THE ANALYSIS OF CAUSAL LINKAGES IN DEMOGRAPHIC THEORY

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ABSTRACT

Many seemingly different questions that interest demographers can be phrased as the same technical question: how, within a given demographic model, would variable y change if the age- or time-specific function f were to change arbitrarily in shape and intensity? At present demography lacks the machinery to answer this question in analytical and general form.

This paper suggests a method, based on modern functional calculus, for deriving closed-form expressions for the sensitivity of demographic variables to changes in input functions or schedules. It uses this "causal linkage method" on three bodies of theory: stable population analysis, non-stable or transient population analysis, and demographic incomplete-data estimation techniques.

In stable theory closed-form expressions are obtained for the response of the intrinsic growth rate, birth rate and age composition to arbitrary marginal changes in the fertility and mortality age patterns.

In non-stable theory, expressions are obtained for the transient response of the age composition to time-varying changes in the birth sequence, and to changing age-specific fertility and mortality patterns. The problem of bias in period vital rates is also looked at.

In incomplete data analysis a general format for robustness or error analysis is suggested; this is applied to a standard Brass estimation technique.

CONTENTS

Many of the questions that appear and reappear in the demographic literature of this century, while seemingly quite different, are but specific instances of a single and fundamental question. *How do the aggregate measures--numbers, rates, and distribution--of a population change, when its underlying behavior at the individual level changes?*

That this question should arise with regularity under different guises is hardly surprising. Much of demography theory aims to translate the events and consequences of individual lives--the timing and number of children, the choice of area of residence, entry to the work-force, time of retirement, age and cause of death--into the grand measures of society itself, its number and growth rate, its scatter over land and town, its vital rates, its proportions by age, sex, work or other category. And since human behavior over the life-cycle, reflecting social habit and environment, is forced to change as society evolves and develops, the demographer in turn is forced to seek analytical ways to translate these shifts in individual behavior into the changes in aggregate population measures he seeks.

Mathematical demography bridges the gap between individual behavior and aggregate measures by observing that human behavior and the main events in human life are closely tied to age. It captures and frames these events by means of demographic schedules or functions--statistical summaries of individual behavior along the age and time dimensions. It then uses these as inputs to mathematical models, sometimes simple, sometimes elaborate, the output or end-result being variables that represent the aggregate measures of growth, distribution, number, and rate. We may therefore pose the question of causal linkage between individual behavior and aggregate measures in a more analytical and precise way. *How, within a given demographic model, would arbitrary changes in its age- and time-specific schedules alter certain output variables that interest us?*

Within the present body of demographic theory there is no way to answer this question. The obstacle is a technical one. To answer, with generality and precision, how a change in age or time function f would affect variable y, the demographer needs a form of sensitivity analysis. Were f a simple variable, or even a vector, analysis would be straightforward. Elementary calculus could be brought to bear, the derivative $\partial y/\partial f$ constructed, and the differential change in y written down as a function of the change in f. But standard calculus allows us no way of taking derivatives with respect to functions, and thus we reach an impasse. Questions of key interest to demographers--how the age composition responds to an arbitrary change in the mortality pattern, or how period vital rates are affected by changes in the birth sequence--therefore remain without analytical solution. What is needed, for questions of causal linkage in demographic theory, is machinery more powerful than standard calculus.

In the absence of such machinery, demographers have developed several ways to investigate the effects of changes in age schedules. None of these is entirely satisfactory. The simplest possibility, blunt but effective, is to calculate numerically the variable y before and after the behavioral change in schedule. But this gives no general expression for an arbitrary change: each case must be calculated anew. A second possibility is to parametrize the age-schedule in question, and try to capture changes in its shape by changes in the parameters. This reduces the problem to the standard-calculus procedure of varying parameters. But parametrization can be tedious, and again no general expression results. A third possibility is to look only at special cases, restricting the change in age-pattern to a certain simple shape--a simple increase in intensity for example. But here again no general insights are guaranteed.

This paper proposes a method of deriving the effect on demographic variables of arbitrary changes in age- and time-functions directly as closed form expressions, without resort to numerical techniques or to parametrization. It draws on concepts from modern functional analysis to construct a "causal linkage method" suited to demographic problems. If it is true that many open questions in demography call for such a method, then we would expect it to yield new results. This turns out to be the case. Some of the results we obtain are quite general; others are for special cases. One or two have been obtained in the literature before; most are new.

The paper is laid out as follows. Section 1 proposes a general linkage method, illustrating it with simple examples. Sections 2 and 3 apply the method to stable theory, in particular to how arbitrary changes in the age patterns of fertility and mortality affect the intrinsic growth rate, birth rate and age composition. These results show, among other things, why fertility has more effect on the age composition than mortality. Section 4 takes up a special case as illustration: age delays in fertility behavior. Section 5 turns to non-stable theory, investigating how the age composition responds to changes in the birth sequence and in fertility and mortality patterns. Section 6 looks at the problem of "bias" in vital rates, due to changes in the age composition and birth sequence, and how this may be partially corrected. Section 7 takes up the problem of incomplete data estimation, and proposes a method for assessing errors in the estimates, given underlying assumptions that are not perfectly fulfilled. It illustrates this with a specific Brass example. The main sections are largely independent, but the reader is urged to understand the method before he turns to any applications.

1. THE CAUSAL LINKAGE METHOD

In this section I shall develop both the vocabulary we need and a general method for linkage analysis in demographic theory. I will avoid abstractions, and will assume (at some cost to full mathematical rigor) that the functions dealt with inhabit appropriate, if unmentioned, spaces and that they are smooth enough to allow the operations we want. I start by reviewing briefly the familiar, standard theory of differential changes, then spend some time extending it to differentials with respect to functions, finally proposing a general method for sensitivity or linkage analysis in demographic theory.

The Standard Theory

Begin with y as a simple function of the variable x:

(1.1) $$y = f(x) \quad .$$

Given that x is increased on amount h, the familiar, standard calculus tells us that a good approximation to the change in y, when h is small, is given by the *differential* δy, defined by

(1.2) $$\delta y[h] = f'(x)h \quad ,$$

where f' is the derivative or gradient taken at x--itself a function of x. (Since δy, the differential is a function of the change h, evaluated at x, we write it $\delta y[x;h]$; or when x is understood, $\delta y[h]$; or when h is also understood, simply as δy.)

If we merely want the change in y, going from x to x+h, why bother with the differential, an approximation? Why not calculate $y(x+h) - y(x)$ directly? This of course is possible. But the differential has two advantages. It applies to all x in the domain of the function and to all changes h--it is general. More important, useful qualitative information is usually contained in the expression for $f'(x)$; the connection between y and x can therefore be usefully interpreted and studied.

One way to define the differential directly, without resort to the gradient, is via the limit

$$(1.3) \qquad y[x;h] = \lim_{\alpha \to 0} \frac{f(x+\alpha h) - f(x)}{\alpha} \quad .$$

Thus the change caused by a small step in the direction of h, divided by the step length, can be shown in the limit to yield the same linear approximation as the differential in (1.2). This fact will be useful below.

Finally, recall that if y is a function of several variables

$$y = f(x_1, \ldots, x_n)$$

and if changes h_i occur in the variables x_i (with indices i in the set I), the others being held constant, the differential in y becomes the summation

$$y = \sum_I \frac{\partial f}{\partial x_i} h_i \quad .$$

This is the familiar "chain rule" of differential calculus.

Functional Differentials

So much for the standard theory. We now proceed to the case of interest in this paper. This time we begin with a function z, whose domain in demographic theory is usually age or time.

At the outset a notational difficulty must be cleared up. Elementary textbooks often write the function z as z(a), where they mean the entire function over the range of a. Since this might be confused with the *value* of z at point a, I shall follow modern notation and reserve the label z for the function itself, using z(a) for its value at point a.

Typically, in demographic theory, models are built out of functions (and variables), the simplest possible being

$$(1.4) \qquad y = F(z) \quad .$$

Here y is a function of the entire curve z--a rule which assigns a real number y to any given curve z. F is called a *functional*. As examples

$$F(z) = \max_{0 \leq t \leq 1} \{z(t)\} \quad .$$

$$R_0(p,m) = \int_0^{\omega} p(a)m(a)da \quad ,$$

are functionals. The first attaches a real value to the curve z, the second, a functional of two functions, assigns a real value, given the curves p and m. Demographers will recognize the second example as the net reproduction rate, given the age-schedules of mortality and fertility respectively.

Now suppose that the function z changes shape (as in Figure 1.1), that it becomes z+h

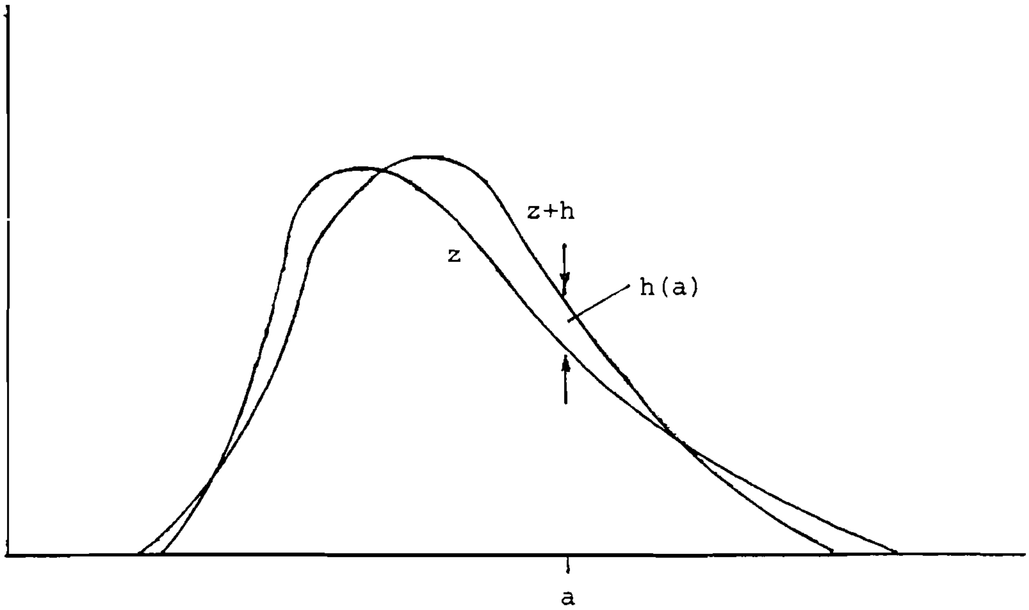

Figure 1.1

where the perturbation h, itself a function, is small. How much will the value y change? By analogy with (1.3), we can simply define the differential (now called a *functional differential*) to be

$$(1.5) \qquad \delta y[z;h] = \lim_{\alpha\to 0} \frac{F(z+\alpha h) - F(z)}{\alpha} \quad ,$$

providing of course this limit exists. Just as the simple differential approximates the change in y when x changes an amount h, the functional differential approximates the change in y if the function z is perturbed or changed by a function h.

