Working Paper

Estimating the Uncertainty in Population Projections by Resampling Methods

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Abstract

This paper proposes a new approach to introducing quantitatively measured uncertainty into population projections. It is to a lesser degree based on past time-series than other approaches, since it uses random walk models for migration, mortality and fertility, for which upper and lower bounds are defined. No parametric distribution is fitted to the observations, but the random walk is resampled from the past data. By putting bounds on the level that fertility can reach in the future, further substantive information is introduced that transcends the information derived from the observed time series. By sampling 10.000 path of the random walks in fertility, mortality and migration, the distributions of population size and structure up to 2050 for Austria, Mauritius and USA are estimated.

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1 Introduction

1.1 The need for new projection approaches

Recent ecological concerns and considerations of sustainable development have brought the notion of the "resilience" of systems to prominence in areas outside ecology itself. It refers to the robustness or shock absorbing capacity of a system. This concept is also applicable to social, economic, and political systems. In the field of social security one may for instance ask how robust the present system is to alternative possible future fertility, mortality and migration trends. An investigation of such issues requires looking at the variance as well as the mean.

Traditionally, population projections have not systematically considered the variance of future population sizes and age structures. Attention has focussed on a medium projection, which is considered to be the most likely variant. When high and low variants are given, it is always emphasized that they should not be considered as statistical confidence intervals of any kind. The underlying logic and basis for alternative assumptions in the high and low variants remain unclear.

Aside from demographers there seem to be three groups of persons interested in the results of population projections: The first group consists of other scientists in the social and natural sciences. The recent upsurge of environmental and global change research has heightened the demand for population projections far into the future. A major reason for this demand lies in the fact that many indicators used in such studies are on a per capita basis, i.e. by definition require a population figure in the denominator. In other cases population size is assumed to have a direct effect as is done in studies on CO2 emissions which combine different assumed future population trends with different assumed per capita emissions to assess alternative possible paths of global warming (e.g Boongaarts (1992), Birdsall (1992), Lutz (1993), Bartiaux and van Ypersele (1993)). Also related to global warming issues is the large group of energy demand models which is probably the greatest scientific consumer of population projection data (e.g. Gouse et al.

(1992), Leontief and Sohn (1984)). The increasing sophistication of scenario approaches in many of these non-demographic studies has increased the demand for alternative population scenarios which requires an explicit consideration of the possible variance in future demographic rates.

The second group of population projections users are planners and public policy makers. Especially in the secotors of health, education, and social security, medium- and long-term planning includes demographic variables as crucial components. In the past, public administrators and planners have been generally satisfied with one most likely population projection, but increasingly aiming at robust policies requires sensitivity analysis including the consideration of alternative demographic trends. A third group of users, finally, are business and the general public. In general, their demand is not too different from that of public planners with a somewhat shorter time horizon. But there is a very specific subgroup, including educational institutions and advocacy groups in the group of environment and family planning, that explicitly wants to use alternative population projections for educational and illustrative purposes.

In summary the different groups interested in population projections seem to expect two different things from the demographers preparing such projections: (1) a single most likely projection, that can be used without further thinking about the problem of uncertainty, and (2) information about alternative less likely but still possible trends for the analysis of sensitivity and ex ante testing of the robustness of certain systems.

How can demographers meet this twofold demand better than has been done in the past? We can see two possible approaches: One approach is the systematic consideration of alternative extreme- case scenarios based on expert opinion as recently applied by Lutz ((1991) for Europe and North America; (1994a) for 12 world regions). Under this approach experts in the fields of fertility, mortality, and migration are asked to discuss on the basis of their full knowledge–which goes far beyond the analysis of past trends–possible alternative future trends in the three components. For the actual projection these alternatives (two for each component) are combined into eight sscenarios plus one central scenario combining all three means. This last scenario meets the demand for one most likely path the others serve the purpose of sensitivity analysis. But still this approach does not yet provide probabilities for the individual point scenarios.

The other approach thus would be the explicit quantification of uncertainty by incorporating information about vital rate variability and possibly the errors of past forecasts. It is evident that both forecasters and users would like to know what confidence to place in specific projections and what the full distribution of possible future population trends look like, but as yet no single technique to do this unambiguously has gained currency. A recent US Bureau of the Census (1989) forecast notes: "Many problems remain before a method can be developed for placing reliable confidence intervals around population projections." To further advance the discussion about probabilistic population projection models this paper proposes a method that combines some of the features of the different categories of models as will be discussed below.

2

1.2 Literature

A number of random models have been proposed for modeling uncertainty in demographic rates. These models fall into two categories: empirical models of forecasting success which measure all forms of rate variation – random and structural – and time-series models which analyze only the random variation in vital rates. In the first category are Keyfitz (1981) and Stoto (1983), who both propose using the observed errors in past forecasts as the basis for statements about future variation. Empirical comparison with forecasts has the advantage of including all sources of forecast error, ranging from unexpected vital rates changes to computational errors. On the other hand, in order to apply the method to current forecasts, a very strong assumption needs to be made: that the errors in future forecasts are of the same magnitude as in the past. This is of particular concern since the most recent forecasts are least represented in the sample of empirical forecasts because their accuracy has yet to be seen. This is problematic because not only do methods of choosing high, low, and medium assumptions change, but so also does the potential variability of vital rates. Unless both rate variability and projection technology stay the same, it is unclear how good an indicator past errors of future uncertainty.

The direct analysis of population trends themselves offers a distinct alternative. Starting with the Lee's (1974) analysis of U.S. fertility rates until today, time-series methods aim to define a structure to the process of changing rates, for example a random walk with drift, or an ARIMA. Tuljapurkar (1989) offers an overview of different stochastic models. Lee (1974) analyzes the structure of variation in U.S. fertility rates. Lee (1993) also examines U.S. fertility rates, but analyzes age-specific rates. Lee and Carter (1992) and McNown and Rogers (1989) both forecast age-specific mortality rates.

Such methods produce not only a central forecast, but also the entire probability distribution, showing where fertility and mortality rates are likely to be at any future specified date contingent on a normal distribution of errors. To date, there have been few attempts to use random rates in making projections [Notable exceptions include Cohen's (1986) work on Sweden and Lee and Tuljapurkar (19xx)] Time-series analysis to date – particularly of fertility trends – has not been particularly convincing, because results have varied so much with model specification. Furthermore, since the models are relatively difficult to understand, it is almost impossible for a potential user to decide which specification he or she has more confidence in.

