lambda_{ij} = \exp\lfloor \beta_{ij0} + \beta_{ij1} Z_1 + \beta_{ij2} Z_2 + \ldots \rfloor$$

The model may be written as a log-linear model:

$$\ln \lambda_{ij} = \beta_{ij0} + \beta_{ij1} Z_1 + \beta_{ij2} Z_2 + \ldots$$

In principle, Z_p can be any covariate. In conventional log-linear analysis, all covariates are discrete or categorical. The observations on transitions may therefore by arranged in a contingency table. The covariates refer to rows, columns, layers and combinations of these (to represent interaction effects).

The log-rate model is a log-linear model with an offset:

$$E\left[\frac{N_{ij}}{PY_i}\right] = \frac{\lambda_{ij}}{PY_i} = \exp\lfloor \beta_{ij0} + \beta_{ij1} Z_1 + \beta_{ij2} Z_2 + \ldots \rfloor$$

where PY_i denotes exposure time in state i (origin state). Since PY_i is fixed, the equation may be rewritten as follows:

$$E\lfloor N_{ij} \rfloor = \lambda_{ij} = PY_i \exp\lfloor \beta_{ij0} + \beta_{ij1} Z_1 + \beta_{ij2} Z_2 + \ldots \rfloor$$

The age dependence may be introduced in two ways: non-parametric and parametric. In the first approach, the population is stratified by age and a transition rate is estimated for each age separately. In the parametric approach, age dependence is represented by a model. A common model is the Gompertz model, which imposes onto the transition rate an exponential change with duration. The Gompertz model has two parameters and each may be made dependent on covariates (For a detailed treatment, see Blossfeld and Rohwer 2002). Other parametric models of duration dependence may be used. In studies of marriage and fertility, the Coale-McNeil model is often used to describe the age dependence of the marriage or first birth rate (eg. Liang 2000). In migration studies, the model migration schedule is a common representation of the age dependence of the migration rate (eg. Rogers and Castro 1986). Each parameter of the model may be related to covariates. In practice, only one or a selection of parameters is assumed to depend on covariates.[4]

In some cases, the researcher is not interested in the age dependence of transition rates, but in the effect of covariates on the level of transition. Rather than omitting age altogether, as in the basic exponential model, the transition rate is allowed to vary with age but the effect of the covariates on the transition rate does not vary with age. The transition rate model that results is a Cox proportional hazard model. It is written as

$$m_{ij}(x) = m_{ijo}(x)\exp\left[\beta_{ij0} + \beta_{ij1}Z_1 + \beta_{ij2}Z_2 + \ldots\right]$$

where $m_{ijo}(x)$ is the baseline hazard. It is the set of age-specific transition rates for the reference category. Note that if the age dependence (age structure) of transition is independent of the dependence on covariates (motivational structure), the baseline hazard may be represented by a parametric model and the two components may be estimated separately.

From Transition Probabilities to Transition Rates

In this section, we assume that transition is measured in discrete-time. Examples include the census (based on the residence at time of census and 5 years prior to the census). From that information, the approximate transition rates can be derived. The problem is equivalent to one in which we are given **P**(x,y) and **M**(x,y) is required. The derivation starts with the exponential expression $\mathbf{P}(x,y) = \exp[-(y-x)\mathbf{M}(x,y)]$. The exponential expression may be approximated by the linear model:

$$\mathbf{P}(\mathrm{x,y}) = \left[\mathbf{I} + \tfrac{1}{2}\mathbf{M}(\mathrm{x,y})\right]^{-1}\left[\mathbf{I} - \tfrac{1}{2}\mathbf{M}(\mathrm{x,y})\right]$$

The approximation is adequate when the transition rates are small or the interval is short.

The derivation of the rate of transition during an interval from information on states occupied at two consecutive points in time is known as the inverse problem: transition rates are derived from transition probabilities (Singer and Spilerman 1979).

$$\mathbf{M}(x,y) = \tfrac{y-x}{2}\left[\mathbf{I} - \mathbf{P}(x,y)\right]\left[\mathbf{I} + \mathbf{P}(x,y)\right]^{-1},$$

provided $[\mathbf{I}+\mathbf{P}(x,y)]^{-1}$ exists. The inverse relation may be used to infer transition probabilities for intervals that are different from the measurement intervals. For instance, if the states occupied are recorded at age x and at age y, the inverse relation may be used to infer the average transition rates **M**(x,y) and to derive the transition probabilities over a one-year period. The expression is $\mathbf{P}(x,x+1)=\exp[-\mathbf{M}(x,y)]$ where **M**(x,y) is estimated from **P**(x,y) using the inverse method. The method assumes that transition rates are constant during the (x,y)-interval and that the linearity assumption is an adequate approximation of the exponential model.