As yet this gives no simple way to derive δy, without taking limits. However, it is easy to show that since $F(x+\alpha h)$ is a simple function of the parameter α, (1.5) can be rewritten as an ordinary derivative in α, evaluated at $\alpha = 0$:[1]

$$(1.6) \qquad \delta y[z;h] = \frac{d}{d\alpha} F(z+\alpha h)\Big|_{\alpha=0} \quad .$$

Usually this gives a convenient way to derive the differential.

Example 1.1 A functional form that often occurs in demography is

$$(1.7) \qquad y(z) = \int_0^{\omega} g(z(a))da$$

an integral of a function g of function z at age a. We may write

$$\begin{aligned} \delta y[z;h] &= \frac{d}{d\alpha}\int_0^{\omega} g(z(a)+\alpha h(a))da\Big|_{\alpha=0} \\ (1.8) \qquad &= \int_0^{\omega} \frac{d}{d\alpha}\, g(z(a)+\alpha h(a))da\Big|_{\alpha=0} \\ &= \int_0^{\omega} \frac{\partial g}{\partial z(a)}\, h(a)da \quad , \end{aligned}$$

the last step following from standard calculus operations. □

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[1] To see this, write the derivative (1.6) as $\lim_{c\to 0} \frac{F(z+(\alpha+c)h) - F(z+\alpha h)}{c}\Big|_{\alpha=0}$. This equals $\lim_{c\to 0} \frac{F(z+ch) - F(z)}{c}$ which is the same as (1.5).

Example 1.2 We may try this formulation on the net reproduction rate example mentioned above.

$$(1.9) \qquad R_0(m,p) = \int_0^{\omega} p(a)m(a)da \quad .$$

Suppose the fertility schedule m is perturbed by a function δm, the mortality schedule remaining fixed; what is the differential in the variable R_0? Applying the rule from the previous example

$$g(m(a)) = p(a)m(a)$$

$$\frac{\partial g}{\partial m(a)} = p(a) \quad ,$$

whence

$$(1.10) \qquad \delta R_0[m;\delta m] = \int_0^{\omega} p(a)\,\delta m(a)da \quad .$$

Knowing the variation in the fertility schedule, we can easily calculate δR_0. □

Functional differentials obey the usual rules for differentials:

(1) $y = aF(z) + bG(z)$ (summation)

$\delta y = a\delta F + b\delta G$

(2) $y = F(z) \cdot G(z)$ (product)

$\delta y = \delta F\ G(z) + F(z)\delta G$

(3) $y = g(F(z))$ (composition)

$\delta y = \frac{\partial g}{\partial F} \cdot \delta F[\delta z]$

(4) $y = F(z_1,z_2,x)$ (z_1,z_2 are functions, x a variable)

$\delta y = \delta F[\delta z_1] + \delta F[\delta z_2] + \delta F[\delta x]$ (chain rule)

(5) $y = \frac{F(z)}{G(z)}$ (quotient)

$$\delta y = \frac{G(z)\delta F - F(z)\delta G}{G^2(z)}$$

Example 1.3 The survival schedule p is connected to the force of mortality schedule μ by

$$(1.11) \qquad p(a) = \exp\left(-\int_0^a \mu(t)dt\right) \quad .$$

The value p(a), in other words, is a *functional* of μ. Given a change δμ in the function μ, caused say by a change in the incidence of a certain disease, how will the survival schedule p change?

Let

$$F(\mu) = -\int_0^a \mu(t)dt$$

so that

$$\delta F[\delta\mu] = -\int_0^a \delta\mu(t)dt \quad .$$

Now,

$$p(a) = e^F \quad ,$$

so that from the composition rule above

$$\delta p(a) = \frac{\partial(e^F)}{\partial F}\cdot\delta F[\delta\mu] = -e^F\int_0^a \delta\mu(t)dt$$

$$(1.12) \qquad \delta p(a) = -p(a)\int_0^a \delta\mu(t)dt \quad .$$

This gives a rule for the differential change δp in the entire function, caused by an alteration δμ of the function μ. □

Each of the examples so far proceeds tediously, step by step. With practice however, as in elementary calculus, it is possible to write down expressions for the differential by inspection.

A final piece of vocabulary will be useful. In the familiar standard calculus we can write the differential as a product

$$\delta y = f'(x)\cdot\delta x \quad ,$$

calling the coefficient of the change in x the derivative. In our examples above we can write the differential in the product form

$$\delta y = \int_0^{\omega} F'(z,a) \cdot \delta z(a) da \quad . \tag{1.13}$$

By analogy we may call the function $F'(z)$, the "coefficient" of the change in z, the *functional derivative* (or Fréchet derivative) of F at function z, understanding that the product here is an inner product. For example, the derivative of the survival schedule at age x, with respect to the force-of-mortality function μ, from the above example is $-p(x)$.

In the functional case it is not always possible to write the differential in this product form, hence a derivative does not always exist. But where it does we need only retain the information F': by taking the inner product of the function F' and the change in z we can summon the differential when needed.

The General Method

We have now assembled enough machinery to construct a fairly simple procedure for analyzing causal linkages in demographic theory.

Assume we have a model that expresses variable y explicitly in terms of functions z_i and variables (or parameters) x_j:

$$y = F[z_1,\ldots,z_m,x_1,\ldots,x_n] \quad . \tag{1.14}$$

If we decide which functions z_i may change independently, say those for i in some set I, and which variables may change independently, say those for j in some set J, we can write the differential change in y as

$$\delta y = \sum_{i\in I} \delta F[\delta z_i] + \sum_{j\in J} \delta F[\delta x_j] \quad . \tag{1.15}$$

We can derive the differentials $\delta F[\delta z_i]$ each separately according to the rules above, and we can derive the differentials $\delta F[\delta x_j]$ quite simply as $\frac{\partial F}{\partial x_j} \delta x_j$. We now have the sought-for expression.

Often, in demographic models, the variable of interest y is contained implicitly in the model. In this case we have the implicit functional model

$$(1.16) \qquad 0 \equiv H[y, z_1, \ldots, z_m, x_1, \ldots, x_n] \quad .$$

As before we allow certain z_i's and x_j's to change. The variable y will respond by the change δy. To maintain the identity at zero all changes must sum to zero. Hence

$$0 = \delta H[\delta y] + \sum_{i \in I} \delta H[\delta z_i] + \sum_{j \in J} \delta H[\delta x_j] \quad ,$$

that is,

$$0 = \frac{\partial H}{\partial y} \cdot \delta y + \sum_{i \in I} \delta H[\delta z_i] + \sum_{j \in J} \delta H[\delta x_j] \quad .$$

$$(1.17) \qquad \delta y = -\left(\frac{\partial H}{\partial y}\right)^{-1} \left\{ \sum_{i \in I} \delta H[\delta z_i] + \sum_{j \in J} \delta H[\delta x_j] \right\} \quad .$$

More generally, there may be several implicit equations H for several variables y. In this case, we can interpret δy to be a vector of changes, $\partial H/\partial y$ to be the (non-singular) Jacobian matrix (of partial derivatives of each H with respect to each y), and the differentials δH to be assembled in vector form. The same expression then holds.

Example 1.4 To illustrate, let us assess the change in the intrinsic rate r when both the fertility and mortality schedules m and p change. The characteristic equation connects r to functions m and p:

$$(1.18) \qquad 0 \equiv \int_0^{\omega} e^{-rx} p(x) m(x) dx - 1 = H(r, p, m) \quad .$$

We calculate

$$\frac{\partial H}{\partial r} = -\int_0^{\omega} x e^{-rx} p(x) m(x) dx$$

recognizing this expression as the average age of childbearing in the population, written A_m. And for perturbations δp and δm we obtain

$$\delta H[\delta p] = \int_0^\omega e^{-rx}\delta p(x)m(x)\,dx$$

$$\delta H[\delta m] = \int_0^\omega e^{-rx}p(x)\,\delta m(x)\,dx \quad .$$

Using (1.17) we may write

$$\delta r = \frac{1}{A_m}\left(\int_0^\omega e^{-rx}(\delta p(x)m(x) + p(x)\,\delta m(x))\,dx\right) \quad . \tag{1.19}$$

We thus have a general analytical expression for the response of the intrinsic growth rate to arbitrary changes in the fertility and mortality patterns. □

We now turn to specific problems in demographic theory.

2. EFFECT OF THE FERTILITY PATTERN ON STABLE POPULATION PARAMETERS

We begin the investigation of causal linkages in demography with stable population theory. How does the fertility pattern determine the growth and age-composition of a stable population?

There have been several attempts to answer this question. Dublin and Lotka (1925) examined the response of the intrinsic growth rate to the special case where the fertility function is multiplied by a constant factor and shifted slightly over age. Some thirty years later, Coale (1956) extended these special-case results to include the effects on age composition. More recently, Demetrius (1969), Goodman (1971), and Keyfitz (1971) derived formulas for the response of various stable parameters to an increase in fertility at a single, arbitrary age x. And in 1977 Keyfitz further derived an approximation for the response of the intrinsic growth rate x to an arbitrary, small perturbation in m, the fertility function, with a result similar to one given below.

Fertility Change and the Intrinsic Growth Rate[1]

A suitable model that connects x with the fertility function m is supplied by the familiar characteristic equation

$$(2.1) \qquad 1 = \int_0^{\omega} e^{-ra} p(a) m(a) da$$

where a is age, ω an upper bound on length of life, and p the survival function.

Suppose the fertility function m changes, to become m', where the difference $m' - m = \delta m$ is itself a function, and assuming the survival schedule p is held fixed, how will r respond?

Write (2.1) in the implicit form

$$(2.2) \qquad H(r,m) = \int_0^{\omega} e^{-ra} p(a) m(a) da - 1 \equiv 0 \quad .$$

---

[1] Although we have already looked at this problem in Example 1.4; I shall for completeness of this section rederive the result.

When m is perturbed an amount δm, r changes by δr. To maintain the identity at zero these changes must offset each other. Therefore

$$(2.3) \qquad \delta H[\delta m] + \delta H[\delta r] = \delta H[\delta m] + \frac{\partial H}{\partial r}\,\delta r = 0 \quad .$$

Evaluating the differential (as in the previous section) and the partial yields

$$\int_0^\omega e^{-ra} p(a)\,\delta m(a)\,da - \delta r \int_0^\omega a e^{-ra} p(a) m(a)\,da = 0 \quad .$$

And since the integral on the right is A_m, the average of childbearing, we obtain our first result:

$$(2.4) \qquad \delta r = \frac{\int_0^\omega e^{-ra} p(a)\,\delta m(a)\,da}{A_m} \quad .$$

We thus have a general, closed-form expression for the response of the intrinsic growth rate to an arbitrary small change in the fertility pattern.[1] This result was arrived at independently by Keyfitz in 1977, by an approximation argument.

