

(KIEFER-WOLFOWITZ PROCEDURE
NUMERICAL ANALYSIS
SEQUENTIAL ANALYSIS)

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STOCHASTIC CONTROL *See* OPTIMAL
STOCHASTIC CONTROL

STOCHASTIC CONVERGENCE *See*
CONVERGENCE OF SEQUENCES OF RANDOM
VARIABLES

STOCHASTIC DEMOGRAPHY

Stochastic demography is the theoretical and empirical study of random variation in demographic processes.

The most fundamental model of demography*, the *life table**, due to Graunt and Halley in the seventeenth century, is essentially probabilistic: it gives 1 minus the *cumulative distribution function* of the duration of life. Yet the practical use of the life table long preceded its interpretation in terms of probability theory. The statistical analysis of the sampling variability of life expectancy, computed from a life table based on a finite number of deaths, is recent (Wilson [105]). Elandt-Johnson and Johnson [23] describe present statistical techniques of life table analysis.

Another early model of stochastic demography, now called the *branching process**, was analyzed by Bienaymé* in 1845. It was independently formulated by Galton and Watson in 1873 to study the extinction of familial lines of descent. The theory of branching processes has undergone enormous mathematical diversification and development. Among demographic users of branching processes, Wachter et al. [103, Chap. 7] measure social mobility in seventeenth and eighteenth century England by comparing extinctions of families holding baronetcies with the predictions of branching processes and of a pure death process (*see* BIRTH AND DEATH PROCESSES).

The modern field of stochastic demography applies equally to human and nonhuman populations, to historical and evolutionary time scales. It emerges largely from the work (1939–1949) of Bartlett [6, 7], Feller [26], and Kendall [50–52]. M'Kendrick [78], in a remarkable but isolated early paper, analyzes pure birth processes in one and two dimensions. He derives, among other results, a partial differential equation for mortality in age-structured populations later attributed to von Foerster, as well as a probabilistic interpretation of the renewal equation for population growth*.

Keyfitz [53], Feichtinger [24], Pollard [87], Ludwig [66], Keiding [48], Menken [75], and Kurtz [55] give reviews. Smith and Keyfitz [95] reprint extracts from classic papers. The mathematics that supports virtually all of stochastic demography appears in Karlin and Taylor [46, 47].

Currently, the interpretation of deterministic population models (*see* MATHEMATICAL THEORY OF POPULATIONS) in terms of modern probability theory continues the task started by M'Kendrick (Hoem [42, 44]). However, this review emphasizes stochastic models for *population projection** developed since 1965. Other stochastic models in demography will be cited or reviewed selectively. Many stochastic models in other social and biomedical sciences that are relevant to demography are omitted entirely. Also largely omitted here are the statistical problems of measuring and estimating the parameters in stochastic models.

POPULATION PROJECTION MODELS

Stochastic models are needed for population projection because deterministic models fail to account for the variability of historical demographic data and to provide probabilistically meaningful estimates of the uncertainty of demographic predictions. Stochastic population projection models may include migration* and mortality as well as fertility*.

Lee [65] reviews comprehensively new techniques for projecting fertility. He concludes that stochastic models of the internal structure of fertility behavior provide a better basis for forecasting than do methods based on behavioral theories or on data about fertility expectations. McDonald [71] supports this conclusion.

Among stochastic projection models, one can distinguish, not always sharply, between structural models* and time-series* models. Structural models attempt to represent some underlying mechanism of population growth. Time-series models apply to demographic data general techniques in which the form of the model need not be based on a theory of demographic processes.

Structural projection models usually describe either or both of two sources of random fluctuation: demographic variation and environmental variation. Additional sources of variation that have been less fully considered in stochastic projection models include the heterogeneity of probability intensities among individuals (but see Keyfitz and Littman [54], Vaupel et al. [101], and Menken et al. [76]) and dependence between individuals (as in marriage; see below) or between factors affecting individuals (Peterson [83], Manton and Stallard [67]).