Keyfitz (1989), tried to combat the complexity of time series models, by incorporating uncertainty into projections using Monte Carlo techniques to simulate vital rate fluctuations. While claiming to be model-free, however, Keyfitz was of course relying on some specification in making his random trials. In particular, the distribution of fertility and migration were assumed to be i.i.d., with distributions equal to their historical distributions. Life expectancy was assumed to grow at a constant, if randomly chosen rate, for the entire sample period.

In this paper we try to follow in the examples of both Keyfitz and the time-series analysts. We use random draws, incorporating the bootstrap of Keyfitz, but rather than drawing levels or constant rates of change we specify processes by which the vital rates evolve and

sample historic differences, either multiplicative or additive. This means that we are able to include the historical information from the data in the distribution as Keyfitz does, while maintaining the link between future rates and the rates at the point of forecast that time-series analysts have achieved.

2 The Model

Forecast models in general – and population forecasts/projections in particular, are usually based on the principle of constancy. The distinction between models – whether they be complex ARIMA models or fixed-rate age structured population models – is *what* they choose to hold constant.

In projecting a vital rate, the most naive guess for the future would be constancy at present levels. A more educated guess – in the sense of incorporating more information – would take into account the recent trends. And an even more sophisticated guess would include information about the changeability in the trend.

How can one measure past variance and include it in our forecast? One way is to fit model probability distributions to empirical data, by estimating a parametric distribution. The approach taken here is to create an empirical distribution and sample from it at random. This is similar to the idea of a bootstrap sample. Our motivation for using the empirical sample instead of some parametric one is that we have no basis for arguing for any particular parametric shape. For example, it would be difficult to argue, on theoretical grounds, that the distribution for changes in fertility rate should be unimodal or bimodal, or whether it should be symmetric or asymetric. In the absence of theory, then, we let the data speak for themselves.

A number of random models have been proposed for modeling the evolution of demographic rates. Both Keyfitz' (1989) model and the one presented here fit into more general frameworks of random population models. Keyfitz' model corresponds to what has been called the "IID Model" in Tuljapurkar (1989, page 231) or a "white noise" process in Lee (1974, page 610). Our model corresponds to either the "Markov Model" (Tuljapurkar, page 231), or a "random walk process" (Lee, page 613).

2.1 The Projection Model

We start with the basic data from the starting year $t = 0$. Let N_x^f resp. N_x^m the female resp. male population at age x, where $x = 0, \ldots, 100$.

Let l_x^s be the number of survivals from life-table valid for the spring-off year normalized to $l_0^s = 1$. Here s stands for the sex: $s = f$ for females and $s = m$ for males.

Let a_x be the person-years lived by those who die in the interval $[x, x + 1]$. We set $a_0 = 0.12; a_1 = 0.37; a_x = 0.5$ for $2 \leq x \leq 100$ and define as usual the death probabilities

q_x and the lived person years L_x as

$$q_x^s = \frac{l_x^s - l_{x+1}^s}{l_x^s} \qquad x = 0, 1, \ldots, 99$$

$$L_x^s = l_{x+1}^s + a_x(l_x^s - l_{x+1}^s) \qquad x = 0, 1, \ldots, 99$$

The person-years lived for ages 100 and older are defined as

$$L_{100}^s =_\infty L_{100}^s = l_{100}^s(\frac{1}{q_{99}} - 0.5)$$

which comes from setting $\mu_{100} = q_{99}$.

As is well known, l_x may be regained from all probabilities q_y by

$$l_x^s = \prod_{y=0}^{x-1}(1 - q_y^s)$$

Let F_x be the age-specific fertility rates in the starting year , i.e. the number of babies born to a woman of age x divided by the average female population of that age.

Denote by f_0 the total fertility rate (TFR)

$$f_0 = \sum_x F_x.$$

2.1.1 The Cohort Component Model

The basic equation

$$\text{population}(t + 1) = \text{population}(t) * \text{survivorship}(t) + \text{births}(t) + \text{migration}(t)$$

reads here (for females)

$$N^f(t + 1) = S^f N^f(t) + 0.49 \cdot f_t \cdot P \cdot N^f(t) + g_t^f \cdot G^f \tag{1}$$

where

$N^s(t)$ is the vector of the population of sex s in year t, i.e.

$$N^s(t) = \begin{pmatrix} N_0^s(t) \\ \vdots \\ N_{100}^s(t) \end{pmatrix};$$

5

S^s is the $[101 \times 101]$ survivorship matrix

$$S^s = \begin{pmatrix} 0 & 0 & 0 & \dots & 0 & 0 \\ s_1^s & 0 & 0 & \dots & 0 & 0 \\ 0 & s_2^s & 0 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & s_{100}^s & 0 \end{pmatrix}, \tag{2}$$

where s_x^s are the age-group specific survival probabilities

$$s_x^s = \frac{Lx + 1^s}{L_x^s};$$

f_t is the total fertility rate in year t;

P is the $[101 \times 101]$ matrix

$$P = \begin{pmatrix} p_0 & p_1 & \dots & p_{100} \\ 0 & 0 & \dots & 0 \\ \vdots & \vdots & \vdots & \vdots \\ 0 & 0 & \dots & 0 \end{pmatrix},$$

where p_x is the probability that (in the spring-off year) a woman, given that she gives birth, is of age x, i.e. $(p_x = \frac{F_x}{f_0})$;

g_t^s are the total net migrations;

G^s is the vector of probabilities G_x^s, that a migrating person of sex s has age x

$$G^s = \begin{pmatrix} G_0^s \\ \vdots \\ G_{100}^s \end{pmatrix}.$$

The values G_x^s are calculated from the age-specific net migrations M_x^s of the spring-off year by

$$G_x^s = \frac{M_x^s}{g_0^s}$$

with $g_0^s = \sum_x M_x^s$.