We can immediately extract a simple theorem from this result. *In a growing population, any given pattern of marginal reduction in fertility has more effect if it is concentrated at younger ages.* To show this, suppose we consider a certain "bite" of shape δm, taken from the fertility function. Recall that c(a), the age distribution density at a, is given in stable theory by

$$(2.5) \qquad c(a) = be^{-ra} p(a)$$

where b is the intrinsic birth rate. Substituting this into (2.4) yields

---

[1] This exercise is one of comparative statics. We must interpret the change in r derived here as the differential between two stable populations that differ only in fertility function; or alternatively as the long-run difference in growth trends in a population with altered fertility.

$$(2.6) \qquad \delta r = \frac{\int_0^{\omega} c(a)\,\delta m(a)\,da}{b \cdot A_m} \quad ,$$

a second and new form of the above result. Since c(a) must decline with age in a growing population, and b and A_m are positive, any given pattern of reduction δm will lower r more if it occurs at earlier ages. Other things equal, a contraceptive method is more effective in reducing growth if it applies to younger women.

A third, and yet more useful form of the above result is possible. The mean level of fertility in the population, $\bar{m}$ can be written as

$$\bar{m} = \int_0^{\omega} c(a)m(a)\,da$$

since c(a) describes the distribution of the population by age. Recalling that $\delta m = m' - m$, we may write (2.6) as

$$(2.7) \qquad \delta r = \frac{1}{bA_m}(\bar{m}' - \bar{m}) \quad .$$

(where both means are taken with respect to the original age density c.) The change of the intrinsic growth rate, in other words, equals the change in the mean level of fertility in the population, normalized appropriately. We could use this, for example, to estimate how much fertility would have to change to achieve some prescribed reduction in the growth rate.

Fertility and Other Stable Population Parameters

One way to extend these results to the effect on the birth rate and the age distribution is to recall that b is a function of r, and c(a) of b and r through

$$(2.8) \qquad b = \frac{1}{\int_0^{\omega} e^{-ra}p(a)\,da}$$

$$(2.9) \qquad c(a) = be^{-ra}p(a) \quad .$$

Thus knowing the change in r, the change in b and c(a) can be easily derived by ordinary calculus.

A more instructive way to proceed, however, is to use the implicit function method, as described in the previous section. Set up the system

$$
\begin{aligned}
H_0(r,m) &= \int_0^{\omega} e^{-ra}p(a)m(a)da - 1 \equiv 0 \\
(2.10) \qquad H_1(r,b) &= b\int_0^{\omega} e^{-ra}p(a)da - 1 \equiv 0 \\
H_2(r,b,c(x)) &= be^{-rx}p(x) - c(x) \equiv 0
\end{aligned}
$$

Let $y = \begin{bmatrix} r \\ b \\ c(x) \end{bmatrix}$, so that the Jacobian matrix $\frac{\partial H}{\partial y}$ is obtained from (2.10) as

$$
(2.11) \qquad \frac{\partial H}{\partial y} = \begin{bmatrix} -A_m & 0 & 0 \\ -A_n & \frac{1}{b} & 0 \\ -xc(x) & \frac{c(x)}{b} & -1 \end{bmatrix}
$$

where A_n is the average age of the population. Given the driving change δm, we then have

$$
(2.12) \qquad \delta y = -\frac{\partial H}{\partial y}^{-1}\{\delta H[\delta m]\} .
$$

We know that $\delta H_0[\delta m] = \int_0^{\omega} e^{-ra}p(a)\delta m(a)da$, and that the other differentials $\delta H_1[\delta m]$, $\delta H_2[\delta m]$ are zero. Inverting $\frac{\partial H}{\partial y}$ yields

$$
(2.13) \qquad \begin{bmatrix} \delta r \\ \delta b \\ \delta c(x) \end{bmatrix} = \begin{bmatrix} \frac{1}{A_m} & 0 & 0 \\ \frac{A_n b}{A_m} & -b & 0 \\ \frac{c(x)(A_n - x)}{A_m} & -c(x) & 1 \end{bmatrix} \begin{bmatrix} \int_0^{\omega} e^{-ra}p(a)\delta m(a)da \\ 0 \\ 0 \end{bmatrix}
$$

So that, multiplying out, we obtain the results

$$(2.14) \qquad \delta r = \frac{1}{A_m}\int_0^{\omega} e^{-ra} p(a)\,\delta m(a)\,da$$

$$(2.15) \qquad \frac{\delta b}{b} = \frac{A_n}{A_m}\int_0^{\omega} e^{-ra} p(a)\,\delta m(a)\,da$$

$$(2.16) \qquad \frac{\delta c(x)}{c(x)} = \frac{(A_n - x)}{A_m}\int_0^{\omega} e^{-ra} p(a)\,\delta m(a)\,da \quad .^1$$

We now have closed-form expressions for the proportional change in the birth rate, and the age distribution, for arbitrary changes in the fertility function. Expressions (2.15) and (2.16) are believed to be new.

Of great interest is the effect of changes in fertility behavior on the age composition. We see from (2.16) that whatever the change in shape of the fertility function, it always has the same type of effect on the age distribution. It pivots it around the average age of the population A_n, a net increase in fertility increasing proportions younger than the average age, decreasing proportions older than it. This tendency of fertility change to pivot the age distribution has been described before, by Lotka (1939) and particularly by Coale (1956 and 1972).

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[1] These results have a straightforward connection with those of Keyfitz in his classic 1971 article on the effects of a change in fertility at the single age a. To obtain Keyfitz's results from ours let $\delta m(a)$ be a unit increase in m, sustained over one age unit at age a. In this case (2.16), for example, would yield $\frac{(A_n - x)}{A_m} e^{-ra} p(a)$, as in Keyfitz. In this paper, however, we consider the case where fertility is changed right across the age dimension. To obtain our results from those of Keyfitz we would need to multiply by the change at age a, $\delta m(a)$, and integrate over age. Stated another way, above we obtain the functional differential; Keyfitz, by other methods, calculates the functional derivative. Since we can construct the more general differential easily from the derivative, we could use Keyfitz's list of expressions to calculate the response for other stable-theory parameters, not treated here.

3. EFFECT OF THE MORTALITY PATTERN ON STABLE POPULATION PARAMETERS

We now turn to the effect of changes in the age-pattern of mortality on stable population parameters. As with fertility there have been several analyses of this problem, most of them of special cases. Coale (1956, 1972) investigated the effect on stable parameters when the force-of-mortality function underwent certain stylized changes close to those observed in real populations. He further provided some empirical results. Keyfitz (1971) looked at the special case of a change in the force-of-mortality function at an arbitrary single, specific age. And in the most general analysis to date, Preston (1974) derived expressions for the proportional change in r, b and c(a) caused by arbitrary changes in the mortality function.[1]

Mortality Change and Stable Parameters

Mortality change can be viewed in two different ways, depending on whether we take the change in the force-of-mortality function μ or in the survival schedule p as the driving change. The two are connected (see example 1.3) in the following one-to-one relation so we use them interchangeably:

$$(3.1) \qquad \delta p(a) = -p(a) \int_0^a \delta\mu(x)dx \quad .$$

We now proceed as before, obtaining δr, δb and $\delta c(x)$ corresponding to δp (or $\delta\mu$), by the implicit function method. This time, keeping m fixed, we have

$$(3.2) \qquad \delta y = -\frac{\partial H}{\partial y}^{-1}\{\delta H[\delta p]\} \quad .$$

and since we know $\frac{\partial H}{\partial y}^{-1}$ from the previous section it remains only to evaluate $\delta H[\delta p]$.

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[1] Preston's expressions appear to be quite general, but they hinge partly on a parameter A that must be separately determined; they are therefore somewhat difficult to interpret.

From (2.10),

$$(3.3) \qquad \begin{aligned} \delta H_0[\delta p] &= \int_0^{\omega} e^{-ra} m(a)\,\delta p(a)\,da \\ \delta H_1[\delta p] &= b\int_0^{\omega} e^{-ra}\,\delta p(a)\,da \\ \delta H_2[\delta p] &= be^{-ra}\,\delta p(x) \quad . \end{aligned}$$

Substituting these into (3.2):

$$(3.4) \qquad \begin{bmatrix} \delta r \\ \delta b \\ \delta c(x) \end{bmatrix} = \begin{bmatrix} \frac{1}{A_m} & 0 & 0 \\ \frac{bA_n}{A_m} & -b & 0 \\ \frac{(A_n-x)c(x)}{A_m} & -c(x) & 1 \end{bmatrix} \begin{bmatrix} \int_0^{\omega} e^{-ra} m(a)\,\delta p(a)\,da \\ b\int_0^{\omega} e^{-ra}\,\delta p(a)\,da \\ be^{-ra}\,\delta p(a) \end{bmatrix}$$

Finally, multiplying out,

$$(3.5) \qquad \delta r = \frac{\int_0^{\omega} e^{-ra} m(a)\,\delta p(a)\,da}{A_m}$$

$$(3.6) \qquad \frac{\delta b}{b} = \frac{A_n}{A_m}\int_0^{\omega} e^{-ra} m(a)\,\delta p(a)\,da - b\int_0^{\omega} e^{-ra}\,\delta p(a)\,da$$

$$(3.7) \qquad \frac{\delta c(x)}{c(x)} = \frac{(A_n-x)}{A_m}\int_0^{\omega} e^{-ra} m(a)\,\delta p(a)\,da - b\int_0^{\omega} e^{-ra}\,\delta p(a)\,da + \frac{\delta p(x)}{p(x)} \; .$$

We now have general closed-form expressions for the change in the growth rate, the birth rate, and the age-distribution, given an arbitrary small change in the life table. These results are believed to be new; some comments on them are in order.

1. The effect of mortality on the growth rate is similar to the effect of fertility. What matters is the numerator in (3.5) or (2.4) and this is the effect of either fertility or mortality on the reproductive value at birth. Note that mortality improvements late in life, a cure to cardiovascular diseases say, would have

little influence on reproductive value, the change in survival would come largely after reproductive years were past, so that r would show negligible change.