Transition Rates: The Bridge to Demographic Scenarios and Stochastic Projections

The transition rates (or in some cases the transition probabilities) also represent the ultimate scenario variables. Scenarios are often formulated in terms of demographic indicators such as life expectancy and TFR, but these measures must be translated into age (and sex) specific transition rates. Scenarios may be expressed directly in terms of the transition rates or in terms of the covariates that predict the transition rates. For instance, if one is interested in future pension payments, the age at retirement may be considered a scenario variable or it may be predicted by a transition rate model with the rate of retirement depending on a set of personal attributes and policy variables.

The transition rates (or transition probabilities) also constitute the ultimate variables for stochastic projection. Predicted values of demographic indicators such as life expectancy or TFR (predicted by expert opinions, a mathematical model extrapolating past values and errors, or a combination) must be translated into age (and sex) specific transition rates. Stochastic projections are based on the assumption that the transition rates are not point estimates but interval estimates following particular probability distributions around means or expected values (e.g. normal distribution or beta distribution). A two-step procedure involving the random selection of values from a distribution and the projection of the population using these values constitutes a simulation experiment. Repeated simulation experiments produce information on the distribution of target variables such as the population aged 65+, the dependency ratio, the number of years spent in pension and the number of years with severe disability.

The coefficients of the regression models predicting the transition rates or transition probabilities may also vary in time or over individuals with the same attributes. In that case the model with fixed effects (fixed effects model) changes into a varying effect model (which includes as a special case the random effects model that describes the distribution of effects of covariates among a group of people with the same attributes). The model may become very complex and may be manageable only in a micro-simulation mode.

Individual Biographies and Microsimulation

The multistate model is also the basis for the prediction of individual biographies. In the previous sections, an individual was represented by k. To project k's biography, information on the attributes of k, on other explanatory variables and maybe some assumptions about patterns of change are used to determine for each age the transition rate experienced by k. Transition rates are predicted from explanatory variables using a regression model (transition rate model). The technique is used extensively in medical sciences (eg. Anderson *et al.* 1990; Mamun 2004). The method is also related to micro-econometric models of labour market dynamics (eg. Flinn and Heckman 1982a; 1982b).

The multistate model specified above is a macro-simulation model that uses point estimates of the transition rates and predicts expected values, e.g. the *expected* number of individuals in a given state at a given future time. The transition rates may depend on covariates, eg. sex. The expected value is the mean value in a population of individuals. Individual values, e.g. states occupied by individuals in a population at a given future point in time, are obtained by randomly allocating events (transitions) to members of the population in a way that is consistent with (a) the point estimates of the transition rates (mean or expected value) (prior estimate) and (b) the distribution of the individual values around the mean. It implies that the transition rates follow a given probability distribution. Individual values are generally not produced for all members of a population but for a (random) sample. Using a random number generator, a unique value is selected from a distribution for each individual in the sample population. If for a given individual, the value is less than the mean value in the population (point estimate), the event is allocated to the individual and the individual makes the transition from the state of origin to the state of destination. If the value drawn from the distribution exceeds the mean value, the individual remains in the state of origin. The transition rates that result after the events have been allocated to the sample population (posterior estimates) generally differ slightly from the prior estimates. The reason is sample variation. If the sample is sufficiently large, the posterior estimates coincide with the prior estimates. That is why microsimulations require large sample populations to produce reliable estimatesfor the population characteristics.