The model for males (which is dependent on the model for females, but not vice-versa) is

$$N^m(t+1) = S^m N^m(t) + 0.51 \cdot f_t \cdot P \cdot N^f(t) + g_t^m \cdot G^m. \tag{3}$$

6

2.1.2 Multiplicative Changes in Mortality and Fertility

In the following, a model of muliplicative changes of the death probabilities q_x is considered: Let r be some factor and set

$$q_x^s(r) = r \cdot q_x^s$$

Using the quantities $q_x^s(r)$ for the calculation of the l_x's and the L_x's we get

$$l_x^s(r) = \prod_{y=0}^{x-1}(1 - q_y^s(r))$$
$$L_x^s(r) = l_{x+1}^s(r) + a_x(l_x^s(r) - l_{x+1}^s(r))$$

The life expectancy e_0 at birth pertaining to this mortality pattern is calculated according to the formula

$$e_0^s(r) = \sum_{x=0}^{100} L_x^s(r) = \sum_{x=0}^{99}(x + a_x)q_x^s(r) \cdot l_x^s(r) + [100 - 0.5 + \frac{1}{q_{99}^s(r)}]l_{100}^s(r) \qquad (4)$$

The life expectancies for the spring-off year are of course $e_0^f(1)$ resp. $e_0^m(1)$.

Since the factors r influence the survorships by

$$s_x^s(r) = \frac{L_{x+1}^s(r)}{L_x^s},$$

the survivorship matrix (2) is a function of r too: $S^s = S^s(r)$.

We will also adopt a multiplicative structure for the age-specific fertility rates:

We assume that the probabilities p_x are constant over time, i.e. given that we know an estimate f of the TFR in some year, the age-specific fertilities in that year are

$$F_x = p_x \cdot f.$$

The final model, which contains the multiplicative factors r_t^s is

$$N^f(t + 1) = S^f(r_t^s)N^f(t) + 0.49 \cdot f_t \cdot P \cdot N^f(t) + g_t^f \cdot G^f$$
$$N^m(t + 1) = S^m(r_t^m)N^m(t) + 0.51 \cdot f_t \cdot P \cdot N^f(t) + g_t^m \cdot G^m.$$

Assuming that $\{r_t^f\}$, $\{r_t^m\}$, $\{f_t\}$, $\{g_t^f\}$, $\{g_t^m\}$ are stochastic processes, with knownprobabilistic structure, one sees that $N^f(t)$ and $N^m(t)$ are stochasticvector processes, with distributions being completely specified by the starting values and by the joint distribution of $\{r_t^f\}$, $\{r_t^m\}$, $\{f_t\}$, $\{g_t^f\}$, $\{g_t^m\}$. In the next section, the specification of these processes will be discussed in detail.

2.2 The structure of Vital Rate Variation

We model the randomness in fertility, mortality and migration rates independently. Although fertility and mortality were inversely-related in pre-transition societies like the pre-industrial England of Malthus, we are not aware of any evidence of covariation of vital rates in post-transition populations.

As mentioned, the input data that constitute our time series are the total fertility rate, life expectancy at birth, and annual net migration. We let each set of age specific rates vary according to a single index parameter. Age-specific rates are calculated using fixed schedules for fertility and mortality. As the TFR and life-expectancy vary, we adjust all age-specific rates by a constant multiplier.

In the following sections we explain, and attempt to justify, the structure of the stochastic processes specified for each vital rate.

2.2.1 Fertility

When dealing with any model of variability in fertility rates over time we need to decide if the magnitude of fertility change is proportional to the current level or of fixed additive size. Here we look at the theoretical and empirical arguments. We conclude that the multiplicative model is a better choice.

Having decided that the fertility level in year t will be a simple function of the level of the previous year, $t - 1$, and some random change, the simplest two models that offer themselves are the additive and multiplicative random walks:

$$f_t = f_{t-1} + \delta \tag{5}$$

$$f_t = f_{t-1} \times \epsilon \tag{6}$$

Both of these are stationary markov processes, where δ is a random variable of additive change, ϵ is a random variable for multiplicative change, and f_t is the level of fertility in year t.

The data can tell us which specification is more appropriate. The choice between an additive and a multiplicative specification boils down to a test for heteroskedacity as is common in regression analysis. One simple way is to plot the ordered TFR values against the absolute changes and then against the proportional changes and to check by eye if there is a pattern. An arithmetic way of doing this is to divide the ordered sample in two halves and see how the average change in the lower half compares to the average change in the upper half.

We see in table 1 concerning U.S. fertility the mean absolute difference is about one-and-a-half times bigger for the larger TFRs than for the smaller TFRs. The mean proportional change, however, is virtually the same despite the change in TFR value. These results support our theoretical argument for a multiplicative model. The same test was performed using Japanese fertility rates 1960-1989 (with a cut–off level at 1.88) and Austrian fertility

8

Table 1: Average change in U.S. fertility rates 1917- 1988,
by type of change and fertility level

	$TFR < 2.54$	$TFR > 2.54$
Number of years	36	35
Mean absolute change: $(f_{t+1} - f_t)$	0.075	0.112
Mean proportional change: $(\frac{f_{t+1}}{f_t})$	1.038	1.035

rates 1953–1992 (with a cut–off level at 2.05) and resulted in similar findings (more so in Ausatria than inm Japan), hence supporting the multiplicative assumption.

We detrend fertility in our projection model. Extrapolation of fertility trends, which have in the long-term been declining, implies that women will soon have no children.[1] On the other hand, extrapolation of the recent short-term upswing in fertility rates in some countries would result in monotonic increases in fertility.

Although in the last century fertility rates have shown a net decline, in the more recent past say since the end of the baby-boom they have oscillated in an apparently random fashion. The theory of the demographic transition, where fertility follows a logistic-like path from a high plateau in natural fertility populations to a low plateau in fertility-controlling populations, also, cautions us against extrapolating from a trend across the two regimes. Furthermore, even since fertility control, which was well established in the time of the first big world-wide dip in fertility in the great depression, there seem to be two distinctly different dynamics pre- and post-baby boom. We intentionally include only the post-baby boom period, which we see as basically trendless. In fact, since the 1970s fertility rates have declined in Austria from 1.87 to 1.50, in the United States they have risen slightly from 1.879 to 1.9321 [note these numbers refer to different time periods], and even in Mauritius, rates have oscillated and risen recently.

Because of the lack of clear trend in the data, we feel that in the near future fertility rates are as likely to fall as they are to rise. We therefore detrend the empirically estimated distributions in such a manner as to preserve the observed variance.

Bounds on fertility

Because there is a significant body of analysis of fertility determinants and scientific information from surveys, etc., which is very relevant for future fertility levels but does not enter our model as defined by the detrended bootstrap, it was decided to set bounds on future fertility levels which are derived from substantive reasoning. In this we follow the choices made for extreme fertility values in the recent scenario population projections conducted by IIASA's Population Project. The reasoning for these choices is given in two books (Future Demographic Trends in Europe and North America: What can we assume today? edited by W. Lutz, 1991; and The Future of World Population: What can we assume today? edited by W. Lutz, 1994) and cannot be summarized here.