2. A special case of mortality change, "neutral" change, is known (see Preston 1974) to have a particularly simple effect on the growth rate. We can verify this easily. Suppose

$$\mu(x) \longrightarrow \mu(x) - \bar{k} \qquad (\bar{k}, \text{ a constant})$$

so that

$$\delta\mu = -\bar{k}$$

$$\delta p(a) = a p(a)\bar{k} \quad .$$

Then

$$\delta r = \frac{\bar{k}\int_0^{\omega} a e^{-ra} m(a)p(a)da}{A_m} = \bar{k}\,\frac{A_m}{A_m} = \bar{k} \quad .$$

Reducing the mortality function by a constant amount, in other words, increases the growth rate the same amount.

3. The effect of mortality change on the age distribution is straightforward to analyze, given the above general closed-form expression. The first term once again "pivots" the age-distribution about A_n. For any given mortality improvement it is linear over age, and negatively sloped. The second term is constant and negative. And the third term directly reflects the change in the survival function. For the usual pattern of mortality change over time, where survival chances improve significantly at ages under five and over forty, the change in the age distribution has the shape shown below in Figure 3.1. Again, this confirms Coale's (1972) analysis of the effects of observed changes in the age-distribution. "Usual" patterns of mortality change tend to pivot the age-distribution clockwise, toward greater proportions in younger age-groups, thus lowering average age.

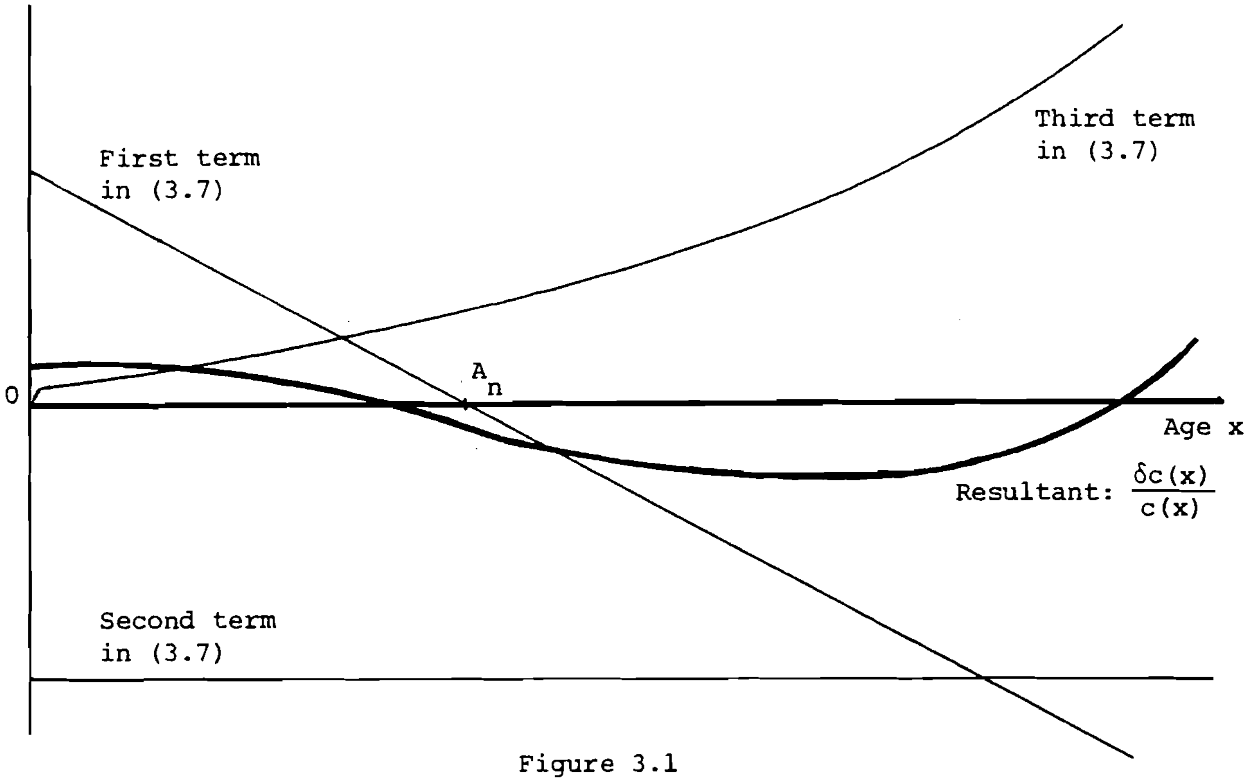

Figure 3.1

4. Survival improvements in the post-reproductive years only, however, pivot the age distribution the other way. The growth effect term disappears and the second term now lowers the age distribution uniformly across the age dimension. The third term again directly reflects the improvement in survival at older ages. The age distribution now pivots anticlockwise, raising average age.

5. Expressions (2.16) and (3.7), taken together explain the empirical observation that fertility affects the age distribution more than mortality does. Taking fertility and mortality changes that have equal effect on growth (term on right of (2.16) equal to first term of (3.7)) we see that in contrast to fertility which acts only through the growth rate, mortality affects the age composition through two other terms. These, in general, tend to offset the first, so that the pivoting of the age distribution is not so pronounced in the mortality case.

6. Finally, the differentials that describe the effects of mortality change and fertility change in any of the stable parameters are additive. We could therefore combine results to find the net effect of both fertility and mortality change, or, working in the opposite direction, decompose a given change in a stable parameter into separate fertility and mortality effects.

Example 3.1 A simple numerical test of the above results is easy to perform. Suppose we start with a stable female population with mortality corresponding to the Coale and Demeny (1966) Model West Level 18 schedule and with growth rate zero. Can we use the above formulae to "predict" the new growth rate, birth rate, and age composition, if mortality were given instead by Level 20?

The differential function δp is obtained numerically from the tables; it is the difference between survival schedules 20 and 18. The Level 18 initial growth rate and birth rate, the new Level 20 values as calculated by (3.5) and (3.6), and the (correct) Level 20 values obtained from the tables compare as follows:

r_{18}	r_{20}(calc.)	r_{20}(tables)	b_{18}	b_{20}(calc.)	b_{20}(tables)
0.00	0.0196	0.0191	16.00	15.86	15.88

The calculated value for r, via the differential, is about 2.5% off in estimating the change, due to the curvature of the functional for r over its argument function p.

The age distributions, old and new, and calculated from (3.7) versus interpolated from the Coale-Demeny tables, compare as follows:

Age Group	0 - 1	1 - 4	5 - 9	10-14	15-20	20-24	25-29	30-34
c_{18}	1.53	5.92	7.29	7.24	7.17	7.09	6.98	6.86
c_{20}(calc.)	1.54	6.00	7.39	7.29	7.18	7.06	6.92	6.78
c_{20}(tables)	1.54	6.02	7.41	7.31	7.19	7.07	6.93	6.79

Age Group	35-40	40-44	45-49	50-54	55-59	60-64	65-69	70-74	75-79
c_{18}	6.72	6.56	6.36	6.11	5.76	5.27	4.61	3.71	2.63
c_{20}(calc.)	6.63	6.46	6.25	6.00	5.67	5.21	4.61	3.76	2.74
c_{20}(tables)	6.63	6.46	6.25	5.99	5.66	5.21	4.60	3.76	2.72

There is of course a discrepancy since the differential is a first-order approximation to the true response. (Part of this discrepancy may be due to the fact that c_{18}, used as the input data for c(x) in (3.7), is already rounded to two decimal places in the tables.) We can conclude that, in this case, for most purposes the differential brings us tolerably close to the true change. If we wanted the *exact* response of r and c, however, for purposes of high-precision tabulation say, we would use a more complicated form of the differential -- the functional line integral -- to be touched on briefly in Section 8. ☐

4. AN ILLUSTRATION: THE EFFECT OF AN AGE-SHIFT IN FERTILITY

Thus far our stable theory results contain "δm" or "δp" in the expressions, reflecting the fact that we developed them for arbitrary changes in m and p. Often though we would want to use these results by specializing δm and δp to a particular type of change in age pattern. I illustrate a case now.

As a country develops, individual demographic behavior persists--a person marries, reproduces, and dies as before--but it often takes place at different times in the lifecycle. Thus the fertility pattern may not change too greatly in shape, but may vary in its overall intensity and its location on the age axis. In demographic theory the consequences of changes in intensity (uniform proportional change over the entire age-schedule) are easy to analyze. But there is no easy method to determine the consequences of simple translation in age-patterns. Using the results of the previous sections however, we can analyze translations in a straightforward way.

Translation of the Net Maternity Schedule

We begin by looking at the simplest case: a pure age-shift in the net maternity schedule, ϕ. See Figure 4.1. This can be regarded as a *rough* indication of what happens when age at marriage is increased.

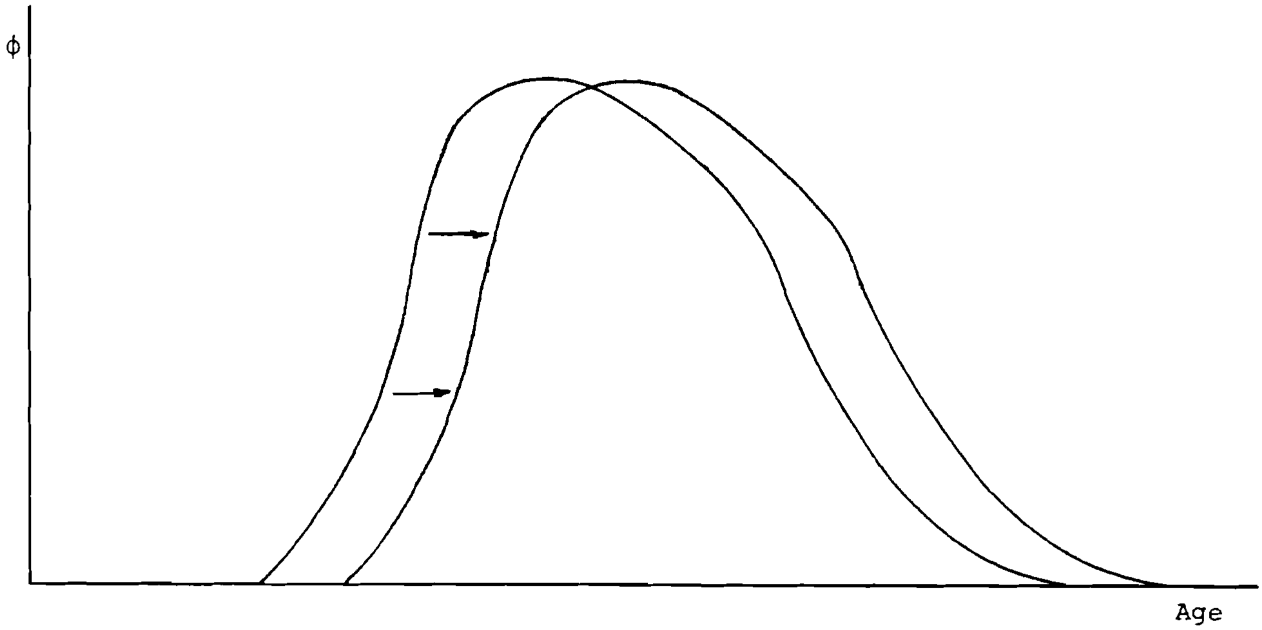

Figure 4.1

Confining our attention to the stable case, and working from the characteristic equation

$$(4.1) \qquad 1 = \int_0^{\omega} e^{-ra} \phi(a)da \quad ,$$

where $\phi = p \cdot m$ is the net maternity function, we find as before that

$$(4.2) \qquad \delta r = \frac{1}{A_m} \int_0^{\omega} e^{-ra} \delta\phi(a)da \quad .$$