Wolf (2000) views microsimulation as the generation of data. He sees microsimulation fundamentally as an exercise in sampling: "Microsimulation consists of drawing a sample of realizations of a prespecified stochastic process" (Wolf 2000:2). The same view is adopted in the MicMac project. The data consists of realizations of an underlying probability mechanism. Probability models constitute the core of microsimulation and predictions generated by the probability models represent the output of microsimulation. Wolf also observed that the emphasis in most microsimulation is on the outputs generated by the simulation, rather than on the process of model development, estimation, and assessment. He argues that microsimulation has much to offer in these modeling steps. The MicMac project is an exercise in model development, estimation and assessment. The estimation of model parameters (transition rates in continuous-time models and transition probabilities in discrete-time models) from data uses the theory of statistical inference when required, i.e. when sampling is involved.

The MicMac Project

The Partners and the Work Packages

The biographic projection model is developed and implemented by a consortium of research institutes in Europe. The following institutes participate (coordinator in parentheses): NIDI in The Hague (Nicole van der Gaag), IIASA and Vienna Institute of Demography (VID) (Wolfgang Lutz), Bocconi University in Milan (Francesco Billari), Department of Public Health, Erasmus Medical Center in Rotterdam (Wilma Nusselder), Max Planck Institute for Demographic Research in Rostock (James Vaupel and Jutta Gampe), University of Rostock (Gabrielle Doblhammer-Reiter), INED in Paris (Laurant Toulemon). General coordination is by the author. Model development is concentrated at NIDI. IIASA will develop methods and procedures to efficiently derive scientifically sound argument-based expert views on future trends of demographic variables utilising insights from the fields of cognitive science, group dynamics and quantitative decision analysis. Other partners will use the instruments developed at IIASA to produce argument-based scenarios and develop uncertainty distributions around most likely values of demographic parameters of multistate models.

The Erasmus Medical Center, in cooperation with the Max Planck Institute for Demographic Research and the University of Rostock, will determine the age (risk) profiles of key events in morbidity and mortality in the life course and determine the relative risks of these events in relation to proximate risk factors (e.g. smoking, blood pressure, body mass index) and to more distant determinants such as socio-economic status (SES.) This will serve as input for the illustrative projections using the MicMac micro-simulation approach. In addition they will develop mortality and morbidity scenarios using the instruments for argument-based scenarios developed at IIASA.

Bocconi University, in cooperation with VID and INED will provide the input needed to make forecasts on fertility and family and household structure. In addition, argument-based scenarios will be developed.

Both the macro-model (Mac) and the micro-model (Mic) project biographies in terms of state occupancies and transitions. Mac projects cohort biographies. It projects the (expected) number of members of a birth cohort that occupy various states at a future date. It uses mean or expected values of transition rates and transition probabilities. Mic projects individual biographies. It predicts the state occupied by a given individual at a given future point in time. To project individual biographies, Mic uses information on the attributes of the individual, on other explanatory variables and maybe some assumptions about patterns of change to determine for each age the transition rate experienced by the individual. The transition rates are predicted from explanatory variables using a regression model (transition rate model).

VID will also prepare multi-state population projections by level of education. This research will deliver to all other components of MicMac a substantive contribution about changes in the educational composition of the total population (with special emphasis on the working age population). It will define alternative scenarios about future transition rates considering ongoing plans for school reforms and it will cover the analysis of interactions between education and the timing of fertility over the life course.

Software Development

A number of software packages for demographic projection already exist (Willekens and Hakkert 1992; http://www.eat.org.mx/software/softpyd.htm for an update). Packages that implement the cohort- component method include PDPM/PC (Population and Development Projection Methods for Microcomputers), developed under auspices of the United Nations, and PEOPLE, developed by Richard Leete, for national and subnational population projections.

Packages for *multistate* demographic modelling have been developed largely as part of methodological research. The first packages were developed at IIASA in the 1970s by Ledent and Willekens (SPA by Willekens and Roger, 1978; LIFEINDEC by Willekens 1979). They included the multistate life table and multistate projections. The work was carried further at NIDI. That resulted in LIPRO by Van Imhoff and Keilman (1992), FAMY by Zeng Yi (1991), PROFAMY by Zeng Yi (Zeng Yi *et al.* 1997) and MUDEA by Willekens (Willekens and Drewe 1984; Willekens 1995). LIPRO was originally developed for multistate household projection but has been designed as to be generally applicable. It is user-friendly and has been applied in several countries of Europe. At IIASA the first interactive user-friendly software for multistate population projections - DIALOG (Scherbov *et al.* 1986) was developed by Scherbov.