The lower limits chosen for total fertility rates are 1.3 for Austria, 1.4 for the USA, and

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[1] For example, Keyfitz(1989) notes that in the case of Canada, "extrapolation from the last 30 years would give zero births within the first quarter of the 21st centry." p. iii.

1.5 for Mauritius. The upper limits were 2.1 for Austria, 2.3 for the USA, and 2.5 for Mauritius. The range within which fertility variation is allowed is greatest in Mauritius with 1.0 children because less seems to be known about the fertility determinants than in Austria, which has a range of only 0.8 children. Whenever the random walk of fertility rates hits a bound, it will be thrown back in the next step by giving the randomly-drawn stepsize a sign that will bring it back into the range. In practice, trial runs without the bounds show that trends based purely on the randomness of past variation hardly go beyond the bounds. In the very long run, however, the bounds force the average fertility assumed towards the arithmetic mean of the two bounds, while originally average fertility is closer to the starting value. This is exactly our intention because the mean of the two extremes is also considered the most likely value (the central scenario) in the assumptions of the IIASA scenarios.

2.2.2 Mortality

The goal of the mortality model is similar to the fertility model in that we would like to incorporate the same amount of variance in the forecast period as in the sample period. Unlike fertility, however, we assume a trend in mortality. The expectation of life at birth is assumed to increase monotonically at either the same rate as the sample period, or at a slower rate (e.g., one-half the speed of recent mortality improvements.) Slowing the rate of increase requires a transformation of the emprical distribution. We prefer subtracting a constant from each sample value, as this changes the mean rate of increase while leaving the variance of the distribution as it was observed.

Expectation of life at birth is chosen as the demographic variable to be modeled. It has the advantage of being widely available in data, well-known, and easily convertible into life table values. Keyfitz (1989) simply changes all age-specific mortality rates by an equal proportion. We do the same.

Letting γ be a random variable representing the proportional change in $e(0)$ from one time period to the next,

$$e_{t+1}(0) = e_t(0) + \gamma_t$$

The justification for an additive random-walk with a strong linear trend is not physiologically based but rather reflects the strong linear trend in the historical data. There are alternative approaches, such as linear extrapolation of age-specific rates, and these result in a life expectancy increase of only half the magnitude of the linear extrapolation of life expectancy itself. There seems to be little theoretical support for linearly extrapolating the age-specific mortality rates rather than life expectancy itself as both are arbitrary statistical measures. Our choice of life expectancy is predicated mainly on the easy availability of life expectancy data as opposed to time series of age-specific rates.

10

2.2.3 Migration

The markovian assumption that the current period fertility and mortality rates would depend in part on the previous period rates seems less suitable for modeling migration. [2]

Time series of migration levels show that policy interventions play a great role in determining migration levels. We are not then modeling large scale social phenomena, as we do with migration and fertility rates, but rather the political system and its interaction with the economy and international migration pressures. In this context, it is reasonable to assume that drastic change, of the sort seen in the pure independence model, is not so easy to dismiss. Accordingly, we model migration not as random walk, but as a simple random draw. Letting g_t be the total number of migrants in a time period, we have

$$g_t = \epsilon,$$

where ϵ is a level of migration selected at random from recent history. The implication of the model is that expected net migration in any time period is the average of the migration during the sample period.[3]

2.2.4 Summary

We can summarize our method in the following four assumptions:

- Future rates of change are based on data from the past.

- Mortality, fertility, and migration are not intercorrelated.

- Mortality and fertility rates depend only on the most recent year's rates (Markovian assumption).

- Migration levels are independent from one year to the next.

2.3 Estimating the resampling distribution

Once the model has been designed, one has to specify the occurring probability distributions. In our case, one has to specify the distribution of $\{r_t^f\}, \{r_t^m\}, \{f_t\}, \{g_t^f\}$ and $\{g_t^m\}$.

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[2] The U.S. Census bureau until recently did not include migration in their forecasts. This was due not only to the link between migration levels and political currents, but because net migration statistics were considered unreliable due to illegal immigration and the lack of record keeping on emigration. "Because changes in these factors are not particularly amenable to quantitative analysis, the assumption has always been made in Census Bureau projections that trends in future international migration levels *could not be predicted.*" (U.S. Bureau of Census (1989), page 25-26) [emphasis added] The U.S. Census' latest projection includes a scenario-based approach to international migration.

[3] From the standpoint of uncertainty, the migration model contains the undesirable feature that we are as uncertain about next year's migration as migration in the year 2023, an alternative would be to this is an issue we will discuss later on.

Let us first discuss the processes $\{r_t\}$. Equation (4) establishes a one-to-one correspondance between the factors r and the life expectancy $e(r)$. This correspondance is nonlinear and concave, its shape for Mauritius 1990 is shown in Figure 1.
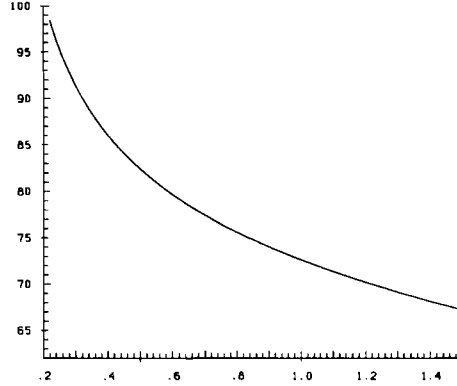

Fig. 1: The relation $r \mapsto e^f(r)$ (females, Mauritius)

It is therefore possible to model the life expectancy processes $\{e_t^f\}$ and $\{e_t^m\}$ and calculate the factors r_t^f and r_t^m from them by inverting the corresponding relations.

We modelled $\{e_t^f\}$ and $\{e_t^m\}$ as additive random walks, $\{f_t\}$ as a multiplicative, truncated random walk with Markov dependencies and $\{g_t^f\}$ resp. $\{g_t^m\}$ as i.i.d. processes.

For the random walk processes we need to specify the distribution of the increment process $\{\eta_t\}$, for the i.i.d. process, the distribution itself has to be determined.

We did not want to make an additional assumption by specifying a parametric class of distributions, but used the "bootstrap idea": Instead offitting a distribution, we take the empirical distribution of the past data as the sampling distribution for the future data.