Now, a pure translation of ϕ to the right (later childbearing by τ years) means that the change in ϕ is given by

$$\delta\phi(a) = \phi(a-\tau) - \phi(a)$$

so that

$$\begin{aligned} \delta r &= \frac{1}{A_m} \left\{ \int_0^{\omega} e^{-ra} \phi(a-\tau)da - \int_0^{\omega} e^{-ra} \phi(a)da \right\} \\ &= \frac{1}{A_m} \left\{ \int_0^{\omega} e^{-r(a+\tau)} \phi(a)da - \int_0^{\omega} e^{-ra} \phi(a)da \right\} \\ &= \frac{(e^{-r\tau}-1)}{A_m} \int_0^{\omega} e^{-ra} \phi(a)da \end{aligned}$$

$$(4.3) \qquad \delta r = (e^{-r\tau}-1)/A_m \quad .$$

This result tells us that if r is positive, later childbearing ($\tau > 0$) necessarily decreases r. If it is negative on the other hand, δr is positive, so that later childbearing actually speeds growth. The reason for this paradoxical result is that a delay in childbearing means that the next generation arrives later. Since it is smaller, the decline in numbers over time is therefore not so rapid.

The above result offers a useful rule of thumb for age-shifts in childbearing. Dividing by r we have

$$\frac{\delta r}{r} = \frac{(e^{-r\tau}-1)}{A_m r} \quad ,$$

and expanding the exponential term and dropping terms of second order and upward (permissable since r is small) we obtain

$$(4.4)\qquad \frac{\delta r}{r} = \frac{-r\tau}{rA_m} = \frac{-\tau}{A_m} = -\frac{\text{Increase in Average Age of Childbearing}}{\text{Average Age of Childbearing}} \quad .$$

Thus the proportional fall in the growth rate equals the proportional rise in the mean age of childbearing. Since A_m is usually about 27 or 28 years, or thereabouts, a year's shift in childbearing causes a proportionate change in the growth rate of $\frac{1}{27.5}$ or about 3.6%. It would therefore take more than a five year delay in childbearing to cause a 20% decline in the growth rate, or to take 8 points off a CBR of 40.

The Fertility Schedule: Age-Shift and Increase in Intensity

We now look at a slightly more difficult case, assuming now that the fertility function shifts by τ years, and increases also by a factor 1+k in intensity. Since differentials are additive we can treat the two changes separately.

Here I make an approximation. Assume that, over the childbearing years, the survival curve declines linearly with slope ρ. That is,

$$(4.5)\qquad p(a+\tau) = (1-\rho\tau)p(a) \quad .$$

From (2.4), with the differential $\delta m = m(a-\tau) - m(a)$

$$\delta r = \frac{1}{A_m}\int_0^\omega e^{-ra}(m(a-\tau) - m(a))p(a)da$$

$$= \frac{1}{A_m}\left\{\int_0^\omega e^{-r(a+\tau)}m(a)p(a+\tau)da - \int_0^\omega e^{-ra}m(a)p(a)da\right\} \quad .$$

So that, using (4.1)

$$(4.6)\qquad \delta r = \frac{1}{A_m}\left\{e^{-r\tau}(1-\rho\tau) - 1\right\} \quad .$$

Neglecting terms of order r^2 and upward, we obtain

$$(4.7)\qquad \delta r = \frac{-\tau}{A_m}(\rho+r) \quad .^1$$

Now we analyze the effect of the second change, $\delta m = km(a)$. Substitution into (4.2) shows that this time

$$\delta r = \frac{k}{A_m} \quad .$$

Adding the two differentials, we obtain

$$(4.8)\qquad \delta r = \frac{k - \tau(\rho+r)}{A_m} \quad .$$

This tells us how much the intrinsic growth rate changes if fertility increases by a factor 1+k, and is shifted along the age axis by τ years, as may happen in the course of development. From (2.16) we can easily write the change in the age-distribution as

$$(4.9)\qquad \frac{\delta c(x)}{c(x)} = \frac{(A_n-x)}{A_m}(k - \tau(r+\rho)) \quad .$$

Example 4.1 In a well-known paper, Coale and Tye (1961) present an example where the 1956-58 fertility patterns of two ethnic groups in Singapore, the Malays and the Chinese, resemble each other closely in shape. The mean age of childbearing for the Chinese is 29.1 years, about 3 years higher than that for the Malays, 26.4. On the other hand the survival schedules, and overall fertility levels differ slightly. The Chinese intrinsic growth rate is 8.3% lower than the Malaysian one. How much difference does the age-shift in childbearing make, compared to the other factors? Using (4.7), with $\rho = 0.0013$, $r = 0.040$, and the Malaysian figures as a base, we find

$$\frac{\delta r}{r} = \frac{-(29.1 - 26.4)}{26.4}\ \frac{(0.0013 + .040)}{.040} = -10.5\% \quad .$$

---

[1] Results (4.6) and (4.7) may be contrasted with Dublin and Lotka's (1925) approximation: $\delta r = \frac{1}{(A_m+\tau)}\left(\ell n\left(\frac{p(a+\tau)}{p(a)}\right) - r\tau\right)$. Where τ is small, the results coincide with Dublin and Lotka's expression.

The higher age of childbearing of the Chinese lowers their growth rate by 10.5%. The Chinese have higher fertility however, and a slightly different survival schedule so that the real difference is not quite so great--it is 8.3%. The age shift difference of 10.5% (or 10.15 if we include second-order terms in the approximation) agrees well with Coale and Tye, who calculate 10% due to this effect. □

5. CAUSAL LINKAGES IN NON-STABLE THEORY

In the previous sections we looked at the response of the age composition and of intrinsic rates to demographic change within a stable-population model. For non-stable populations the theory is no more difficult. But the non-stable case, being more general, has less mathematical structure than the stable case, and for this reason closed-form mathematical results are not always possible to obtain.

This section takes up two problems. It derives the transient response of the age composition to underlying changes in the birth sequence and to temporal changes in the fertility pattern. And it examines the more difficult problem of the transient response of the age composition to temporal changes in mortality.

Response of the Age Composition to Changes in the Birth Sequence

The age composition of the population, c(a,t) is given in the general, non-stable case by

$$(5.1) \qquad c(a,t) = \frac{N(a,t)}{N(t)} = \frac{B(t-a)p(a,t)}{\int_0^{\omega} B(t-a)p(a,t)da}$$

where N(a,t) is the population density at age a, time t, N(t) is the total population at time t, and p(a,t) is the probability that a person (born at t-a) survives to be aged a at time t.

Suppose there is a given nominal birth sequence, B(t). It may be an arbitrary function of time, or it may follow some particular form, such as exponential growth. How will the age composition respond, over time, to an arbitrary change in this function -- a baby boom, for example, or a deviation from exponential growth?

Let $\delta B(t)$ be the given perturbation in the birth sequence (see Figure 5.1).

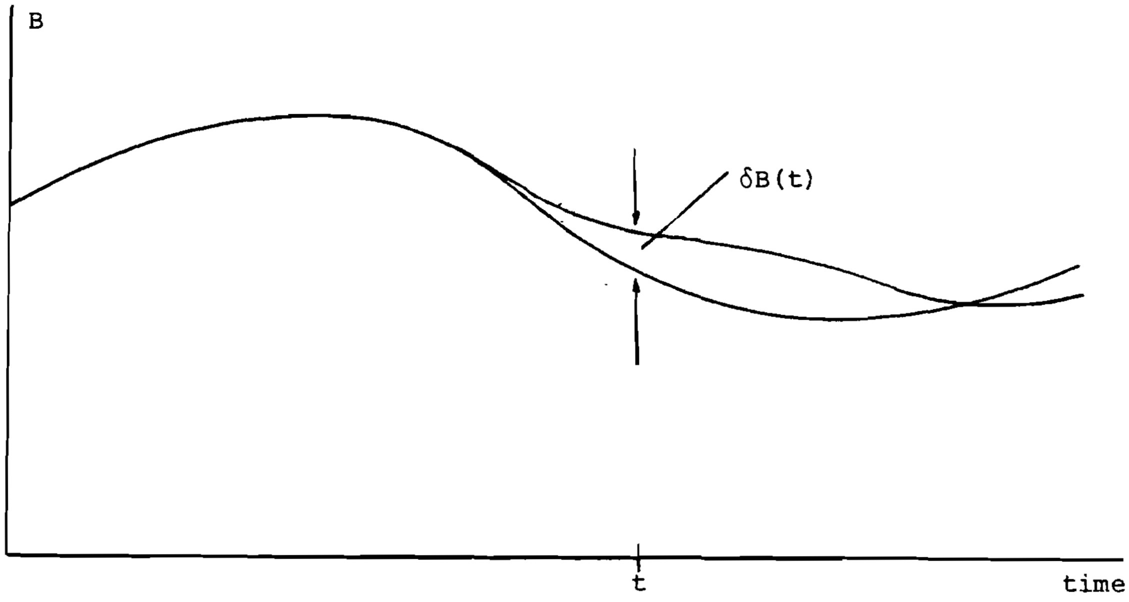

Figure 5.1

The response of c(a,t) to the alteration in the birth sequence δB is obtained from (5.1) by the quotient rule:

$$\delta c(a,t)[\delta B] = (N(t)\delta N(a,t) - N(a,t)\delta N(t))/N(t)^2$$

$$(5.2) \qquad \delta c(a,t) = \frac{1}{N(t)}\left(\delta B(t-a)p(a,t) - c(a,t)\int_0^{\omega}\delta B(t-a)p(a,t)da\right).$$

Dividing through by c(a,t) this becomes our first, non-stable-theory result:

$$(5.3) \qquad \frac{\delta c(a,t)}{c(a,t)} = \frac{\delta B(t-a)}{B(t-a)} - \frac{\int_0^{\omega}\delta B(t-a)p(a,t)da}{N(t)} ,$$

or,

$$(5.4) \qquad \frac{\delta c(a,t)}{c(a,t)} = \frac{\delta B(t-a)}{B(t-a)} - \frac{\delta N(t)}{N(t)} .$$

The proportional change in the age composition at time t equals the proportional change in the cohort aged a, less the total proportional change in the population. We thus see the transient response of the age composition to a sequence of cohorts larger than normal as a bulge that passes through the age composition progressively over time.

