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ABSTRACT

Population projections are simply extrapolations of demographic patterns that have remained constant in the past into the future. This observation by Keyfitz simultaneously provides a philosophical base for forecasting techniques and sets off a search for demographic patterns. We begin with a discussion of the reasons for disaggregate projections, how the reasons effect data requirements, and how models relieve the strain. The next section discusses advances in demographic models, especially extensions of the relational methods developed by Brass. Finally, we discuss how time-series models, in conjunction with model patterns, can be used to make forecasts with appropriate confidence intervals. The paper motivates the techniques through examples of Swedish life tables, and describes appropriate mathematical properties for projection models.

ADVANCES IN MATHEMATICAL MODELS FOR POPULATION PROJECTIONS

INTRODUCTION

Population projections are simply extrapolations of demographic patterns that have remained constant in the past. This simple observation of Nathan Keyfitz[1] simultaneously provides a philosophical base that moves forecasting from the realm of crystal balls to that of modern computers, and sets off a scientific search for demographic patterns to improve our ability to forecast the future.

Forecasters must consider two sorts of patterns; age patterns and temporal patterns. The first involves relationships between simultaneous demographic variables, such as mortality rates for various ages. In applying population dynamics to forecasting, demographers have learned to disaggregate data. But disaggregation requires detailed data that is often either not reliable, or not available. The development of model schedules helps to fill this gap. Model schedules abstract the pattern of, say, age-specific fertility rates that is common to all populations.

The second type of pattern concerns how variables change over time. Forecasting would be simple if all key variables changed according to a simple pattern. Part of the reason for disaggregation is to find simple trends at low levels of aggregation that do not appear at higher levels.

Trends, too, are of two types. Most basically, forecasters try to identify demographic variables that grow linearly, or perhaps exponentially, and extrapolate these into the future. On another level, forecasters must also consider the time pattern of variances and covariances of demographic variables in order to construct confidence intervals for population forecasts. Modern methods of time series analysis help identify both trends and the covariance structure of observations in time.

This paper begins with a discussion of the reasons for disaggregate models, and how they affect data needs. The next section discusses some new tools for specifying model patterns in mortality data, especially the relational methods pioneered by William Brass, and their extensions. As an example of these techniques, the paper makes and evaluates forecasts of Swedish life tables. The following section discusses similar methods for fertility forecasts, and then the paper considers the role of time series analysis, which, in conjunction with model parameters, leads to forecasts with appropriate confidence intervals.

Although producers of population projections frequently distinguish their work from predictions of forecasts, users do not always understand the distinction.[2] Throughout this paper, the terms "forecast," "prediction," and "projection" are used interchangeably, and refer to estimates of future population variables extrapolated from the past. In addition, the paper only considers purely demographic projections that do not rely on exogenous forecasts of economic or other variables.

THE ROLE OF DISAGGREGATION

Disaggregating demographic data leads to better projections, but causes data problems. Let us examine the reasons for disaggregations, and then see how relational models relieve some of the associated problems.

Component methods allow forecasters to isolate or more easily interpret time trends. Perhaps the simplest application of this idea is to independently consider birth, death, immigration, and emigration rates. The key idea is that trends in these variables may be simpler to forecast than the overall growth rate. For instance, ideas about economic conditions and contraceptive behavior help us to explain trends in the birth rate and predict what will happen in the future. A slightly more complex component method makes a separate analysis and projection for each ethnic, racial, or socioeconomic group. The idea here is that simple but different demographic trends apply to each group, and that the simplicity is hidden in the aggregate data.

Disaggregation also permits forecasters to apply the mathematics of population dynamics to predict the effect of a population's age structure. For instance, given the same set of age-specific fertility rates, populations with a large proportion of young women will, in the short run, have more births than other, older populations. Thus age-disaggregation, together with the mathematics of population dynamics, leads to a more realistic model of demographic growth. In addition, age-specific models also lead to simplicity in time patterns. For instance, fluctuations in the birth rate reflect both age structure and age-specific fertility. The total fertility rate, on the other hand, reflects only fertility behavior, and thus may have simpler and more easily interpretable trends.

Finally, disaggregation is often important if projections are to respond to policy questions. For instance, if we are to study the effect of an immigration policy or a family planning program on the overall growth rate and the future age distribution, all of the above variables must be explicitly modeled. As another example, forecasts of the school-age population obviously must depend on age-specific projections.