Here is how it was done. Let $e_{-1}^f, e_{-2}^f, \ldots, e_{-T}^f$ be the recorded life expectancy data of the past T years. The empirical distribution of the differences puts mass $1/(T-1)$ on each of the differences $e_{-t}^f - e_{-t-1}^f; t = 1, \ldots T - 1$. The model for the life-expectancy is

$$e_{t+1}^f = e_t^f + \eta_t, \qquad t \geq 0,$$

where $\{\eta_t\}$ is independently identically distributed according to the forementioned empirical distribution. The process $\{e_t^m\}$ is constructed similarly. Figure 2 shows the past data e_{-s}^f and five typical trajectories of the life expectancy process (females) for Mauritius. Here the lower resp. upper truncation point was set to 1.5 resp. 2.5.
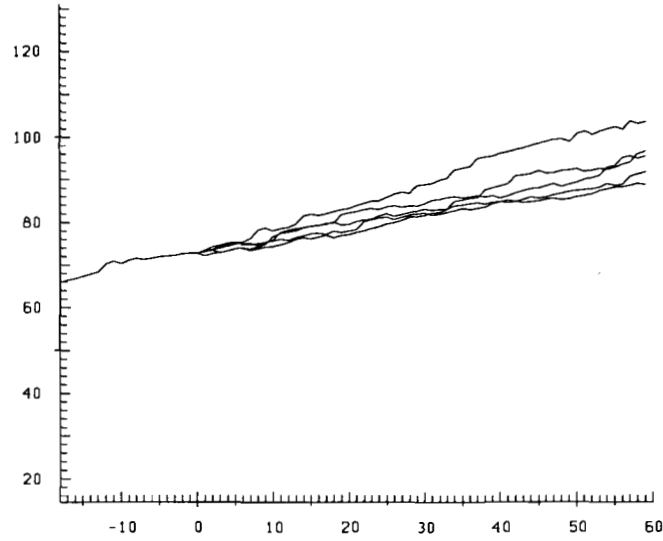
12

Fig. 2: Five trajectories of process of (female) life expectancies
modelled as additive random walk (Mauritius)

2.3.1 Resampling a random walk with Markov dependencies

Since the fertility process was modelled as multiplicative random walk with Markov de-
pendencies, we took the differences of the logarithms of subsequent past total fertilities
as the basis of our considerations. To eliminate the trend, the differences are addidively
corrected to have mean zero:

$$d_{-t} = \log(f_{-t}) - \log(f_{-t-1}) - \frac{1}{T-1}(\log(f_{-T}) - \log(f_{-1})), \qquad t = 1, \ldots T - 1.$$

The emprical transition distribution is obtained by putting mass $1/(T-1)$ on each of the
pairs (d_{-t}, d_{-t+1}). Here is a picture of the emprical transition density:
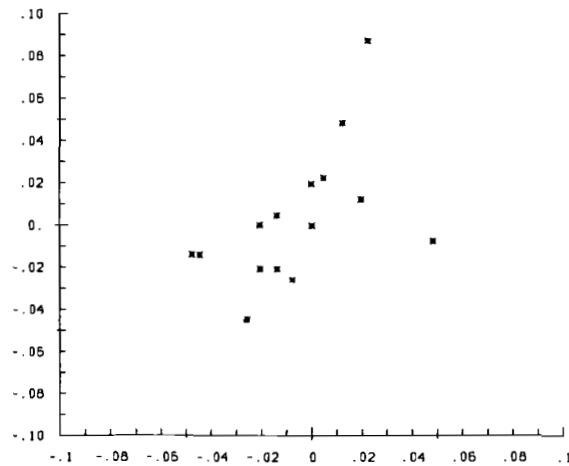

Fig. 3: The empirical transition of the logarithmic total fertility rates (Austria)

13

How can the process of differences be simulated according to this empirical transition? Suppose that f_t and f_{t-1} are the current and the previous simulated values of the fertility process. Let $\xi_t = \log(f_t) - \log(f_{t-1})$. The idea is that the new difference ξ_{t+1} should be with high probabilty a past difference, say d_{-s}, for which d_{-s-1} is close to ξ_t. Define the weights $w(\cdot)$ on the past differences such that w_{-s} is proportional to $\exp(-\gamma(\xi_t - d_{-s})^2))$, where the weights are normalized to 1 and γ is an appropriate smoothing factor. Then choose the old difference d_{-s} with probability w_{-s}. If we set the parameter γ equal to 0, we get an equal distribution over all past differences and we model a pure random walk. If we set γ very large, we will just reproduce the past trajectory. For our bootstrap simulation, we have chosen γ such that the serial correlation of ξ_t coincides with the serial correlation of the past differences d_{-s}. (The value of γ was 5000 for Austria).

The final simulated value for f_{t+1} is $f_t \cdot \exp(d_{-s})$. Here are five typical trajectories:
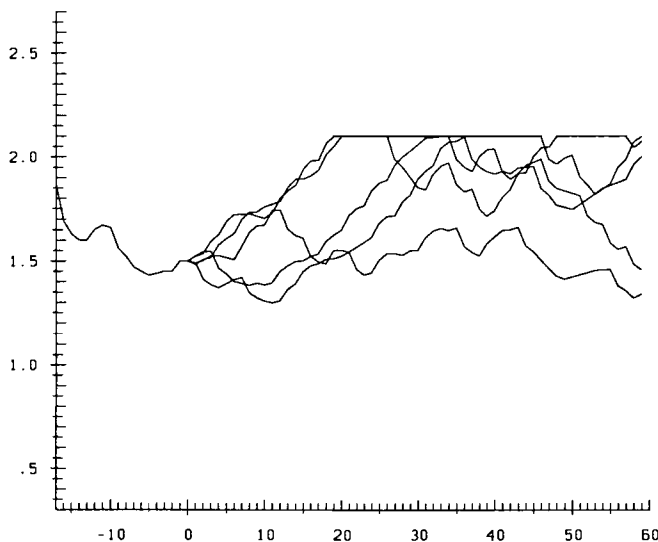

Fig. 4: Five trajectories of the total fertility process
modelled as a multiplicative truncated random walk with Markov dependencies
(Austria)