Demographic variation arises in ensembles of populations from the stochastic operation of mechanisms with fixed vital rates. For example (Pollard [85]), in populations each of $N = 1,000,000$ people, if the probability of dying within one year is $q = 0.002$, uniformly and homogeneously for all people, then the (binomial*) variance among populations in the number who die after one year in $Nq(1 - q) = 1996$. This demographic variability should not be confused with sampling variability (though it is unfortunately sometimes given the same name), which is the variation in the properties of a sample of individuals randomly selected from a population. Whereas sampling variability arises from the procedures for observing a population, demographic variability arises intrinsically in an ensemble of populations each governed by a stochastic process*.

Environmental variation arises when the demographic rates themselves are governed by a stochastic process. To continue the example, if q is a random variable with mean 0.002, as before, and with standard deviation 0.0001, then, ignoring demographic variation, the variance in the expected number of deaths among populations of a million people is $\text{var}(Nq) = N^2 \text{var}(q) = 10,000$. In this example, the purely environmental variation is more than five times the demographic variation, although the standard deviation of q , the fraction who die, is only 5% of the mean.

Generally, in large populations, fluctuations in vital rates cause fluctuations in population size that appear to dominate the fluctuations arising from demographic variation.

POPULATION PROJECTION WITH DEMOGRAPHIC VARIATION

Deterministic projections of populations closed to migration commonly use the recurrence relation

$$y(t+1) = L(t+1)y(t),$$

$$t = 0, 1, 2, \dots, \quad (1)$$

where $y(t)$ is a vector in which the i th component is the number of females in age class i at time t , $i = 1, \dots, k$, $y(0)$ is a given initial age census* of the female population, and $L(t)$ is a $k \times k$ nonnegative matrix, conventionally called a *Leslie matrix*. All elements of L are 0 except those in the first row and those just below the diagonal. $L_{1i}(t+1)$ specifies the effective fertility of females in age class i at time t (the average number of daughters born between t and $t+1$ who survive to time $t+1$, per female aged i at t) and $L_{i+1,i}(t+1)$ gives the proportion of females in age class i at time t who survive to age class $i+1$ at time $t+1$ (Keyfitz [53]).

Taking L to be independent of t , i.e., constant in time, Pollard [84] reinterprets (1)

as a multitype branching process. $L_{1i}(t+1)$ becomes the probability that a female in age group i at time t will give birth during the time interval $(t, t+1)$ to a single daughter, and that this daughter will be alive in age group 1 at time $t+1$; and $L_{i+1,i}(t+1)$ becomes the probability that a female from age group i at time t will survive to be in age group $i+1$ at time $t+1$. The survival and fertility of each female are assumed independent of each other and of the survival and fertility of all other females. Then $y(t)$ in (1) can be interpreted as the expectation of the age census at time t . A linear recurrence relation that uses the direct or Kronecker product* of two matrices describes the variances and covariances of each census of females. Goodman [35] computes the probability in Pollard's model that the line of descendants of an individual of any given age will eventually become extinct.

The multitype branching process model does not require that $L(t)$ in (1) have the form of a Leslie matrix. See Goodman [36] for a linear treatment of two sexes; Breev and Staroverov [12] for labor force migration; Wu and Botkin [106] for elephants. Deistler and Feichtinger [21] show that the multitype branching process model may be viewed as a special case of a model of additive errors proposed for population dynamics by Sykes [98].

Mode [80] develops population projection models using renewal theory* rather than matrix methods. Underlying these models are discrete-time versions of the Crump-Mode-Jagers age-dependent branching process.

The continuous-time stochastic theory analogous to what has just been described is presented by Keiding and Hoem [49] and Braun [11], with extensions to parity-dependent birth rates and multiregional populations.

Branching processes have been criticized as models of human and nonhuman populations. The criticisms have been directed at both assumptions and predictions. The best studied branching processes share two assumptions: stationarity and independence.