Software for stochastic population projections is not generally available. PEP (Program for Error Propagation) developed by Alho (n.d.) is not generally accessible but has been extensively documented. It is used in the DEMWEL project in the Fifth Framework Programme of the European Commission. The manual is available on the internet: http://joyx.joensuu.fi/~ek/pep/userpep.htm

Dynamic longitudinal microsimulation models simulate life histories of individuals and families. Macro-simulation models, such as demographic projection models, deal with individuals grouped by concerned attributes, for instance a group of persons of the same age and parity and/or marital status. Micro-simulation models simulate life course events and keep detailed records of demographic status transitions for each individual of the sample population. The models trace the influence of a large number of decisions or events on the life course of people. Microsimulation models that are designed to simulate life histories adopt a life course perspective and involve behavioural rules that determine the occurrence of events and ages at events. Dynamic longitudinal microsimulation models have been the subject of extensive reviews (Van Imhoff and Post 1998). Recent reviews were presented at the *Dynamic Microsimulation Modelling Technical Workshop*, held in January 2002 at the London School of Economics (http://www.lse.ac.uk/ Depts/sage/conference/workshop.htm) and at the *International Micro-simulation Conference on Population Ageing and Health: Modelling Our Future*, held in Canberra, Australia in December 2003. Among the microsimulation models, SOCSIM, developed at the University of California at Berkeley, is one of the oldest but continuously updated models, and LifePaths of Statistics Canada is one of the best known. The latter has inspired the development of microsimulation models in several countries. Other models are SABRE in the UK, DESTINIE in France, NATSIM in Australia, SWITCH in Ireland and MOSART in Norway. MicMac differs from these models in the special interest in micro-macro linkages.

As part of the MicMac project, a user-friendly software package will be developed for biographic forecasting (cohort biographies and individual biographies). Biographic projections provide a generic approach to functional population projections. The software implementing Mac includes a facility to link the rates/probabilities to explanatory variables using rate models or probability models (regression models). The link is operationalized in a separate module that can be activated by the user.

The software will be object-oriented. Three broad objects are distinguished: a **pre-processor** to produce the data base for projection (input), the **processor** that represents the projection engine and stores the results in a data base (output), and the **post-processor** to process the projection results. At a more specific level, objects refer to algorithms or procedures to obtain particular estimates or predictions, to determine prediction error, to impose empirical regularities (e.g. using model schedules), to calculate summary indicators, etc. The individual objects will be documented and assembled in an **object library**. That approach enables and simplifies the further development of MicMac after the project is completed (by persons not involved in the initial development). It is an important strategy towards sustainability.

What Does the Project Contribute?

The proposed project signifies a step change in projection methodology. It specifically adds the following:

1. The multistate cohort-component model will be extended to project cohort biographies covering a number of domains of life (e.g health, family and education) that constitutes the basis for integrated demographic projections involving a number of domains of life.
2. The multistate cohort-component model will be extended to project individual biographies. This represents a scientifically sound strategy towards disaggregated demographic projections that cover several domains of life and that consider detailed characteristics of the population.
3. Uncertainty will be dealt with in an innovative way, using recent findings from cognitive science and the study of group dynamics. In addition, uncertainty will be measured at the level of demographic events. That level is appropriate since demographic forecasting errors are caused by errors in predicting births, deaths and other demographic events. An important advantage of this approach is that it will be easier to communicate the results of stochastic projections to policy makers and the general public.
4. For the first time ever, demographic projection models will be available that take advantage of the important advances during past decades in the statistical analysis of lifetime data and event histories. That development concentrated on the explanation of transition rates (hazard rates) and transition probabilities.
5. For the first time ever, a generic software package will become available to explore demographic futures of Europe that cover detailed population categories. Although the software will be presented as a easy-to-use package, it has a modular structure and consists of a large number of objects. The availability of an object library will enhance the further development of MicMac and other demographic software that may use these objects.
6. MicMac will be readily applicable to investigate the impact of lifestyle factors and other major health determinants on specific chronic diseases and the health status in general, and to assess the effects of different types of interventions on the health status of different groups in the population. What differentiates the proposed methodology from

other projection and impact assessment methods is (1) the focus on incidence (transitions) rather than prevalence and (2) the correct treatment of the effects of competing risks by adopting a multistate setting.