The difficulty with disaggregation is that as more and more realism is gained by making more detailed models, the forecaster must estimate more data points. These data include both a detailed description of base-year population figures and rates as well as a large set of future demographic rates. The practical difficulties of gathering and analyzing these data, as well as small sample problems that arise, soon overcome the benefits of disaggregation.

Mathematical models of demographic rates offer a compromise position. Such models represent an entire set of fertility, mortality, or migration rates with a small number of parameters. To the extent that these models adequately represent the true rates, they reduce and simplify the work involved in estimating future rates.

The next sections describe some recent progress in the development of models for demographic rates. We begin with mortality because this area is most developed, and because the models we describe can be adapted to other sets of demographic rates.

DEMOGRAPHIC MODELS FOR MORTALITY

Demographers have generally taken one of three approaches to developing mortality models. The first—mathematical—approach attempts to find a mathematical formula to adequately describe some life table function, usually the force of mortality, μ_t. The relatively simple Makeham and Gompertz curves often work well over age 30, but not at earlier ages. Recently, Pollard[3] has developed a six-parameter model for the complete age span, but no simpler version seems adequate.

The second—empirical—approach attempts to statistically develop a set of numerical life tables that cover the range of observed tables.[4] For many populations these models are quite successful, but the numerical form constrains the flexibility and ease of application of these systems.

The third approach, Brass's "relational" model and its extensions, offers a compromise between the flexibility of the mathematical approach and the empirical nature of the second approach. Because it is based on comparisons of similar life tables it is especially appropriate for a forecasting model.

The relational system assumes the existence of a common "standard" life table, $l_s(x)$. In forecasting problems, we have a series of previous tables, $l_i(t)$, for time periods (or cohorts) denoted by i. The system relates each of the $l_i(t)$ to the standard by a simple function, hence it is called a "relational system."[5] Specifically, let

$$\text{logit }(p) = \frac{1}{2} \log \left(\frac{p}{1-p}\right) \quad .$$

The relationship of a given life table to the standard is

$$\text{logit}\left[l_i(t)\right] = \alpha_i + \beta_i \text{ logit}\left[l_s(t)\right] \quad . \qquad (1)$$

Let us first consider under what conditions a group of similar life tables can be described by equation (1). We begin with an unrealistic assumption that we will soon drop. Let T be a random variable, the length of life. The life table values, $l_i(x)$ are

$$l_i(t) = \text{Prob }(T \geq t)$$

the probability that a life exceeds t years. The unrealistic assumption is that T has a logistic distribution with parameters α_i and β_i, that is, that $l_i(t)$ has the form

$$l_i(t) = \frac{e^{2(\alpha_i + \beta_i t)}}{1 + e^{2(\alpha_i + \beta_i t)}} \quad .$$

The logit function is the inverse of the logistic life table function;

$$\text{logit}\left[l_i(t)\right] = \frac{1}{2} \log e^{2(\alpha_i + \beta_i t)}$$

$$= \alpha_i + \beta_i t \quad .$$

If all life tables represented logistic distributions, logits of all life tables would be linear functions of t. Thus, if we define

$$l_s(x) = \frac{e^{2t}}{1 + e^{2t}}$$

then

$$\text{logit}\left[l_s(t)\right] = t \quad .$$

Hence for all $l_i(t)$,

$$\text{logit}\left[l_i(t)\right] = \alpha_i + \beta_i \left\{\text{logit}\left[l_s(t)\right]\right\} \quad .$$

Under the restrictive assumptions, a relational system represents all life tables.

But we can substantially relax the assumptions and still maintain the linear relationship. For any specific $l_i(t)$ we can find a transformation of the time axis, $g(t)$, such that

$$l_i(t) = \frac{e^{2[\alpha_i + \beta_i g(t)]}}{1 + e^{2[\alpha_i + \beta_i g(t)]}} \quad .$$

The transformation $g(t)$ may be simple, for instance, taking logarithms of the time scale, or it may be complex. If the same $g(t)$ transforms each of a set of distributions to a logistic shape, we can represent each table as

$$\text{logit}\left[l_i(t)\right] = \alpha_i + \beta_i \, g(t) \quad . \tag{2}$$

If we set the standard as

$$g(t) = \text{logit}\left[l_s(t)\right] \quad ,$$

equation (1) still holds.