Stationarity means that the underlying rates (e.g., of survival or of giving birth) are constant in time, though they may change with, e.g., age or parity; in branching processes in random environments (e.g., Pollard [85]), survival and birth rates may fluctuate, but the fluctuations are controlled by a stochastic process that is stationary in time. Independence means that the life history of one individual is independent of the life history of every other individual, though fecundity and survival may interact within one individual's life history and both fecundity and survival may depend on a fluctuating environment.

Of the assumptions, stationarity is the easiest target for criticism. For example, it has been objected that even a few human generations span a period of historical time in which social, political, and economic systems change so markedly and migration is so influential that any model based on unchanging rates or a stationary pattern of environmental fluctuations must be irrelevant. This objection would be valid if the long-run properties of branching processes occurred only when rates or environmental fluctuations had been stationary for all time. However, stochastic weak ergodic theorems* (Cohen [17]) suggest by analogy that even if the stochastic process governing vital rates is not stationary (but is ergodic), the behavior of a multitype branching process (specifically, the inhomogeneous product of the mean value matrices) should (under suitable conditions) depend on the recent past much more than on the remote past. Thus, loosely speaking, if the rate of historical change is slow relative to the smoothing effects of demographic processes, it may be adequate to model the present and recent past as if demographic processes were stationary, as long as no one assumes that today's conditions will extend indefinitely into the future. Thus the assumption of stationarity is not a priori disabling if its limitations are respected and if it leads to confirmed predictions.

The assumption of independence between individuals seems ineluctable in branching processes (but see Staroverov [96] for an

example of how it can be modified). Independence seems easiest to defend in large populations and more difficult to defend in small ones because interactions seem more apparent in small populations, yet the demographic variation described by branching processes is most relevant to small populations and nearly irrelevant to large. Independence precludes a description of monogamous mating in a two-sex population. In studies of fish and wildlife* populations, it is widely assumed that population size must be stationary, on the average, over a long period of time, in part because of interactions between individuals that adjust birth and death rates. The assumption of independence is probably a greater obstacle to the success of branching process models than the assumption of stationarity.

If their assumptions are not grounds for dismissing branching processes a priori as population models, the empirical task remains of evaluating the predictions. Since existing populations are not extinct by definition, a supercritical branching process is usually chosen as a model and the asymptotic theory is applied (for a counterexample, see Wachter et al. [103, Chap. 11]).

In Pollard's model, the branching process is supercritical if the dominant eigenvalue $r(L)$ of the expected value matrix L exceeds 1 (so that the population asymptotically increases exponentially in size). In this case, if, for some t , every element of L^t is positive, then, with probability 1, the random vector that gives the number of females in each age class, divided by $(r(L))^t$, asymptotically becomes proportional to the stable age structure of the deterministic model with projection matrix L . It is obvious that no real population can forever grow exponentially and that $t \rightarrow \infty$ is never observed. At finite times large enough for the predictions of the model to be relevant, it appears that many real age censuses for human and nonhuman populations (e.g., elephant: Wu and Botkin [106]) deviate markedly from the stable age structure implied by current vital rates. This finding suggests that the age census is in-

fluenced by sources of variation in addition to purely demographic ones.

Projections of the Norwegian population as a multitype branching process give estimates of uncertainty that Schweder [91] considers unrealistically low.

Independently of Pollard [84], Staroverov [96] considers exactly the same model. Because the model variances are implausibly small compared to the historical variation in Soviet birth rates, Staroverov replaces the assumption that each individual evolves independently with the assumption that groups of c individuals evolve as units, independently of other groups. As c increases, the variance of numbers in each age group increases while the means remain unaltered. A comparison of observed and projected births from 1960 to 1973 suggests that even $c = 100,000$ is too small, and that it is necessary to allow for temporal variation in the fertility and mortality parameters.