The response of the age composition to temporal changes in fertility behavior is now easy to obtain. The standard Lotka equation links the birth sequence with the fertility function m:

$$(5.5) \qquad B(t) = \int_0^{\omega} B(t-a)p(a,t)m(a,t)da$$

with the initial birth sequence given. For a temporal change in the fertility pattern, $\delta m(a,t)$, the birth sequence is therefore perturbed an amount

$$(5.6) \qquad \delta B(t) = \int_0^{\omega} \delta B(t-a)p(a,t)m(a,t)da + \int_0^{\omega} B(t-a)p(a,t)\,\delta m(a,t)da \ ,$$

with the initial sequence δB zero before the change occurs. Changes in fertility behavior thus affect the birth sequence both directly (second term on the right) and indirectly through the "echo effect" of the change itself (first term on the right). The perturbation δB is thus given by a Lotka-type renewal equation, with a non-homogeneous or forcing term.[1]

Temporal age-pattern changes in fertility, we can conclude, change the age composition in two stages. They alter first the birth sequence, according to (5.6); this then alters the age composition, as in (5.3) or (5.4).

Response of the Age Composition to Changes in Mortality Rates

Temporal age-pattern changes in mortality affect the age composition through a more complex mechanism: they alter both the birth sequence B and the survival function p in (5.1). Here I take the force-of-mortality function μ as the starting link of the causal chain; improvements in public health, the incidence of epidemics, of wars and natural disasters, the partial cure of certain diseases and the shift between one cause of death and

---

[1] Here we run up against an inherent limitation of differential analysis. The term δB is a first-order approximation to the actual change in birth sequence, and since it also appears on the right side any error compounds over time. Hence we may think of (5.6) as being "valid" only over the space of two or three generations.

another are most directly seen as acting either temporarily or permanently on μ, the probabilities of death at given ages in a given year. I split the analysis into two questions: first, how does a temporal change in the force-of-mortality function μ affect the survival function p over time? Second, how does the resulting transient change in p affect the age composition over time?

The force-of-mortality, or probability of death per unit time, for the cohort aged x at time t_0 is written $\mu(x,t_0)$. It determines the probability of survival p(a,t) to age a, at time t, for the cohort born at t-a, by the relation

$$p(a,t) = \exp\left(-\int_{t-a}^{t} \mu(a-(t-\tau),\tau)d\tau\right) .$$

The survival probability p, in other words, is a function of the cohort's force-of-mortality history at previous times τ over its life span up to age a.

Let us now suppose the force of mortality is altered over the age and time dimensions by $\delta\mu(x,\tau)$, at age x and time τ. Then, as in Example 1.3, the transient response in the survival function p is obtained as

$$(5.9) \qquad \delta p(a,t) = -p(a,t)\int_{t-a}^{t} \delta\mu(a-(t-\tau),\tau)d\tau .$$

The survival probability is therefore altered over time to a degree proportional to itself times a summation of the force-of-mortality changes that apply to the cohort in question in all its previous years from birth onward. To gain some insight into how this linkage works, suppose a change in μ for one year only at some past time τ_0 for the cohort then aged a_0. At future time t this cohort will be aged $a = a_0 + (t-\tau_0)$ and from (5.9) we obtain the alteration in its survival probability as

$$(5.10) \qquad \delta p(a_0+t-\tau_0,t) = -p(a_0+t-\tau_0,\tau)\,\delta\mu(a_0,\tau_0) ,$$

other changes in the survival function being zero. Thus the one-year alteration in the force of mortality affects one cohort only and it ripples along the survival function with this cohort as it ages. More generally, the effect of a temporary or a sustained change over the entire age dimension in the force of mortality on the survival function is the summation of such cohort ripple effects.

We now take the alteration in the survival function over time, $\delta p(a,t)$, as given or determined. It affects the birth sequence over time as in (5.6) by

$$\delta B(t) = \int_0^{\omega} \delta B(t-a)p(a,t)m(a,t)da + \int_0^{\omega} B(t-a)\delta p(a,t)m(a,t)da \tag{5.11}$$

with δB zero before the change in survival happens. It also alters the total population,

$$N(t) = \int_0^{\omega} B(t-a)p(a,t)da \quad ,$$

over time by an amount

$$\delta N(t) = \int_0^{\omega} \delta B(t-a)p(a,t)da + \int_0^{\omega} B(t-a)\delta p(a,t)da \quad . \tag{5.12}$$

Finally, using the quotient rule, we obtain the change in the age composition as

$$\delta c(a,t) = \frac{1}{N(t)^2}\left\{N(t)B(t-a)\delta p(a,t) + N(t)\delta B(t-a)p(a,t) - B(t-a)p(a,t)\delta N(t)\right\}.$$

Dividing through by $c(a,t)$ we have the result:

$$\frac{\delta c(a,t)}{c(a,t)} = \frac{\delta p(a,t)}{p(a,t)} + \frac{\delta B(t-a)}{B(t-a)} - \frac{\delta N(t)}{N(t)} \quad . \tag{5.13}$$

Thus the proportional change in the age composition at age a and time t equals the proportional change in the survival function at that age and time, plus the proportional change, if any, in the numbers at birth of the cohort aged a at time t, less an adjustment term for the proportional change in the total population. To sum up the causal sequence, changes in death rates, seen as changes in μ, affect the survival function through (5.9). This affects in turn both the birth sequence through (5.11), and the total population size through (5.12). The response of the age composition is given in (5.13) as the summation of these effects.

Mortality changes that affect only post-reproductive ages allow a closed-form result. In this case the change in the birth sequence, δB, is zero and (5.13) reduces to

$$\frac{\delta c(a,t)}{c(a,t)} = \frac{\delta p(a,t)}{p(a,t)} - \frac{\delta N(t)}{N(t)}$$

$$= -\frac{p(a,t)\int_{t-a}^{t} \delta\mu(a-(t-\tau),\tau)d\tau}{p(a,t)} - \frac{\int_0^\omega B(t-a)\delta p(a,t)da}{\int_0^\omega B(t-a)p(a,t)da}$$

$$= -\int_{t-a}^{t} \delta\mu(a-(t-\tau),\tau)d\tau - \int_0^\omega c(a,t)\delta p(a,t)da$$

(5.14)

$$\frac{\delta c(a,t)}{c(a,t)} = -\int_{t-a}^{t} \delta\mu(a-(t-\tau),\tau)d\tau + \left[p(a,t)\int_{t-a}^{t} \delta\mu(a-(t-\tau),\tau)d\tau\right]_c$$

where the square brackets signify the average value of the function within them, taken with respect to the age distribution c at time t.

Example 5.1 To illustrate the transient response of the age composition to a change in mortality probabilities, suppose that cardiovascular diseases had been abruptly eliminated as a cause of death in the United States in 1966, and that this improvement in mortality were sustained in all subsequent years:[1]

Age	45	50	55	60	65	70	75	80
$-\delta\mu$	.00346	.00606	.01004	.01545	.02445	.03564	.05254	.08196

---

[1] This change in μ is obtained from Preston, Keyfitz and Schoen (1972, p.768) by eliminating cardio-vascular diseases as a cause of death in the U.S. 1964 Male tables and making corrections for the effect of competing risks.

Using the Keyfitz and Flieger (1971) U.S. 1966 Male life table and population projections, how would the survival function and age composition respond over time to this sudden but sustained improvement in mortality?

From (5.9) we can compute the response in the survival function as:

	Age x	45	50	55	60	65	70	75	80
$p(x)$	1966	.89404	.86081	.80954	.73493	.63747	.51314	.37576	.24400
	1971	.90951	.88689	.85018	.79170	.71540	.60458	.47447	.34399
	1976	.91778	.90178	.87471	.82860	.76468	.66731	.54143	.40809
	1981	.92162	.90975	.88871	.85087	.79665	.70695	.58737	.45157

The projected age compositions, without the mortality improvement, are obtained from Keyfitz and Flieger (p.335) as:

	Age Group	50-55	55-60	60-65	65-70	70-75	75-80
c %	1971	5.34	4.78	3.97	3.13	2.23	1.56
	1976	5.24	4.68	4.02	3.16	2.29	1.47
	1981	4.61	4.58	3.92	3.18	2.29	1.50

From (5.14) we can compute the changes in these projections, due to the mortality improvement as:

	Age Group	50-55	55-60	60-65	65-70	70-75	75-80
δc %	1971	.130	.228	.333	.421	.455	.501
	1976	.197	.362	.551	.705	.788	.777
	1981	.209	.438	.674	.896	1.005	1.011

Notice that the influence on the age composition grows through time, as cohorts are exposed to the mortality improvement over progressively longer periods of their life span. The response would stabilize about forty years or so after the onset of the improvement: all cohorts in this case would be subject to the entire new mortality function over their life history. □

6. DEMOGRAPHIC CHANGE AND VITAL RATES

The easiest demographic measures to obtain for a population are its vital rates -- the number of occurrences of a vital phenomenon in year t, divided by the total population. Standard measures of this type are the crude death rate, DR, and crude birth rate, BR:

$$(6.1) \qquad DR(t) = \frac{D(t)}{N(t)} \quad ; \qquad BR(t) = \frac{B(t)}{N(t)}$$

where D(t) is total deaths in year t. Other behavioral rates, such as the crime rate in the population may be similarly defined and measured.

In general we suppose some age- and time-related phenomenon, with an age-specific rate $g(a,t)$ for the cohort aged a at time t. Summing over all cohorts we obtain the vital rate for this phenomenon at the benchmark time, t_0, as

$$(6.2) \qquad G(t_0) = \frac{\int_0^{\omega} g(a,t_0)B(t_0-a)p(a,t_0)\,da}{N(t_0)} = \int_0^{\omega} g(a,t_0)c(a,t_0)\,da.$$

Suppose we measure this rate again at some later time, t, we obtain

$$(6.3) \qquad G(t) = \int_0^{\omega} g(a,t)c(a,t)\,da \quad .$$

The rate will have changed on two counts: first the function g itself will have changed with time and this is what we hope to measure, and second the age composition c will have changed. Ideally we would like to measure the overall change in G, without bias introduced by underlying changes in the age composition.