The search for a transformation of the age axis to make each of the observed life tables logistic is equivalent to the search for a standard life table for equation (1). If a series of empirical life tables exactly meet the above conditions, any one table may serve as a standard distribution. Forecasting in this case simply implies estimating the historical series of α_i and β_i and projecting them into the future. A multidimensional problem has been reduced to a much simpler two-dimensional problem.

The form of the relational model is especially convenient for forecasting. First, if an appropriate standard can be found, all of the temporal variation is described by the trajectory of α_i and β_i. Often these trajectories are close to straight lines over reasonable periods of time, and can simply be extrapolated. Second, α_i and β_i have convenient interpretations: α is directly, but not linearly, related to the life expectancy; β is inversely related to the spread of the distribution around the life expectancy. These interpretations allow forecasters to bring subjective knowledge of likely changes in mortality into the projection. Or forecasters can set target values of α and β from similar, but more advanced, countries, and interpolate to these values. Third, with a sufficiently long series of tables, the choice of a standard life table, as we will see below, allows the forecaster to tune the forecast to a specific country, rather than relying on mathematical or "universal" patterns. Finally, the relational model describes a closed system; any value of α_i together with a positive value of β_i represents a permissible life table. Life table values of $l_i(t)$ must be, by definition, between one and zero. But logit $[l_i(t)]$ varies from plus to minus infinity. The form of the relational system, where logit $[l_i(t)]$ is a linear function of logit $[l_s(t)]$, means that as long as $l_s(t)$ is monotone and between one and zero, logit $[l_s(t)]$ and thus logit $[l_i(t)]$ range from plus to minus infinity, hence $l_i(t)$ has the mathematical form of a life table as well. This means that forecasters can extrapolate α and β far from the bounds of historical experience, and still have a projected $l_i(t)$ of the proper form.

CHOOSING A STANDARD LIFE TABLE

An appropriate standard life table is essential for good mortality forecasts, and recent work has focused on this choice. Originally Brass developed two standards, one that reflects African mortality patterns, and another based on European patterns. Recently Clarin *et al.* have developed a set of five standard curves for geographical regions.[6] But in many forecasting situations, the availability of a reasonably long series of historical life tables can lead to a more appropriate choice of standard. The simplest method is to pick one of the series as a standard. If equation (1) were exact, the choice would not matter. But in reality the model never holds exactly, and a better choice can be developed as a sort of average of the observed tables. In this way, peculiarities of the individual tables can be eliminated. To develop such a standard, consider the data as a rectangular array of values, $l_i(t_j)$, the i^{th} life table evaluated at the j^{th} age. The age points, t_j, are the same for each table. Let us define

$$y_{ij} = \text{logit}\left[l_i(t_j)\right]$$

and

$$x_j = \text{logit}\left[l_s(t_j)\right] \quad .$$

We calculate the y_{ij} from the original data, but at the start the x_j are unknown. The implication of the Brass model, equation (1), is the linear model

$$y_{ij} = \alpha_i + \beta_i \, x_j \quad .$$

Since the x_j as well as the α_i and β_i are unknown, the model is actually a simple case of factor analysis.

An estimation algorithm for the standard and parameters can consist of the interation of two steps.[7] If the x_j were known, we would regress the values in the i^{th} column of y_{ij} on the x_j values to estimate α_i and β_i. If α_i and β_i were known, we could construct $y_{ij} - \alpha_i$ for the j^{th} row of y_{ij}, and regress (through the origin) these values on β_i for an estimate of x_j.

Another approach to developing a standard is to increase the number of parameters in the system. Zaba[8] has extended Brass's relational system by developing, through a Gram-Charlier expansion, two standard patterns of deviations from the basic standard, k(t) and s(t). She then defines a new standard

$$l_n(t) = l_s(t) + \psi_i \, k(t) + \chi_i \, s(t)$$

Then the model is

$$\text{logit}\left[l_i(t)\right] = \alpha_i + \beta_i \, \text{logit}\left[l_n(t)\right] \quad .$$

This four-parameter model fits a wide range of life tables, but the additional parameters are difficult to interpret and to estimate without a computerized minimization procedure.