POPULATION PROJECTION WITH ENVIRONMENTAL VARIATION

In a large population, the effects of demographic variation are normally negligible compared to those of apparent changes in vital rates. In a model of multiplicative errors, Sykes [98] supposes that, given $L(t+1)$, $y(t)$ determines $y(t+1)$ exactly, but that there is no correlation between $L(t)$ and $L(s)$, $s \neq t$. He assumes an arbitrary covariance structure for the elements within a matrix, subject to the constraint that $L(t)$ be a Leslie matrix. Sykes computes the means and covariances of the age censuses, allowing the means and covariances of the sequence $\{L(t)\}$ to be inhomogeneous in time. Seneta [92] pursues the computation of variances in the models of Sykes [98] and Pollard [84]. Lee [63] discusses the numerical example that Sykes gives.

LeBras [61] considers populations satisfying (1) in which the sequence $\{L(t)\}$ is governed by a stationary stochastic process* with independence between Leslie matrices

sufficiently distant in time. Under additional conditions on a finite sample space of Leslie matrices, he argues that for every sample path, $\lim_{t \rightarrow \infty} [t^{-1} \log y_1(t)]$ is a constant independent of the sample path, i.e., that the number of births asymptotically changes exponentially in every sample path.

Assuming that $\{L(t)\}$ is determined by a finite-state irreducible Markov chain of arbitrary fixed finite order, LeBras [61] computes the moments of $y(t)$ of all orders, for both finite t and as $t \rightarrow \infty$. He argues that the distribution of the number $y_1(t)$ of births at a given large time t is approximately log-normal*.

Independently of LeBras, Cohen [16] proves that when the Leslie matrices $L(t)$ are chosen from a denumerable set according to a Markov chain that is not necessarily stationary or homogeneous in time, the moments of age structure eventually become independent of the initial age census $y(0)$ and initial vital rates $L(1)$.

Cohen [16] also points out the relevance to stochastic demography of products of *random matrices** (Furstenberg and Kesten [29]). Under exactly stated conditions more general than those of LeBras, Furstenberg and Kesten prove theorems that imply that $y(t)$ changes asymptotically exponentially and that the elements of $y(t)$ are, for large t , asymptotically log normal.

Cohen [17] generalizes (1) to allow $L(t)$ to be *contractive operators* on the space of age structures, chosen by a first-order irreducible aperiodic Markov chain from a general (i.e., possibly uncountably infinite) state space of operators. When the Markov chain is time-homogeneous, the solution of a linear renewal integral equation* gives the limiting probability distribution of age structure. Even when the Markov chain that chooses $L(t)$ is inhomogeneous but suitably ergodic, the probability distribution of age structure asymptotically becomes independent of initial conditions. This weak stochastic ergodic theorem is the probabilistic analog of the deterministic weak ergodic theorem of Coale and Lopez (Pollard [87, pp.51–55]).

The use of products of random matrices to model environmental variability in age-structured populations is generalized and refined by, among other, Cohen [18], Lange [58], and Tuljapurkar and Orzack [99].

An elementary but important observation emerging from these studies is a distinction between two measures of the long-run rate of growth of a population in a stochastic environment. One measure, studied by Furstenberg and Kesten [29], is the average of the long-run rates of growth along each sample path,

$$\log \lambda = \lim_{t \rightarrow \infty} t^{-1} E(\log y_1(t)).$$

Another measure is the long-run rate of growth of the average populations,

$$\log \mu = \lim_{t \rightarrow \infty} t^{-1} \log E(y_1(t)).$$

For deterministic models $\lambda = \mu$, but in general, in stochastic models, $\lambda \leq \mu$ with strict inequality in most examples.

DEMOGRAPHIC AND ENVIRONMENTAL VARIATION

Demographic variation and environmental variation both exist in reality. If the probabilities of giving birth and of surviving in a multitype branching process are themselves random variables (Pollard [85], Bartholomew [3]), the moments of the numbers of individuals in each age class can be computed from a modification of a recurrence relation derived by Pollard [84].