Suppose we know the change in the age composition between t_0 and t, either directly, or by evaluating it as in the previous section from changes in the birth sequence or in fertility or mortality behavior. Expanding G(t) about t_0, to first order, by Taylor series we obtain

$$(6.4) \quad G(t) = G(t_0) + \int_0^{\omega} g(a,t_0)\delta c(a,t_0)\,da + \int_0^{\omega} \delta g(a,t_0)c(a,t_0)\,da.$$

The second integral on the right is what we seek: it is the change in the phenomenon itself, averaged over the population. Denoting this as ΔG, we can write it as

$$(6.5) \qquad \Delta G = G(t) - G(t_0) - \int_0^{\omega} g(a,t_0)\,\delta c(a,t_0)\,da \quad .$$

We have now obtained the result we need. The "true" change in the vital phenomenon is given by the measured changes in the rates less a correction factor for the change in age composition. This correction factor in general may not be easy to compute; some knowledge of the age-specific phenomenon and the change in the age composition would be necessary. One or both of these may have to be approximated on an incomplete data basis: this however is a standard task in demographic work.

Example 6.1 We can use a similar type of analysis to find how period rates differ from the "correct" cohort rates given fluctuations in the birth sequence.[1] To look at the question with precision, suppose (i) a stationary population, with $N(t) = N$, $B(t) = B$, and (ii) mortality functions p and μ that are constant over time. By virtue of (ii), all birth cohorts face the same lifetable, the same mortality experience, regardless of the birth sequence. And by virtue of (i), in the absence of perturbations in B, the crude death rate DR will equal the correct, cohort rate d; it will show no bias.

Now,

$$DR(t) = \frac{D(t)}{N(t)} = \frac{\int_0^{\omega} B(t-a)p(a)\mu(a)\,da}{N} = d$$

which responds to an arbitrary perturbation δB in the birth sequence by

$$(6.6) \qquad \delta DR(t) = \frac{\int_0^{\omega} \delta B(t-a)p(a)\mu(a)\,da}{N} - d\,\frac{\int_0^{\omega} \delta B(t-a)p(a)\,da}{N} \quad .$$

---

[1] Preston (1972) analyzed a related, special case: the response of the crude death rate to exponential growth of the birth sequence.

This expression gives the deviation of DR from the cohort rate d, given a fluctuation in the birth sequence. We can gain further insight by specializing δB to be a single-year "boom" in the birth sequence; a cohort boom in year t_0, larger by δB than the usual sequence B. (Since we are perfectly free to examine the response to any perturbation in B as an analytical experiment, for simplicity I shall ignore any echo effect.) We now have

$$\delta B(t) = \begin{cases} \delta B & t_0 \leqq t \leqq t+1 \\ 0 & \text{otherwise} \end{cases} .$$

And for this particular change, (6.6) on integrating out, becomes

$$\delta DR(t) = \frac{\delta B}{N} \cdot p(t-t_0)\mu(t-t_0) - d \cdot \frac{\delta B}{N} \cdot p(t-t_0) .$$

Letting $\frac{\delta B}{B}$ be β, and $\frac{B}{N}$ be b, we find

$$\delta DR(t) = b\beta p(t-t_0)(\mu(t-t_0) - d) . \tag{6.7}$$

We have thus found an expression for the bias in the crude death rate caused by a controlled baby-boom--an additional "pulse" of births born at t_0. Notice the effect. The bias in CDR shows as strongly positive, at time t just after t_0, then negative as time progresses further, then positive again as t reaches $t_0 + 60$ fading then gradually to zero. The short pulse of births in

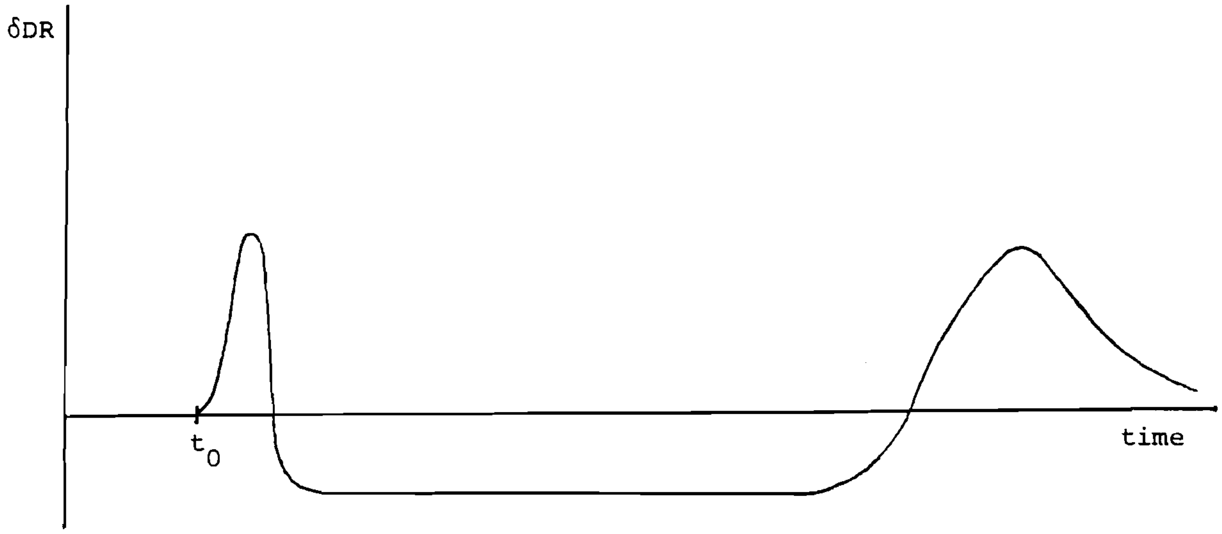

Figure 6.1

other words, causes the crude death rate to be more positive than the cohort rate due to higher mortality in the infant years. Then, as it swells population numbers in its middle years but shows few deaths, the CDR falls below the "true" cohort rate. Finally it biases CDR positively again as it reaches the older, high mortality years, the effect fading as the cohort passes out of the population. These changes are summarized in Figure 6.1. ☐

7. TOWARD A THEORY OF ERROR IN DEMOGRAPHIC ESTIMATES[1]

In the last fifteen years or so, since the seminal work of Brass and Coale (1968), demographers have become highly skilled at estimating vital rates from census data that are fragmentary or incomplete. Normally in statistics it is impossible to base an estimation technique on data that are largely missing. But in demography a fortuitous circumstance makes this possible. By and large demographic behavior follows highly regular age-patterns. The demographer need only use the available data to select an approximate age pattern from a standard and known family of such patterns. Knowing the approximate pattern he can then fill in the blanks as it were, and calculate the desired rates or parameters.

It is useful to view this procedure abstractly. The demographer begins with a standard schedule, of mortality or fertility say, which can be varied by one or two parameters to create a family of model schedules. His observed data tell him how to adjust these parameters to transform the standard schedule into one that approximates the "true" but unknown schedule in the population under study. Thus any particular estimation procedure may be viewed as mapping certain observations plus one or more standard schedules into the real numbers to produce the desired estimate. More precisely then, the estimate can be viewed as a functional of the standard schedules and a function of the observed data:

$$\hat{q} = F(O_1,\ldots,O_n,L_1^s,\ldots,L_m^s)$$

where q is the parameter to be estimated, $\hat{q}$ the estimate, O the observed data, and L^s the standard age-schedules. The particular functional form of F of course depends on the demographic identities on which the estimation procedure is based, and these in turn depend on the demographic assumptions that underlie the procedure.

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[1] Here I thank Griffith Feeney, who suggested that causal linkage analysis might be used to estimate errors in these techniques. Collaborative work with Michael Stoto has also helped clarify my thinking in this section. A more complete and precise account of the notions explored here will appear in a forthcoming paper by Arthur and Stoto (1980).

The statistician interested in such estimation procedures might well ask two questions. First, how robust is the estimation procedure, given that not all the necessary assumptions can be perfectly fulfilled? Second, how might we "correct" the estimate, given different and known sources of error in the technique. Mathematically, a theory of error or of robustness for demographic estimates can be based on analysis of the linkages between the estimate $\hat{q}$ and the standard functions it depends on. To illustrate this, I carry out such analysis on a well-known incomplete data technique -- estimation of mortality from the Brass Child Survivorship technique. I choose this technique because it uses a minimum of notation. Other Brass techniques are much the same in structure -- the type of analysis applied here and some of the general conclusions would just as well apply to them.

The Brass Child Survivorship Technique

Suppose we want to estimate the mortality parameter q(M), the probability of death between birth and age M, where M is less than 10 years say. In many countries where births and infant deaths are poorly recorded it is not possible to evaluate q(M) by direct counting. Brass (1975) suggests the following technique.

1. Question mothers, aged x, on the proportion of their children who have failed to survive, D_x. This is the single observation used; but notice that it is already a rough indicator of mortality in the childhood years.

2. Choose model schedules of mortality q' and fertility m', and estimate q(M), the probability of death before age M by the expression

$$(7.1) \qquad \hat{q}(M) = \frac{q'(M)\int_0^x m'(y)\,dy}{\int_0^x m'(y)\,q'(x-y)\,dy} \cdot D_x \quad .$$

There are several ways to see why this procedure should work. One way is to suppose we have chosen the model schedule q' fairly well as regards its shape, but are unsure as to what level to set it at to read off q(M). Now, D_x, the proportion of children dead for mothers aged x is given by

$$(7.2) \qquad D_x = \frac{\int_0^x m(y)q(x-y)dy}{\int_0^x m(y)dy}$$

where m(y) is the true fertility rate for mothers aged y, and q(x-y) is the true probability a child will die during the interval x-y, between mother's age y at birth and her age x at the time of interview. The estimation procedure (7.1) therefore corrects the guessed or model level q'(M) by a factor

$$\frac{D_x\int_0^x m'(y)dy}{\int_0^x m'(y)q'(x-y)dy} = \frac{\underline{\text{Observed proportions dead}}}{\text{Model proportions dead}}$$

which, if the model schedules m' and q' have the right shape, equals the observed or actual mortality level over the model mortality level. The estimation therefore "adjusts" the value q'(M) to a level that corresponds with the observed mortality.

Before proceeding further, it will help to normalize the estimation formula. Let $m'(y)/\int_0^x m'(y)dy$ be f'(y), the (model) probability density of childbearing at age y, before age x. Similarly define f(y), the true density of childbearing at age y, before age x. We may then write the estimate as

$$(7.3) \qquad \hat{q}(M) = \frac{q'(M)}{\int_0^x f'(y)q'(x-y)dy} D_x$$

where, if the observation D_x has been measured correctly, we have

$$(7.4) \qquad D_x = \int_0^x f(y)q(x-y)dy \quad .$$

Finally, following Brass (1975) we can express (7.4) in a useful approximate form as

$$(7.5) \qquad \int_0^x f(y)q(x-y)dy \simeq q(x-A)$$

where A is the average age of childbearing for mothers aged x, that is, the average age under the density function f.[1] Thus D_x approximately measures the probability of death at the average age, x-A, of the childhood deaths being reported.