Conclusion

Biographic forecasting is a new approach to demographic forecasting that integrates traditional forecasting of the population by age and sex and functional population forecasting. Demographic change is increasingly difficult to forecast because the idiosyncratic nature of demographic behaviour. Family formation, migration and attempts to grow old healthy are part of a lifestyle that also includes work and other domains of life. The interest in life strategies originates from the awareness that critical decisions in life, i.e. decisions related to life events, are not taken in isolation but are based on lessons learned from past experiences (antecedents) and general conceptions about future developments in different life domains. Increasingly, demographic events are embedded in a life plan. The individual programming of life events, viewed by Légaré and Marcil-Gratton (1990) as a challenge for demographers in the twenty-first century, may be situated within the broader context of the individual design and implementation of life strategies. The second demographic transition, with its emphasis on choice biographies and changing interpersonal relationships, may also be viewed as a consequence of individualization and the emergence of individual life strategies.

The new demographic regime characterized by choice biographies and life planning raises new challenges for demographic forecasters. Traditional projections by age and sex do not adequately capture the complexity of life. As a result the uncertainty increases. Probabilistic projections quantify the uncertainty but are not able to reduce the uncertainty. Reduction of uncertainty and increase of forecasting performance require more realistic projection models, i.e. models that are better able to integrate substantive knowledge and to capture the causal links that underlie childbirth, death, migration and the other events that shape the lives of people. This new generation of models consists of transition models or multistate models that capture transitions people make in life and the developmental processes and pathways that characterize individual lives. The multistate life table and the multistate projection model, combined with regression models of transition rates, are adequate candidates for the development of a new generation of demographic projection models. Cox's (1972) paper on regression models for life tables caused a revolution in survival analysis. The emerging discipline of survival analysis was provided with tools it needed for studying the effects of prognostic factors on individual survival in clinical trials designed to evaluate new cancer therapies. The model became a central research tool. The paper by Gill (1992) on regression models for multistate life tables went largely unnoticed although it showed that the Cox model and the associated techniques of statistical inference can be immediately applied to studying transitions in multistate demographic models. It is time to move away from narrow perspectives in demographic forecasting and to broaden the perspective by bridging micro- and macro-level analysis and by effectively integrating substantive knowledge and statistical perspectives and techniques into demographic modeling. The life course provides the logical framework, from a substantive and an analytical perspective. Techniques of statistical inference may be used to obtain parameters of projection models from observational data to complement vital statistics and census data and to provide for a richer empirical basis for demographic forecasts.

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Notes

1. The concept of cohort biography was introduced by Ryder (1965).

2. In demography, this condition is referred to as the "pure state".

3. The intensity is a conditional probability of a move during a small interval: $\lambda_{ij}(x) = \lim \dfrac{P(x \le X < x + \Delta x, J = j \mid X \ge x, I = i)}{\Delta x}$ where X, I and J are random variables denoting age, state of origin and state of destination, respectively.

4. TDA (Transition Data Analysis) has a facility for user-defined rate models (Rohwer and Pötter, 1999, Section 6.17.5). The programme may be downloaded from prof. Rohwer's homepage: http://www.stat.ruhr-uni-bochum.de/ The manual (extensive) can be downloaded from the same site. Willekens (2002) has written a brief introduction to TDA with examples.

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Annex I
The linear model as an approximation of the exponential model

Using Taylor series expansion, it can be shown that the linear model is an approximation of the exponential model. Two methods are considered

i. Method 1

The exponent exp[-h**M**] can be written as

$$\exp[-h\mathbf{M}] = 1 - h\mathbf{M} + \tfrac{1}{2}(h\mathbf{M})^2 - \tfrac{1}{6}(h\mathbf{M})^3 + ... = \sum_{k=0}^{\infty} \frac{-(h\mathbf{M})^k}{k!}$$