For a multitype branching process such that the offspring probability generating functions* at all times are independently and identically distributed, Weissner [104] gives some necessary and some sufficient conditions for almost sure extinction of the population (see also Namkoong [81]). In a multitype branching process with probability generating functions determined by a stationary metrically transitive process (subject to certain bounds), the Furstenberg–Kesten

limit of the product of expectation matrices determines whether the probability of extinction of all types is 1 or less than 1 (Athreya and Karlin [2]). Weissner, Athreya, and Karlin do not discuss the application of these results to age-structured populations.

A thorough empirical test of the merits for prediction of (1) when $L(t)$ has sequentially dependent, e.g., Markovian, random variation, in comparison with deterministic methods (Siegel [94]) of *population projection**, has yet to be performed. An outstanding example of the evaluation of a projection procedure, though it predicts only total population size, is given by Henry and Gutierrez [41]. In evaluating stochastic projections of age-structured populations, it will be necessary to consider, in addition to demographic variation and environmental variation, the uncertainty in specifying the form of a model that governs the $\{L(t)\}$ sequence and the uncertainty in estimating the parameter values of the model (Schweder [91], Hoem [43], Bartholomew [3]).

Time-Series Models

The application of modern stochastic *time-series* methods to demographic data originates with Lee [62] and Pollard [86]. Lee (see ref. 64 for summary) uses long time series, for example, of births and marriages or of mortality and wages, to test alternative historical theories of demographic and economic dynamics. Pollard [86] develops a second-order autoregressive model of the growth rate of total population size for Australia.

Lee's [63] analysis of births from 1917 to 1972 in the United States demonstrates that the distinction between structural models and time-series models is not sharp. Equation (1) implies that each birth may be attributed to the fertility of the survivors of some preceding birth cohort. Hence the sequence of births $\{y_1(t)\}$ is described by a renewal equation. By a sequence of approximations to this renewal equation, Lee transforms the residuals of births from their long-run trend into an autoregressive process for which

variations in the net reproduction rate are the error term. Among the several stochastic models Lee considers for the net reproduction rate, a white-noise process and a first-order autoregressive (Markovian) model lead to poorer descriptions of births than a second-order autoregressive process.

Independently of Lee, Saboia [89] develops autoregressive moving average* (ARMA) models using *Box-Jenkins** techniques for the total population of Sweden. Based on data from 1780 to 1960 at five-year intervals, his projections for 1965 compare favorably with some standard demographic projections.

Saboia [90] relates ARMA models to the renewal equation for forecasting births. In these models, the age-specific vital rates can vary over time; migration is recognized. Using the female birth time series for Norway, 1919–1975, he gives forecasts with confidence intervals up to 2000. However, Saboia's [90] models are not the simplest required to describe the data (McDonald [70]). McDonald [69] describes the relationships among the renewal equation model, with migration added, structural stochastic econometric* models, and ARMA models.

Using Australian data from 1921 to 1965, he finds that the number of females aged 15 to 39 years does not help explain the number of births given the time series of past births, but that some additional explanatory power is obtained from the number of females aged 20 to 34 years. The ARMA models do not predict a sharp decline that occurred in the number of Australian births after 1971. McDonald suggests that exogenous, perhaps economic, variables will have to be invoked to explain this turning point. Land [56] similarly suggests incorporating exogenous variables in structural stochastic projection models with environmental variation.

The long-term forecasts of the time-series models have very wide confidence intervals* (e.g., McDonald [69], McNeil [74]). In view of the uncertainty of the demographic future, policy that depends on population size and structure should be flexible enough to allow for different possible futures.