Error Theory

Where the model schedules q' and f' coincide with the true functions q and f, and where D_x has been measured correctly so that it conforms with (7.4), $\hat{q}(M)$ estimates q(M) exactly:

$$(7.6) \qquad \hat{q}(M) = \frac{q(M)}{\int_0^x f(y)q(x-y)dy} \int_0^x f(y)q(x-y)dy = q(M) \quad .$$

Errors can arise from three and only three sources. First, and most likely, the observation D_x will be in error, due say to sampling bias, age misreporting, and underreporting of deaths. Errors here have a directly proportional effect on the estimate and we have no need to consider them here. We will assume that D_x has been correctly measured. Second, the model schedule f', which must be guessed, will be in error. It will deviate from the true f function by the function $\delta f = f' - f$. And third, the model schedule q', which must also be guessed, will be in error. It will deviate from the true q function by the function $\delta q = q' - q$. We may take these last two sources of error separately, for they are additive in differential form.

1. Error in f. Assume for the moment that the mortality function has been chosen correctly, that is, that q' = q. If f' deviates from the true fertility function f by δf, then the deviation in the estimate, $\hat{q}(M) - q(M)$, is approximated by the differential $\delta\hat{q}(M)[\delta f]$, evaluated at the function f. Using the quotient rule on (7.3), we can write the differential, at f, as

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[1] To see this, expand q(x-y) by Taylor series around q(x-A): $q(x-y) = q(x-A) + (y-A)q'(x-A) + O^2$. Whence $\int f(y)q(x-y)dy = q(x-A)\int f(y)dy + q'(x-A)\int (y-A)f(y)dy + O^2 \simeq q(x-A)$, since the second term is zero. Where q is relatively linear, this approximation is good.

$$(7.7) \qquad \delta\hat{q}(M) = -\frac{q(M)\int_0^x \delta f(y)q(x-y)dy}{\int_0^x f(y)q(x-y)dy} .$$

Calling $\delta\hat{q}/q$, the relative error, Err $\hat{q}(M)$, we have the result:

$$(7.8) \qquad \text{Err } \hat{q}(M) = -\frac{\int_0^x \delta f(y)q(x-y)dy}{\int_0^x f(y)q(x-y)dy} .$$

Knowing the form of δf, as we would in a given application, we could use (7.8) to calculate error bounds on the estimate.

We can gain further insight by using the approximation formula (7.5). Let A' be average age under the guessed schedule f'. Then we have

$$(7.9) \qquad \text{Err } \hat{q}(M) = -\frac{\int_0^x (f'(y)-f(y))q(x-y)dy}{\int_0^x f(y)q(x-y)dy} \simeq \frac{q(x-A) - q(x-A')}{q(x-A)} .$$

We can conclude that poor choice of the normalized fertility density f' matters if (i) the model density f' has an average age that differs from that of the true density f, and (ii) if the mortality function q is sloped around the age x-A (or its proxy, M).

2. *Error in* q. Now assume that the fertility model schedule has been guessed correctly, so that f' = f, but that the model mortality schedule q' deviates from the true schedule q by δq. Again using the quotient rule on (7.3) we obtain the differential caused in the estimate, $\delta\hat{q}(M)[\delta q]$ as

$$(7.10) \qquad \delta\hat{q}(M) = \delta q(M) - q(M)\frac{\int_0^x f(y)\,\delta q(x-y)dy}{\int_0^x f(y)q(x-y)dy}$$

so that, in this case

$$(7.11) \qquad \text{Err } \hat{q}(M) = \frac{\delta q(M)}{q(M)} - \frac{\int_0^x f(y)\,\delta q(x-y)dy}{\int_0^x f(y)q(x-y)dy} .$$

Again, using the average age approximation:

$$(7.12) \qquad \mathrm{Err}\ \hat{q}(M) \simeq \frac{\delta q(M)}{q(M)} - \frac{\delta q(x-A)}{q(x-A)} \quad .$$

We can conclude that error in choice of the model mortality schedule q' matters (i) if the estimation age M differs from the average age of the childhood deaths being reported, x-A, and (ii) if the model schedule has a shape different from the true one, so that the terms in (7.12) do not cancel.

Error expressions (7.7) and (7.11) carry specific implications for the robustness of the Brass technique: the model childbearing density f' should be chosen that its average age is close to that of the true density f; the model mortality schedule q' should if possible have the same shape as the true schedule q; M, the estimation age should be chosen equal to the average age of childhood deaths being reported, and not too small so that q is highly sloped around M. These conclusions are general.

We can go further with this type of analysis. The Brass technique rests on several specific assumptions, for example, that the mortality experience of the different cohorts entering the estimate is the same. Violated assumptions usually cause specific and characteristic errors in the choice of model schedules f' and q'. Their effect on the estimate can be analyzed (see Arthur and Stoto (1980)) via the error expressions developed in this section.

8. THREE FORMS OF LINKAGE ANALYSIS: SOME FURTHER REMARKS

Throughout this paper I have deliberately presented the various linkage expressions in the form of functional differentials. This is not the usual practice in sensitivity analysis and I owe the reader some explanation for this. There are three forms in which one can write the response to a change in function, each with a different purpose: the derivative, the differential, and the line integral.

For the models that interest us in demography, recall from (1.13) that the differential can usually be written as an inner product of some expression F'(z) with the driving perturbation δz:

$$\delta y = \int_0^{\omega} F'(z,a) \cdot \delta z(a)da \quad .$$

To be truely parsimonious, we need therefore only present and preserve the derivative F', it being a trivial matter to recover the differential by taking the inner product. This, in fact, is the usual way linkages are presented in physics or economics, at least when the driving change occurs in a single or vector variable. The differential though gives a clearer view of the linkage between the output variable and the function that alters it. It emphasizes that the change in y depends not only on the properties of F', but in this functional case also on the shape and character of the driving perturbation δz in the age or time pattern. This is why I have used the differential form.

The differential has one major disadvantage though. It is a first-order approximation, and thus is valid only to the extent the functional in question remains linear over the schedule or function being perturbed. It is perfectly serviceable for many numerical applications and it shows the structure of the linkage clearly and correctly; but it would not be always suited for high-precision arithmetic.

There is a closely connected form of result that is *exact* for large perturbations. This is the functional line integral. I shall not describe it in detail, but it works roughly as follows. Suppose instead of calculating the differential response to a full perturbation δz, we first allow only a scaled-down perturbation, $1/10\delta z$ say, and calculate the response to this. Now we update all parameters and functions, so that the initial function z_0 becomes $z_0 + 1/10\delta z$, and calculate the response to the next $1/10\delta z$, updating again and repeating this until we have arrived at the tenth and last $1/10\delta z$. As output we have ten smaller differentials in y, which we can add together to form a total differential δy. This new differential will be more accurate as a measure of the total change, since we have continually followed function and parameter changes as the function is perturbed. If we made the step size Δs smaller, 1/100 instead of 1/10, then 1/1000 instead of 1/100, this sum (under certain conditions) of the resulting small differentials will tend to a limit, which we can call, by analogy with standard calculus, an integral. It measures *exactly* the change in y. For the case $y = F(z)$, with $F'(z)$ known, with initial input function z_0 and final function z_1 and the difference $z_1 - z_0 = h$, we can, following this procedure, write the exact change in F as

$$(8.1) \qquad y(z_1) - y(z_0) = F(z_1) - F(z_0) = \int_0^1\int_0^\omega F'(z(a,s))h(a)\,da\,ds \quad ,$$

where

$$z(a,s) = z_0(a) + sh(a) \quad .$$

At the cost of a more complicated expression -- a double integral now -- the response to large changes in argument function is exact.

As illustration, suppose a not necessarily small change in the fertility schedule m_0, with the new schedule m_1 and the difference $m_1 - m_0$. Then using (2.4) and (8.1), the difference in intrinsic growth rates is

$$(8.2) \qquad r(m_1) - r(m_0) = \int_0^1\int_0^\omega \frac{e^{-r(m(s))a}p(a)(m_1(a) - m_0(a))\,da\,ds}{A_m(m(s), r(m(s)))}$$

where

$$m(s) = m_0 + s(m_1 - m_0) \quad .$$

This result, not an approximation, could be used to update the intrinsic growth rate in a precise numerical calculation, given an arbitrary change in the fertility schedule.

In sum, for efficient storage of information all we need is the functional derivative. For insight into the linkage mechanism itself the differential is clearest. And for high-precision numerical work or for large changes in the input schedules, we would need the more complicated integral. All three forms are related and are equivalent.

9. CONCLUSION

In this paper I have attempted to show that several classes of problems in mathematical demography fall into a common format--that of estimating or analyzing the linkage between certain aggregate variables of interest and changes in the age schedules or time sequences that describe individual demographic behavior. I have also attempted to provide a method that obtains closed-form expressions for such linkages. Several illustrations were shown: linkages of stable parameters to general changes in fertility and mortality schedules and to an age-shift in fertility; the transient response of the age composition and of vital rates to short-run changes in demographic behavior; and the analysis of errors in demographic estimation techniques. While much is known qualitatively about these linkages, in some instances with considerable analysis of special cases, the results in these notes apply more generally than before, and they are believed to be new.

There are several uses for linkage analysis. Not only do closed-form expressions for demographic linkages allow the analyst to compute changes--the difference that a new contraceptive would make for example--but they also afford him considerable qualitative insight into the mechanisms at work. They give him a story to tell, one whose structure may be impossible to discern without them. In some cases they are useful numerically; they offer a direct computational method for updating parameters without the repeated numerical solution of implicit equations. In other cases they lead to general statements, or theorems, on the response to change.

Throughout I have presented the various linkage mechanisms in the form of functional differentials. These, while they show the linkage clearly and are perfectly serviceable for many numerical purposes, are still, of course, first-order approximations to the true response. They hold best for marginal changes. Should we require the exact response to large changes in age or time schedules though, the line-integral form is available, albeit at extra computational and notational expense.

For the most part, in this exploratory paper I have chosen problems for analysis about which much is already known. This allowed us to compare our results with experience already gained on these problems. Several other problems could have been as easily looked at. For example, given an appropriate economic-demographic model it is possible to analyze the economic consequences of arbitrary changes in mortality risks (see Arthur (1979)). It would be possible also to look at the spatial consequences of changing migration patterns, or the economic consequences of changing labor-participation patterns. And given appropriate biological theory, it might be possible to investigate why the mortality and reproductive age-patterns of a given species should provide for evolutionary success.

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