Finally, the total net migration processes $\{g_t^f\}$ and $\{g_t^m\}$ are modelled jointly:
Let $g_{-1}^f, g_{-2}^f, \dots, g_{-T}^f$ and $g_{-1}^m, g_{-2}^m, \dots, g_{-T}^m$ the past total net migration data. The emprical joint distribution puts mass $1/T$ on each of the pairs (g_{-t}^f, g_{-t}^m). The projected process (g_t^f, g_t^m) is i.i.d. distributed with the empicrical joint distribution.
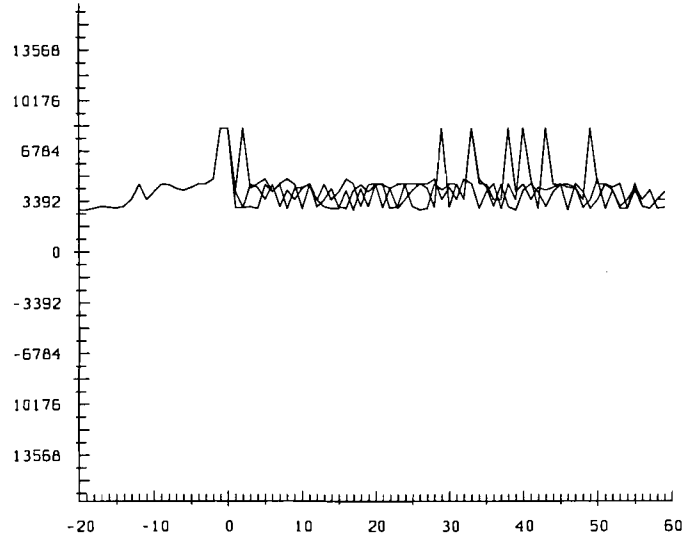
14

Fig. 5: Five trajectories of the (female) net migration process
modelled as i.i.d. process (USA)

3 Results

The method as described above has been applied to three very different countries, Austria, the USA, and Mauritius. These three countries from three different continents, however, have one important characteristic in common: They all have completed their process of demographic transition, i.e., a fertility transition has followed the mortality transition and fertility rates are now fluctuating at levels around or below replacement level. The completion of the fertility transition was an important criterion for picking the countries because it is only after this transition that the assumption of fertility fluctuations without a clear trend makes sense.

As described earlier, the time series considered for the three countries are of different length (ranging from 17 to 20 years). Also different bounds have been set for fertility (see section 2.2.1).

In the following we will discuss the projection results in terms of total population size and projected old age dependency ratio for the three countries individually and compare them to other projections for these countries.

To allow a direct comparison with other projections, the tables below show our 10%, 50% and 90% quantiles together with the projection published by the world bank (WB) as well as the three UN scenarios (low: UNl, middle: UNm and high: UNh).

Austria:

The Austrian census of 1991 provided us with a starting population for the projection of 7.82 million inhabitants. For 2025 our projections based on the bootstrap as described above shown a range of between 8.00 and 8.42 covering 80% of the projected cases with

15

the median at 8.42 million. For 2050 this range is naturally wider because of increased uncertainty with time. While the median is almost identical, the lower decile is at 7.44 million and the higher at 9.32 million.

Table 2: Total population for Austria

	10%	50%	90%	WB	UNl	UNm	UNh
1991		7.82					
2025	8.00	8.42	8.78	7.8	7.69	8.26	8.75
2050	7.44	8.25	9.32	7.3			

This projection clearly gives higher total population figures than the World Bank, which does not consider recent immigration and also tends to be lower than the UN projection, which also assumes lower immigration and lower increases in life expectancy. The official population projection of the Austrian Statistical Office projects 8.2 million by 2025 under the medium variant, 7.9 under the low immigration variant and 8.5 under the high immigration variant. For mortality and fertility assumptions only one specific path is assumed under these assumptions. Another set of alternative scenarios projections produced by IIASA (Prinz and Lutz 1994) for the Council of Europe combines widely differing assumptions on mortality, fertility and migration. Under these projections the central scenario yields 7.9 million in 2030 and 7.6 million by 2050. The most extreme values result from the combinations of low fertility, high mortality and low immigration (6.7 million in 2030 and 5.4 in 2050) on the one side and high fertility, low mortality, and high immigration (9.1 million in 2030 and 10.1 in 2050). The other scenarios lie within this range of extremes.

Hence for Austria, the total population size projected according to our probabilistic bootstrap model tends to be somewhat higher than the UN and the World Bank because of higher immigration, and also a bit higher than the national projections due to slightly quicker improvements in mortality resulting from our method. The IIASA scenarios cover a wider range than our deciles, but the likelihood of these extreme scenarios are explicitly more at the order of 1% than 10%.

As to the age structure resulting from the projections, Figure 6 indicates how little the variation in the old age dependency ratio is over time. It will almost certainly increase from presently 24.9% to between 36% and 40% by 2030, and even 60% and 76% by 2050. This low degree of future variability is due to the fact that the trend of this ratio, at least over the next 40 years, is largely a function of the cohort sizes of people already born. Uncertainty increases visibly only beyond 2030. Another reason for this amazingly low variance is the fact that our bootstrap method does not yield very high variability with respect to future mortality trends, because the past trend increased so smoothly. But generally, other population projections confirm this pattern of a high degree of certainty of significant increases in the old age dependency ratio around 2020 in Western European low fertility populations.
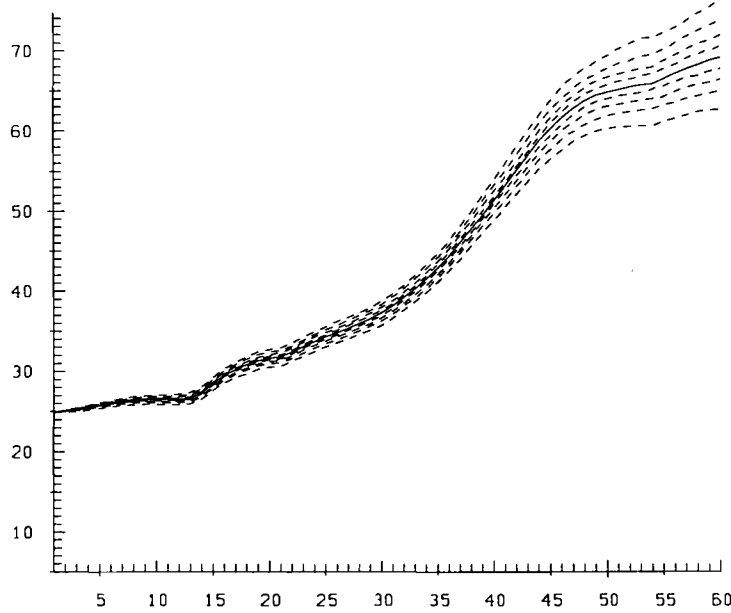
Fig 6: The deciles of the projected oadr-rates (Austria)

USA:

For the United States of America our probabilistic bootstrap- based projections yield a median total population size of 323 million in 2025 and 391 million in 2050. For 2025 this is approximately the same result as given by the UN medium variant. The low variant gives 302 million, the high one 346 million. The only projection given by the World Bank, however, is significantly lower and estimates only 324 million by 2050.