Ewbank *et al.*[9] have developed another four-parameter system that has more easily interpreted and estimated parameters. Define

$$T(p;\kappa,\lambda) = \begin{cases} \dfrac{\left(\frac{p}{1-p}\right)^{\kappa} - 1}{2\kappa} & p \geq 0.5 \\[2ex] \dfrac{1 - \left(\frac{1-p}{p}\right)^{\lambda}}{2\lambda} & p < 0.5 \end{cases} \quad .$$

Then, instead of equation (1), model

$$\text{logit}\left[l_i(t)\right] = \alpha_i + \beta_i \, T\left[l_s(t);\, \kappa_i,\, \lambda_i\right] \quad . \qquad (3)$$

In the limit, as κ and λ go to zero, $T(p;\kappa,\lambda)$ goes to logit (p). Thus, $T(p;\kappa,\lambda)$ is a generalization of the logit function. Heuristically, α and β represent differences in location and scale between $l_i(t)$ and the standard, and κ and λ represent changes in the shape of the distribution in each tail.

Using this sytem, strong, linear, temporal patterns often appear in the parameters, suggesting the regular progression necessary for extrapolation. In addition, regularities in the age pattern also appear. For instance, in Swedish life tables, both κ and λ have been consistently linearly related to β for over two hundred years. This suggests that a two-parameter model (given the linear relationships) is sufficient to describe changes in Swedish mortality.

EXAMPLE: MORTALITY FORECASTS FOR SWEDEN

Let us consider an example that illustrates many of the difficulties of demographic forecasting, and the advantages of relational methods. Suppose a demographer in 1965 wanted to forecast changes in the life table for Swedish males. I choose this date so that we can compare the forecasts to the eventual life tables which are now known. We have at our disposal a long historical series of five-year life tables, but for the moment concentrate our attention on the seven tables from 1931 on. Figure 1a shows the time trend of five values: $l_i(1)$, $l_i(20)$, $l_i(50)$, $l_i(65)$, and $l_i(80)$. Simple linear extrapolation of these trends would soon lead to impossible values of $l_i(t)$ greater than one. Similar problems would arise with q(t) values going below zero.

One alternative is to calculate the values

$$r_i(t) = \frac{l_i(t)}{\left[1 - l_{i(t)}\right]} \quad ,$$

plotted in Figure 1b. The r(t) values have no upper bound, so extrapolation does not lead to impossible values. But both the slope and the degree of variability for $r_i(1)$ is much larger than for $r_i(80)$, and this heterogeneity could lead to confusion and inefficiences in forecasting. The third panel of Figure 1 plots

$$y_i(t) = \text{logit}\left[l_i(t)\right] = \frac{1}{2} \log r_i(t) \quad .$$

This transformation leads to similar slopes and variances. Since forecasts rely on consistency, extrapolating trends in $y_i(t)$ may lead to better projections. There is some curvature in the trends in Figure 1, but the last four observations (those after the Second World War) appear reasonably linear. Extrapolation of these trends by least squares regression leads to Projections 1, 2, and 3 of $l_i(t)$ for '66-'70 and '71-'75 in Table 1.

Alternative projections rely on relational models. Figure 2a shows the time trend of the four parameters, α_i, β_i, κ_i, and λ_i, from the model of equation (3). Here again, trends in the fitted parameters are reasonably linear from '46-'50 on. One projection comes from simply extrapolating each series, then calculating the implied values of $l_i(t)$. The result appears in Table 1 as Projection 4. On the other hand, Figure 2b indicates that α_i, κ_i, and λ_i are each nearly linearly related to β_i, consistent with the results of Ewbank *et al.*[10] Projection 5 in Table 1 is based on the linear extrapolation of the last four

Table 1 Time series and projections for five selected Swedish male life table values. Projections are: 1) extrapolation of $l_i(t)$; 2) extrapolation of $r(t)$; 3) extrapolation of $y(t)$; 4) extrapolation of α, β, κ, λ; and 5) extrapolation of β, and estimation of α, κ, and λ as a function of β.