In addition to spectral methods and *Box-Jenkins* techniques, other recent approaches to population time-series modelling include a stochastic version of the logistic equation (McNeil [74]) as a model of United States Census total population counts; the *Karhunen-Loève procedure* (Basilevsky and Hum [8]) for quarterly records of births on two Jamaican parishes, 1880 to 1938; and an age- and density-dependent structural model, estimated by use of the *Kalman-Bucy filter* (Brillinger et al. [13]) for age-aggregated counts of the sheep *blow-fly*. In the study of blow-flies, even after the best of seven models for death rates had been fitted, the weighted residuals of the time series of deaths revealed substantial autocorrelation. Applying an ARMA model to these residuals improved the description of the data (Brillinger et al. [13, p. 75]). Hybrid models like this one, which combine demographic theory with general-purpose statistical descriptions, deserve further study in conjunction with efforts to determine empirically what exogenous nondemographic variables need to be incorporated. Granger and Newbold [38, Chap. 8.2] analyze the combination of forecasts in an economic context, which is relevant here.

Evaluation of Stochastic Population Projections

Prediction is the ultimate test of scientific understanding. Good population projection procedures might be found faster if two procedures were more systematically exploited: historical pseudo-experiments and multiple criteria.

To illustrate the meaning of historical pseudo-experiments, suppose one has data, demographic and otherwise, from year a to year b , and one wishes to forecast one or more components of the data. Using all the data from a to b to forecast for years $b + 1$, $b + 2$, ... permits publication long before the model can be rejected. Using part of the data, from a to $b_1 < b$, at least permits a test of predictions against what happened in years $b_1 + 1$, $b_1 + 2$, ..., b . Why not pick a

subinterval of the data for the years a_1 to b_1 , $a \leq a_1 \leq b_1 \leq b$, fit the model to the years a_1 to b_1 and project forward, and then systematically vary *both* a_1 and b_1 ? The different tests of the model will not be independent, but one will have squeezed more information about the model's behavior out of the data. By varying a_1 for each value of b_1 , one will learn how much knowledge of the past is relevant to a good prediction of the future, and whether the amount of the past that is relevant to the future itself changes over time.

Multiple criteria would help in deciding which models are good for which purposes under what conditions. One model may predict births well for the next five years; another, retirement age classes 20 years in the future. Instead of comparing a family of models by one criterion only, e.g., mean-squared deviations of observed from predicted age structure, why not look at median-absolute and maximum as well as mean-squared deviations, for each age class individually, for a whole flock of different intervals projected into the future? Flexibility is needed here to discover what are good criteria for evaluation.

Many of the general issues that arise in evaluating economic forecasts (Granger and Newbold [38, Chap. 8.3] arise equally here.

STOCHASTIC MODELS OF SPECIFIC PROCESSES

Several components of population change have been studied through the use of stochastic models. We shall sketch some models of human reproduction and of marriage. In addition to these, stochastic models have been developed to describe, among other topics, social mobility and the work force (Bartholomew [4], Bartholomew and Forbes [5], McClean [68]); the succession of rulers in an atoll society (Frauenthal and Goldman [28]); changes of residence (Ginsberg [32-34]); the population composition of the descendants of a collection of identical clones (Blackwell and Kendall [9], Cohen [15]);

cause-specific but age-aggregated mortality indices (Land and McMillen [57]); property crime rates (Cohen et al. [19]); dose-mortality curves in radiation biology (Turner [100], Miller [77]); and the frequencies of various *kinship* relations (Goodman et al. [37]; Feichtinger and Hansluwka [25], Wachter [102]).

Human Reproduction

In human reproduction a woman of appropriate age may be supposed to move from a state (state 1) of susceptibility to conception into one of two states: a state of conception (state 2) that does not end in a live birth and a state of conception (state 3) that does end in a live birth. From state 2, the woman returns to state 1, and from state 3, the woman enters a nonsusceptible state of postpartum amenorrhea, from which she eventually returns to state 1. Durations of stay in each state need not be exponentially distributed and rates of transition among states need not be homogeneous across women. This schema may be modeled as a renewal process (Sheps and Menken [93], who also refer to the pioneering work of Gini, Pearl, Henry, and Vincent; Das Gupta [20], Ginsberg [30, 31], Mode [79], Lange and Johnson [59]). This class of models has been used to analyze interbirth intervals and to evaluate the demographic consequences of contraception and abortion (Potter [88]). For example, models indicate that an effective contraceptive used by a small proportion of a population reduces birth rates more than a less effective contraceptive used by a much higher proportion of the population.