Table 3: Total population (USA)

	10%	50%	90%	WB	UNl	UNm	UNh
1989		248					
2025	319	334	340	314	302	322	346
2050	356	391	401	324			

Table 4: Old age dependency ratio (USA)

	10%	50%	90%
1989		21.18	
2030	29.36	30.34	31.31
2050	41.05	43.17	46.91

Figure 7 plots the distribution of projected total population sizes for the USA. It opens in a trumpet-like manner, much more so than that of the old age dependency ratio (see Figure 6 for Austria above). Uncertainty seems to increase regularly with time. While in the first 25 years or so it is only the uncertainty in fertility, mortality and migration rates

17

that matters, beyond that it is also the uncertainty in the size of the cohorts to which future rates will be applied.
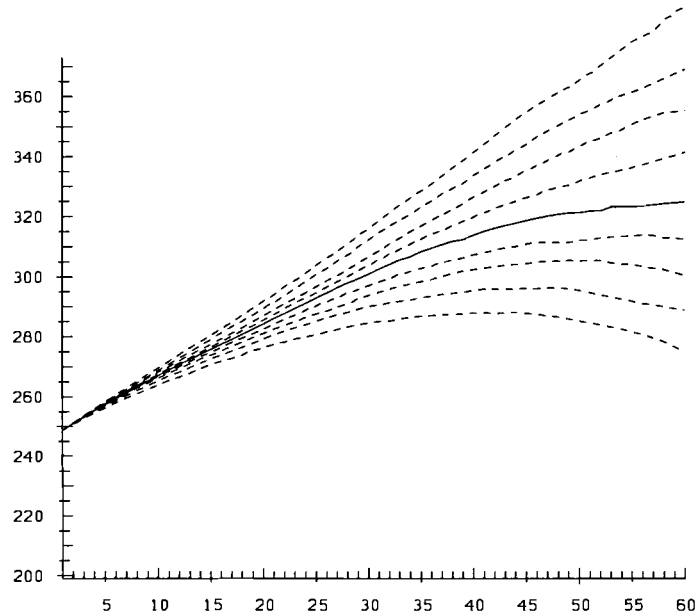

Fig. 7: The deciles of the projected total population process (USA)

As in Austria the old age dependency ratio will certainly increase further in the USA. But the increase will be very irregular. For the next 20-25 years the ratio is expected to stay almost constant on average and also shows very little random variation. By 2030 it will already have increased from presently 21% to around 30%. This rapid increase over the next 25 to 50 years also shows amazingly little variation. It is only after 2040 that random variation begins to play a major role, i.e., when uncertainty about cohort size is added to the uncertainty about mortality, which dominates the picture during the first decades. As in Austria past mortality trends, from which the sample was drawn, improved rather regularly, hence inducing only little random variation in the projection.

Mauritius:

The Indian Ocean island of Mauritius has an amazing demographic history. During the 1960s it had one of the world's most rapid rates of population growth which resulted from formidable increases in life expectancy combined with continued high or even somewhat increasing fertility. Then during the late 1960s and early 1970s Mauritius experienced what was probably the world's most rapid fertility decline (see analysis in Lutz 1994b). Since the late 1970s the Total Fertility Rate in Mauritius is below 3.0 and even reached sub-replacement level in the mid-1980s. But due to the very high growth rates in the recent past, the age structure of Mauritius is still very young. This resulted in the fact that during the late 1980s the population of Mauritius was still growing at a rate of more than 1% per year despite fertility rates below replacement level, because rapidly increasing numbers of young women entered the prime reproductive ages. Hence Mauritius is a very good example for the momentum of population growth.

18

Our projection model applied to Mauritius also shows that the population will most likely increase further from the 1.05 million in 1990 to around 1.5 million in 2050. This median trend is very close to that projected by the UN and the World Bank. The 80% probability range in 2050 extends from 1.24 to 1.68. This means a higher degree of uncertainty in Mauritius than in the USA and Austria. The range between the 10th and 90th percentiles is in Mauritius 29% of the median level in 2050. In Austria it is 22% and in the USA only 12%. In Mauritius this higher uncertainty is due to the greater empirically-observed changes in fertility and mortality during the observation period from which the bootstrap was drawn. In Austria the uncertainty is mostly due to irregularity in migration streams.

Table 5: Total population (Mauritius)

	10%	50%	90%	WB	UNl	UNm	UNh
1990		1.05					
2025	1.26	1.37	1.44	1.40	1.29	1.40	1.52
2050	1.24	1.50	1.68	1.48			

Table 6: Old age dependency ratio (Mauritius)

	10%	50%	90%
1990		9.62	
2030	18.39	19.62	20.95
2050	34.52	46.96	58.67

The old age dependency ratio in Mauritius shows a pattern similar to that in Austria and the USA. It is also close to constant with little variation for the next 20-25 years and increases sharply thereafter. Because of the young age structure in Mauritius the dependency ratio presently is still extremely low (only 9.6%) but by 2050 it is likely to increase to a level (median 47%) that is higher than that in the USA in that year. This also illustrates the fact that aging in high fertility countries that have a rapid fertility decline will be a much more dramatic phenomenon than in Europe and North America.

4 Summary and Discussion

This paper proposes a new approach to introducing quantitatively-measured uncertainty into population projections. As most similar approaches, it is also based on the information provided by past time series, but to a lesser degree. For fertility and migration, it does not take into account the past trends but only the past variation, i.e., the size of the steps by which fertility, mortality and migration changed in the past. By putting bounds on the level that fertility can reach in the future, further substantive information was introduced that transcends the information derived from time series analysis. Hence this approach lies somewhere between a set of scenarios to which no probability distribution can be attached, and a probabilistic model based entirely on time series.