		'31-'35	'36-'40	'41-'45	'46-'50	'51-'55	'56-'60	'61-'65	'66-'70	(error)	'71-'75	(error)
$l_i(1)$	Actual	.9451	.9530	.9659	.9734	.9776	.9813	.9834	.9860	.	.9887	
	Projection 1								.9947	.0087	1.0012	.0125
	2								.9852	-.0008	.9867	-.0020
	3								.9876	.0016	.9900	.0013
	4								.9874	.0014	.9893	.0006
	5								.9872	.0012	.9893	.0006
$l_i(20)$	Actual	.9048	.9176	.9375	.9544	.9622	.9675	.9714	.9752		.9788	
	Projection 1								.9914	.0162	1.0030	.0242
	2								.9759	.0007	.9786	-.0002
	3								.9790	.0038	.9831	.0043
	4								.9765	.0013	.9799	.0011
	5								.9768	.0016	.9805	.0017
$l_i(50)$	Actual	.7896	.8112	.8443	.8808	.9005	.9109	.9165	.9164		.9178	
	Projection 1								.9557	.0393	.9785	.0607
	2								.9265	.0101	.9330	.0152
	3								.9367	.0203	.9473	.0295
	4								.9286	.0122	.9369	.0191
	5								.9309	.0145	.9397	.0219
$l_i(65)$	Actual	.6298	.6429	.6891	.7219	.7475	.7605	.7660	.7667		.7685	
	Projection 1								.7657	-.0020	.7694	.0009
	2								.7875	.0198	.7999	.0314
	3								.7995	.0318	.8182	.0497
	4								.7899	.0222	.8036	.0351
	5								.7963	.0286	.8122	.0437
$l_i(80)$	Actual	.2554	.2532	.2987	.3080	.3307	.3386	.3395	.3428		.3437	
	Projection 1								.3685	.0257	.3847	.0410
	2								.3636	.0208	.3768	.0331
	3								.3719	.0291	.3903	.0466
	4								.3425	-.0003	.3533	.0096
	5								.3590	.0162	.3772	.0335

SOURCE: United Nations Demographic Yearbook.

observations of β_i and an estimate of λ_i and κ_i as linear functions of β_i, the line based on all seven periods.

Some values of $l_i(t)$ are easier to predict than others. The changes in $l_i(1)$ and $l_i(20)$ are so small that each projection method gives good results, except that the extrapolation of the $l_i(1)$ values leads to values greater than one by '71-'75. The values of $l_i(50)$, $l_i(65)$, and $l_i(80)$ are in general harder to predict; the actual change in these values was generally smaller than the previous changes.

But given these differences, the relational methods perform reasonably well. Projection 4, individual extrapolation of the parameters, gives the best results, with an average absolute error in $l_i(t)$ of 0.0103. The second best results are from Projection 2, extrapolation of the $r_i(t)$ values (0.0134), and the third best are from Projection 5, extrapolation of α_i, κ_i, and λ_i as functions of β_i (0.0164). Extrapolation of the $l_i(t)$ values and the $y_i(t)$ values lead to substantially worse errors (0.0241 and 0.0218).

The point of this exercise is to illustrate the use of relational methods in population projections, and demonstrate that they lead to competitive results. More comprehensive prospective tests would help to determine the sorts of models that are likely to lead to decent mortality forecasts. But demographic forecasters will always remain in the position of extrapolating trends, and no matter how consistent patterns have been in the past, there is never a guarantee that they will continue into the future.

DEMOGRAPHIC MODELS FOR FERTILITY

Demographic studies of the age pattern of fertility differ from mortality studies in two important aspects. First, fertility models must take into account that fertility, unlike mortality, is a repeatable event. Second, a description of fertility often involves more socioeconomic or biological predictors and intermediate steps.

In mortality work models frequently represent l(t), a cumulative variable, rather than μ_t, an age-specific variable. The reasons for this are that (1) l(t), and especially logit [l(t)], are convenient to model mathematically, and (2) l(t) hides some small irregularities in μ_t that are hard to model and not important for projection or estimation. The cost is that changes in cumulative variables, like l(t), are harder to understand than changes in age-specific functions such as μ_t. Since fertility is repeatable, its fundamental measure is the intensity of fertility at age t, f(t), which is analogous to μ_t rather than to l(t). To gain the advantages of a cumulated function, demographers often study

$$F(t) = \int_0^t f(s)\,ds \quad .$$

But, unlike l(t), F(t) is not constrained between zero and one. To achieve the form of a cumulative probability distribution, demographers calculate F'(t) = F(t)/F(50), and model F'(t) by methods similar to those developed for l(t). The cost is an additional parameter, F(50), external to the model.

Because of the many theories about the determinants of fertility, and data availability by age, marital status, parity, marital duration, and other descriptors, there is a wide variety of functions to model. In addition, there is frequently a choice between period and cohort measures. All of these choices can be expressed by a function of the form F(t), so the models described below are potentially applicable to any of these functions. Three criteria should decide the choice of fertility function: (1) data availability, (2) theoretical considerations, and (3) an examination of historical values to determine if the model fits well and yields sensible parametric trends.