Braun [11] analyzes three sets of historical data on birth interval sequences using a different approach based on linear regression*.

Marriage

The standardized distribution by age of the frequency of first marriage* in a female cohort is well approximated by the convolu-

tion of a normal distribution of age of entry into a marriageable state and three exponentially distributed delays: the delay until the woman starts to keep frequent company with the eventual husband; the delay until engagement; and the delay until marriage (Coale and McNeil [14]).

Given the age distributions of brides and grooms separately in any period, how can the correlation in age of spouses be explained? Henry [40] models the two-way contingency table* of marriage frequencies categorized by age of bride and age of groom as a sum of contingency tables each with independence between rows and columns. Each summand is supposed to describe age-independent marriage choices within "panmictic circles."

Other probabilistic marriage models are developed by Hajnal [39], McFarland [72, 73], and Asmussen [1].

As Keiding and Hoem [49] point out, the assumption of stochastic independence between individuals is crucial to their probabilistic formulation of stable population theory, as well as to many other stochastic population models. A tractable and realistic stochastic formulation of marriage, which must drop the assumption of independence between individuals, is an open challenge.

COMPUTER SIMULATIONS

In addition to models that can be written down in what is accepted as "closed form," complex stochastic models of demographic processes are embodied in computer simulations. Menken [75] reviews simulation and other models. Wachter et al. [103, Chap. 1-5 and 11] use population simulations in historical demography; Orcutt et al. [82] in economics; Dyke and MacCluer [22] in population genetics; Howell [45] in anthropology; Feichtinger and Hansluwka [25] and Suchindran et al. [97] in demography proper.

Such simulations reveal the behavior of models when "realistic" assumptions preclude mathematical analysis. In addition, simulation of relatively simple models whose

asymptotic behavior is understood may shed useful light on their transient behavior. For example, in simulations of the critical multi-type branching process treated analytically by Pollard [84], Wachter et al. [103, Chap. 11] find that the interquartile range* in the size of individual age groups is very nearly steady, after a simulated generation or so, for more than a century. This so-called pre-asymptotic stochastic plateau is not described by asymptotic theory.

Simulations can also help test the field-worthiness of demographic estimation procedures derived from deterministic models (Wachter [102]).

Novel techniques make it possible to improve the precision (i.e., reduce the variance) of estimates derived from population simulations by replacing random numbers drawn independently for each replication or run with random numbers having a carefully chosen dependence (Fishman [27]).

ASSESSMENT AND PROSPECTS

A major lesson that has been learned from the testing against data of stochastic models for population projection and for other demographic processes is that it is frequently unsatisfactory to assume constancy over time and homogeneity over individuals in the vital rates or in the other forces of transition that directly affect individuals. Yet the purpose of theory, as Einstein said, is to make nature stand still when our back is turned. So constancy must be assumed at some level, probably far deeper than the rates that affect individuals, perhaps only in the form of causal relations. The question is: where?

The sheer diversity of the stochastic models that have been cited indicates part of the answer. There is a great need to integrate demographic with biological, social, and economic models, and with each other. For example, the fertility rates that serve as parameters in demographic models are the objects to be explained by biological models of fecundity in conjunction with sociological models of marriage and family formation

and with economic models, e.g., of health services or food supply. Perhaps when the component models are correctly chosen and integrated with others correctly chosen, the total amount of variation remaining that must be attributed to pure randomness will be reduced. Even the empirical study of which local models of particular demographic processes are correct might be more successful if each model were not approached in isolation from all others.

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