The geometric progression of $[\mathbf{I} + \tfrac{1}{2}h\mathbf{M}]^{-1}$ is

$$[\mathbf{I} + \tfrac{1}{2}h\mathbf{M}]^{-1} = \mathbf{I} - \tfrac{1}{2}h\mathbf{M} + \tfrac{1}{4}(h\mathbf{M})^2 - \tfrac{1}{8}(h\mathbf{M})^3 + ... \text{ provided that } \left|\tfrac{1}{2}h\mathbf{M}\right| < 1$$

$$[\mathbf{I} + \tfrac{1}{2}h\mathbf{M}]^{-1}[\mathbf{I} - \tfrac{1}{2}h\mathbf{M}] = \mathbf{I} - h\mathbf{M} + \tfrac{1}{2}(h\mathbf{M})^2 - \tfrac{1}{4}(h\mathbf{M})^3 + \tfrac{1}{8}(h\mathbf{M})^4 - .... = \sum_{k=0}^{\infty} \frac{-(h\mathbf{M})^k}{(k-1)!}$$

with (-1)! = 1

ii. Method 2

Liaw and Ledent (1980) show that a method developed in engineering for the discrete approximation of continuous-time state equations may be applied to show the relation between the exponential model and the linear model. It is the Matrix Continued Fraction (MCF) method developed by Shieh *et.al.* (1978). To make the MCF method transparent, Liaw and Ledent consider the expansion of the number 1.2345 into a continued fraction:

$$1.2345 = 1 + \frac{2345}{10000} = 1 + \frac{1}{100000/2345} = 1 + \cfrac{1}{4 + \cfrac{620}{2345}} = ...$$

After a few divisions, one gets

$$1.2345 = 1 + \cfrac{1}{4 + \cfrac{1}{3 + \cfrac{1}{1 + \cfrac{1}{3 + ...}}}} = H_1 + \left[H_2 + \left[H_3 + \left[H_4 + ... \right]^{-1}\right]^{-1}\right]^{-1}$$

The retention of the first few H_j results in a fairly good approximation of the original number. For instance, the retention of the first three H_j gives the number 1.2308.

Application of the MCF method to approximate exp[-(y-x)**M**(x,y)] gives

$$\exp[-(y-x)\mathbf{M}(x,y)] = \mathbf{H}_1 + \left[\mathbf{H}_2 + \left[\mathbf{H}_3 + [\mathbf{H}_4 + \ldots\ ]^{-1}\right]^{-1}\right]$$

Shieh *et al.* (1978) show that

$$\mathbf{H}_1 = \mathbf{I},\ \mathbf{H}_2 = [-(y-x)\mathbf{M}(x,y)]^{-1},\ \mathbf{H}_3 = -2\mathbf{I},\ \mathbf{H}_4 = [-3(y-x)\mathbf{M}(x,y)]^{-1},\ \mathbf{H}_5 = 2\mathbf{I}$$

Let $\mathbf{G}_j$ be the estimate of exp[-(y-x)**M**(x,y)] by retaining only the first j **H** matrices. Then we get

$$\mathbf{G}_2 = \mathbf{H}_1 + [\mathbf{H}_2]^{-1} = \mathbf{I} - (y-x)\mathbf{M}(x,y)$$

$$\mathbf{G}_3 = \mathbf{H}_1 + \left[\mathbf{H}_2 + [\mathbf{H}_3]^{-1}\right]^{-1} = [\mathbf{H}_2\mathbf{H}_3 + \mathbf{I}]^{-1}[\mathbf{H}_1\mathbf{H}_2\mathbf{H}_3 + \mathbf{H}_1 + \mathbf{H}_3]$$

$$\mathbf{G}_3 = \left[\mathbf{I} + \frac{y-x}{2}\mathbf{M}(x,y)\right]^{-1}\left[\mathbf{I} - \frac{y-x}{2}\mathbf{M}(x,y)\right]$$

which is the linear approximation of the exponential model. The linear model is therefore obtained by retention of the first three $\mathbf{H}_j$ in the MCF method.

There is a difference between ignoring the higher $\mathbf{H}_j$ in the MCF method and disregarding the tail of the Taylor series expansion. Shieh *et al.* (1978) observe that

$$\mathbf{G}_3 = \mathbf{I} + [-(y-x)\mathbf{M}(x,y)] + \frac{1}{2!}[-(y-x)\mathbf{M}(x,y)]^2 + \sum_{j=3}^{\infty}\frac{1}{2^{j-1}}[-(y-x)\mathbf{M}(x,y)]^j$$

which differs from the Taylor series expansion.