As for mortality, there are a number of mathematical and empirical models for fertility. Hoem *et al.* discuss and test a number of these models, including mathematical curves such as the Hadwigen function, gamma and beta densities, polynomials, splines, Gompertz curves, and the empirical Coale-Trussell model.[11] The number of parameters in these models ranges from three to ten.

For the same reasons as in mortality studies, relational methods show promise for forecasting. The raw material for relational fertility projections is a set of historical cumulative fertility curves, $F_i(t)$, where t can be age, duration of marriage, or some other variable, and i indexes time. The first step is to divide $F_i(t)$ by $F_i(50)$, and project $F_i(50)$ as a separate parameter. Then apply relational methods to the normalized cumulative, $F_i'(t)$.

There is no mathematical reason why the logit-based methods of the previous sections could not be applied to fertility studies. There is, of course, the question of choosing an appropriate standard.

For empirical reasons, a slightly different form is often used. Brass has introduced the relational Gompertz form in which the function log [- log (p)] replaced logit (p).[12] The reasoning is similar to that developed earlier for the logit model. If all fertility curves had a Gompertz shape

$$F_i'(t) = A_i^{B_i^{(t-t_o)}} ,$$

then for all i

$$\log\left\{- \log\left[F_i'(t)\right]\right\} = \log\left[- \log (A_i)\right] + (t - t_o) \log (B_i)$$
$$= \alpha_i + \beta_i (t - t_o) .$$

Hence for some standard distribution $F_s'(t)$

$$\log\left\{- \log\left[F_i'(t)\right]\right\} = \alpha_i + \beta_i \log\left\{- \log\left[F_s'(t)\right]\right\} . \quad (4)$$

As long as there is some transformation of the time scale to make all of the curves into the Gompertz form, equation (4) holds. The key idea is that for a historical series of related fertility curves such a transformation is likely to exist. The mechanics of fitting α_i, β_i, and the standard $F_s'(t)$ are just as in mortality analysis.

Breckenridge has introduced a similar, but more general, model in the study of changes in the age pattern of Swedish fertility between 1775 and 1959.[13] Defining y_{ij} as

$$y_{ij} = \left[F_t'(t_j)\right]^{1/2} - \left[1 - F_i'(t_j)\right]^{1/2} ,$$

she fits the model

$$y_{ij} = \alpha_i A_j + \beta_i B_j$$

to the time series of fertility curves, estimating both the time parameters α_i and β_i and age functions A_j and B_j. The flexibility of this model, in that "standards" A_j and B_j are estimated from the data series rather than taken as given, leads to closer fits. Breckenridge's analysis of cohort and period marital and total fertility leads to stable and predictable trends in α_i and β_i.

TIME SERIES ANALYSIS

Modern methods of time series analysis and forecasting,[14] are becoming increasingly used in demography.[15] Two conditions must apply for these methods to be used. First, the covariance structure of the time series variable must be stable, and second, the number of data points must be large enough, usually at least 50, to identify the structure. Checking for stability and identifying the structure of the series requires a good deal of exploration and thought. Relational methods reduce the dimensionality of the problem. If the models adequately represent the changes in age-specific rates, forecasters can concentrate their effects on analyzing and projecting a much smaller number of parameters.

There are three sorts of errors in population projections. First, there are errors in the starting values and estimates of current vital rates. Second, there is stochastic variation in the actual number of births and deaths, given the projected fertility and mortality rates. Third, and perhaps most important, there are errors in the predicted fertility and mortality rates themselves. If the time series analysis of the relational parameters is successul in capturing the variation in vital rates, confidence intervals for the parameter forecasts from the time series anlaysis could lead to realistic intervals for the projected population.

DEMOGRAPHIC PATTERNS

In the introduction we considered two types of demographic patterns: age and time. Linearity is the key to detecting and extrapolating patterns, and relational methods provide this linearity.

For effective projection, models must meet two criteria. First, the models should adequately fit the historical series of age-specific rates. Only if this is true do we have any confidence in the extrapolation technique. All of the relational methods have the property that some function—logit $[l_i(t)]$, $\log\{-\log [F_i'(t)]\}$ or $[F_i'(t)]^{1/2} - [1 - F_i'(t)]^{1/2}$—is linearly related to a "standard." Linearity means that graphical analysis provides an effective test of model validity, or suggests more appropriate alternatives. The ability to choose a standard based on the series being projected increases the likelihood of a good fit.