Much more work needs to be done on this issue in the future. This paper only suggests one possibility of combining the attractive features of both approaches. With respect to fertility, the proposed combination of information on "step- height" from the past and information on level from external substantive expertise makes a flexible and promising model. As far as mortality is concerned, the model is less satisfactory. The empirical bootstrap has not been detrended because clearly further improvements in mortality are expected. But the trend has been halved by setting every second step to zero, because it is also unlikely that improvement will continue at such a rapid pace as observed in the past. An undesirable consequence of this, together with the smoothness of the past trend, is that very little mortality variation is introduced into the model. Substantive considerations, such as the uncertainty whether we are approaching a biological limit to life or not, imply a much higher degree of uncertainty in the future than the bootstrap sample in our model suggests. Here is clearly room for further improvement. As to migration, very little substantive theory exists as to how future migration levels should be. For this reason the chosen sampling of past absolute levels of migration seems to be a straightforward and empirically-based choice.

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Random Walks with Markov dependencies

Let $\{\eta_t\}$ be a sequence of i.i.d. random variables. The stochastic process $\{z_t\}$ is called an (additive) random walk, if

$$z_{t+1} = z_t + \eta_t.$$

A nonnegative process $\{z_t\}$ is called a multiplicative random walk, if $\{\log z_t\}$ is an additive random walk.

The process $\{z_t\}$ is called a truncated random walk, if

$$z_{t+1} = [z_t + \eta_t]_a^b,$$

where $[x]_a^b = \begin{cases} b & \text{if} & x > b \\ x & \text{if} & a \le x \le b \\ a & \text{if} & x < a \end{cases}$

a resp. b are the lower resp. upper truncation points.

A nonnegative process $\{z_t\}$ is called a truncated multiplicative random walk, if $\{\log z_t\}$ is a truncated random walk.

A process $\{z_t\}$ is called a random walk with Markov dependencies (RWMD), if the steps $\{\eta_t\}$ stem from a homogeneous ergodic Markov process.

Since an i.i.d. sequence is a special case of a homogeneous ergodic Markov process, random walks with Markov dependencies are generalizations of ordinary random walks.

A pure random walk can never be stationary, since $\text{Var}(z_{t+1}) = \text{Var}(z_t) + \text{Var}(\eta_t) > \text{Var}(z_t)$ unless η_t is identically zero.

A truncated random walk or RWMD however has a unique stationary distribution. In particular, the following properties hold:

- If $\{\eta_t\}$ is ergodic, then $\{z_t\}$ is ergodic.

- Irrepective of the starting value, z_t converges exponentially fast to the unique stationary distribution.

- A small perturbation of the increment process $\{\eta_t\}$ leads to a small perturbation in the stationary distribution of z_t

The proof will be illustrated under the condition, that for each pair x_1, x_2 one may find a pair $\eta_t^{(1)}$ and $\eta_t^{(2}$ such that and and suppose that $0 < \delta \le P\{\eta_t^{(1)} > b - a$ and $\eta_t^{(2)} > b - a | \eta_{t-1}^{(1)} = x_1, \eta_{t-2}^{(2)}\}$ for all t. Consider the two sequences

$$z_{t+1}^{(1)} = [z_t^{(1)} + \eta_t^{(1)}]_a^b$$

$$z_{t+1}^{(2)} = [z_t^{(2)} + \eta_t^{(2)}]_a^b$$

started at $z_1^{(1)}$ resp. $z_1^{(2)}$. We will prove that for all t

$$E(|z_{t+1}^{(1)} - z_{t+1}^{(2)}|) \leq (1 - \delta)E(|z_t^{(1)} - z_t^{(2)}|) + E(|\eta_t^{(1)} - \eta_t^{(2)}|) \qquad (7)$$

where E denotes the expectation.

For the proof set $A = \{\eta_t^{(1)} > b - a \text{ and } \eta_t^{(2)} > b - a\}$ and notice that

$$
\begin{aligned}
E(|z_{t+1}^{(1)} - z_{t+1}^{(2)}|) &= E(|[z_t^{(1)} + \eta_t^{(1)}]_a^b - [z_t^{(2)} + \eta_t^{(2)}]_a^b|) \\
&\leq E(1_{A^c}|[z_t^{(1)} + \eta_t^{(1)} - z_t^{(2)} - \eta_t^{(2)}|) + E(1_A|[z_t^{(1)} + \eta_t^{(1)}]_a^b - [z_t^{(2)} + \eta_t^{(2)}]_a^b|) \\
&\leq (1 - \delta)[E(|z_t^{(1)} - z_t^{(2)}|) + E(|\eta_t^{(1)} - \eta_t^{(2)}|)] + \int_A |b - b|\, dP \\
&\leq (1 - \delta)E(|z_t^{(1)} - z_t^{(2)}|) + E(|\eta_t^{(1)} - \eta_t^{(2)}|).
\end{aligned}
$$

Here we have used the inequality

$$|[x]_a^b - [y]_a^b| \leq |x - y|.$$

From inequality (7) we may draw two different conclusions. First, choosing different starting values for $\eta_t^{(1)}$ and $\eta_t^{(2)}$ and assuming that by ergodicity $E(|\eta_t^{(1)} - \eta_t^{(2)}|)$, one sees that also

$$E(|z_t^{(1)} - z_t^{(2)}|) \to 0.$$

Secondly, if $\eta_t^{(1)}$ and $\eta_t^{(2)}$, then

$$E(|z_t^{(1)} - z_t^{(2)}|) \leq \sum_{i=1}^{t} E(|\eta_t^{(1)} - \eta_t^{(2)}|)(1 - \delta)^i + E[|z_1^{(1)} - z_1^{(2)}|](1 - \delta)^t,$$

which implies that

$$\sup_t E(|z_t^{(1)} - z_t^{(2)}|) \leq \frac{1}{\delta} \sup_t E(|\eta_t^{(1)} - \eta_t^{(2)}|) + E[|z_1^{(1)} - z_1^{(2)}|].$$

We see that due to the truncation, the process $\{z_t^{(1)}\}$ is closed to $\{z_t^{(2)}\}$, for all t, if the $\{\eta_t^{(1)}\}$ is closed to $\{\eta_t^{(2)}\}$. Without the truncation, $\{z_t^{(1)}\}$ and $\{z_t^{(2)}\}$ would drift away as $t \to \infty$. Thus, a slight misspecification of the step process $\{\eta_t\}$ does not lead to a dramatic error for larger t for the model with truncation.