Second, the models should involve a small number of interpretable parameters that vary systematically in time. Interpretability means that external, subjective information can be brought into the forecasting process. The simplest systematic temporal pattern to detect and project is a line, and the time pattern of relational parameters often is linear. Furthermore, the mathematical form of relational models ensures that, for a wide range of observed and extrapolated parameter values, the models represent realistic age patterns of mortality and fertility.

In conclusion, the combination of flexibility, interpretability, and linearity in relational models makes them a good choice for the study and projection of fertility and mortality rates.

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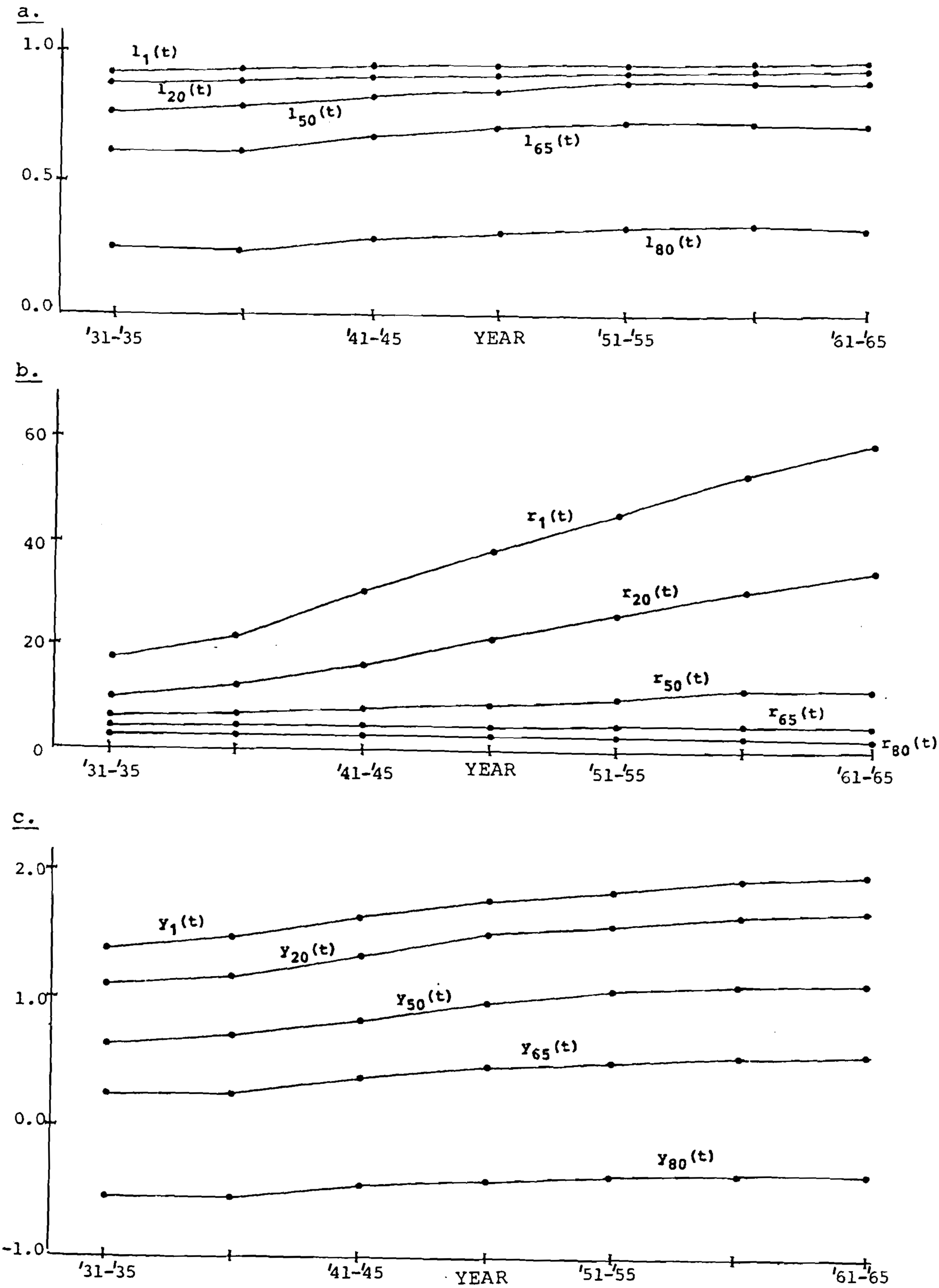

Figure 1. Time trends in $l_i(t)$, $r_i(t)$ and $y_i(t)$ for Swedish male life tables.

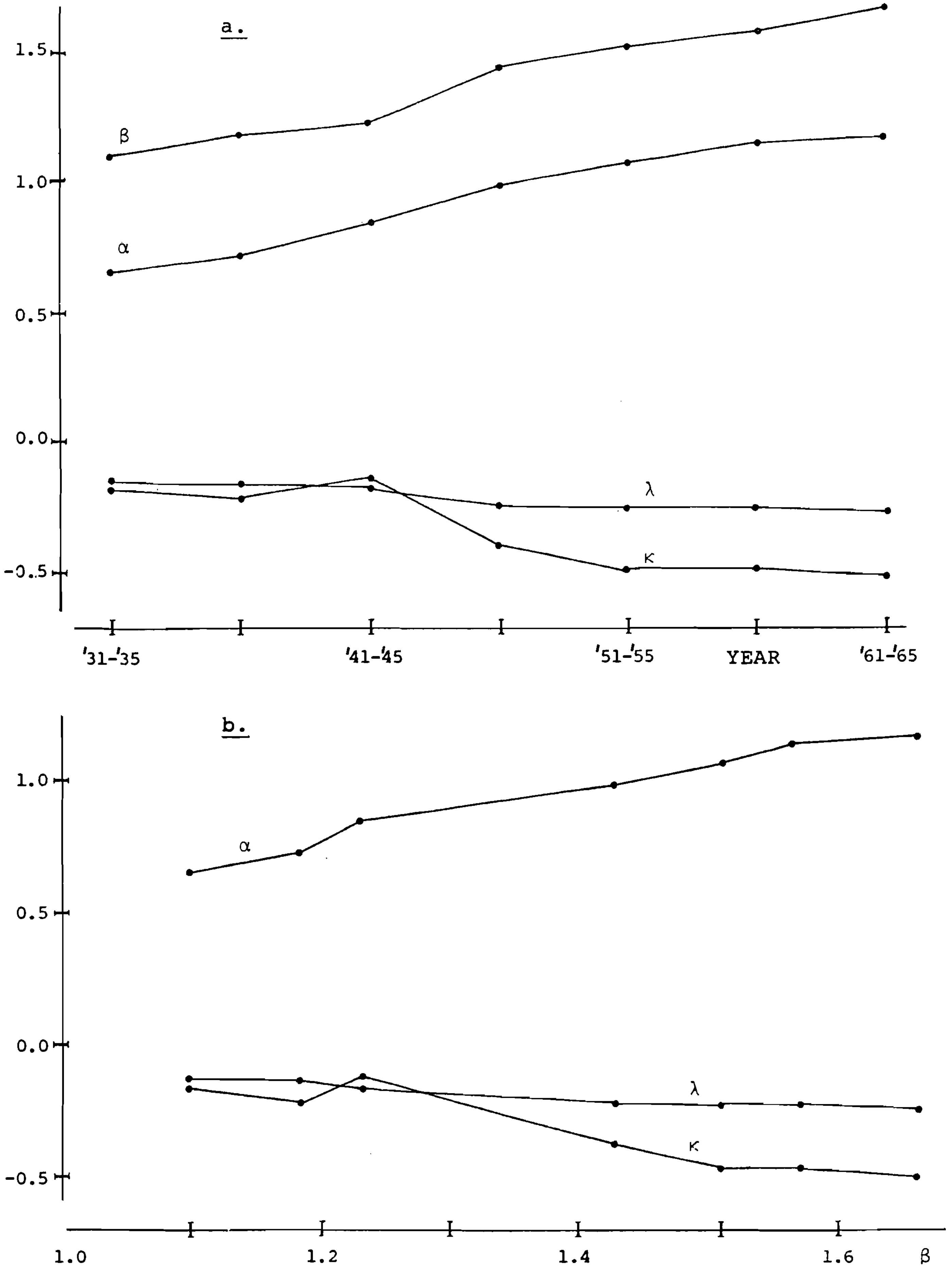

Figure 2. Time trends in parameters of Swedish male life tables (a), and relationship of α, λ, and κ to β (b).