The Determination of Mortality Rates from Observed Data

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DECLARATION

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ABSTRACT

This thesis considers the determination of the mortality rate q_x from full data for the year of age x to x+1 in which some lives enter or leave observation during the year of age. It commences with a survey of previous literature concerned with mortality rate estimators.

New aspects of the conventional actuarial, method of moments, product limit and maximum likelihood mortality rate estimators are identified and discussed. In particular, a fresh rationale of the conventional actuarial estimator is developed and it is argued that Hoem (1984) is incorrect in claiming that this estimator is flawed. It is also argued that Hoem's suggested approximated "operational moment relations" estimators are not satisfactory.

The rectangular hyperbolic mortality law, a two-parameter mortality law embracing three common mortality assumptions as special cases, is developed and investigated. Its application in the estimation of q_x is considered, including by means of the maximum likelihood estimation of the two parameters, a method included in the later simulations. Similar attention is also given to the Gompertz law.

A general theory of mortality rate estimators is developed which generates most, if not all, established mortality rate estimators that assume parametric mortality laws, particular estimators being obtained by the choice of appropriate weighting functions applied to the elements of the year of age. It is shown that all estimators, assuming a one-parameter mortality law, obtained from the general theory are asymptotically unbiased, when the correct mortality law has been assumed. Use of the general theory also identifies the mortality law assumptions for which different mortality rate estimators coincide.

A number of new mortality rate estimators are identified in the thesis, some through application of the general theory.

Computer models are used to generate simulated mortality data in order to examine the performance of a wide range of mortality rate estimators, including a number developed in the thesis. Among other things, the results support the view that the conventional actuarial estimator is not flawed.

CHAPTER I

Introduction

1.1 Introduction

The author of this thesis had been intrigued by the conclusion drawn by Hoem (1984), that there was a flaw in conventional exposed-to-risk theory, and although there seemed little alternative initially but to accept this disconcerting view, it gave a strong feeling of unease, particularly about the apparently accepted interpretation of the "conventional actuarial estimator". This estimator generally seems to be regarded as arising from a modified application of the method of moments, the essense of Hoem's argument being that the modification is unsatisfactory.

The author began to conjecture that it was not adequate to view the conventional estimator as a modified form of the method of moments estimator and that a better understanding of the conventional estimator ought to be possible.

It is believed that this has been achieved and one consequence is a conviction, contrary to Hoem (1984), that the conventional actuarial estimator is not flawed.

A number of further developments have flowed from the intellectual investigations stimulated by this initial work and are discussed in this thesis:

(a) The approximated "operational moment relations" estimators proposed by Hoem (1984) are not believed to be satisfactory.

(b) New aspects of the conventional actuarial, method of moments, product limit and maximum likelihood mortality rate estimators are identified and discussed.

(c) The rectangular hyperbolic mortality law, a two parameter mortality law embracing three common mortality assumptions as special cases, is developed and investigated.

(d) A general theory of mortality rate estimators is developed which enables most mortality rate estimators to be derived by a common method, each distinctive estimator being created by the particular choice of a variable weighting function.

(e) A number of new mortality rate estimators are developed, some through application of the general theory.

(f) The general theory leads to theoretical results concerning the asymptotic unbiasedness, or otherwise, of mortality rate estimators derived using the general theory, when one-parameter mortality laws apply, and to results concerning the mortality assumptions under which different mortality rate estimators coincide.

(g) Computer models are used to generate simulated mortality data in order to examine the performance of a wide range of mortality rate estimators, including a number developed in the thesis. Among other things, the results support the view that the conventional actuarial estimator is not flawed.

The development of the general theory of mortality rate estimators is regarded by the author as the most important result of the research reported in this thesis.

1.2 Structure of the thesis

Chapter 1 of the thesis introduces the area of research and presents a survey and discussion of previous literature concerned with mortality rate estimators.

Chapter 2 considers aspects of the conventional actuarial estimator and of the method of moments, product limit and maximum likelihood mortality rate estimators. Particular attention is paid to their rationales and, where appropriate, to the comments of Hoem (1984) who has alleged that there is a flaw in conventional exposed-to-risk theory. A further estimator design is also considered.

Chapter 3 introduces the rectangular hyperbolic mortality distribution, a two-parameter mortality law that embraces three common mortality assumptions as special cases. The properties of the distribution are investigated and it is applied in association with various statistical criteria to produce formulae for the estimation of q_x. Similar attention is also given to the Gompertz law.

Chapter 4 develops a general theory of mortality rate estimators which generates most, if not all, established mortality rate estimators that assume parametric mortality laws, particular estimators being obtained by the choice of appropriate weighting functions applied to the elements of the year of age. A wide range of such functions and their corresponding estimators are examined. Other theoretical implications of the general theory are also considered.

Chapter 5 describes the simulation studies that were undertaken in association with the theoretical work and presents a detailed review and analysis of the results obtained.

Chapter 6 sets out the important conclusions from the research.

Appendix I shows the derivation of a number of results, quoted in *Chapter* 3, relating to the rectangular hyperbolic mortality distribution.

Appendix II gives the printouts of the simulations, together with a key to the details shown.

Finally, the "*references and bibliography*" section follows.

1.3 Preliminary assumptions and definitions

This thesis will consider the determination from observed data of the value of the mortality rate q_x, ie the proportion of lives in the life table aged x exact who will die before reaching age x+1.

Throughout it will be assumed that full data is available about movements in and out of the observed population during the year of age from age x to age x+1.

Therefore we assume that, for the i^{th} life in the investigation, we know exactly the age $x+s_i$ at which the life entered the investigation ($0 \leq s_i < 1$) and the age $x+t_i$ at which the life left the investigation, and whether this was due to death or withdrawal ($0 < t_i \leq 1$) or by survival ($t_i = 1$).

Generally we will not distinguish between withdrawals whose exit at the observed value of t_i was scheduled to occur, of which "enders" in UK terminology is a major example, and those whose exit at the observed value of t_i was not scheduled in advance.

Throughout we will assume that the behaviour of a life is independent of the behaviour of any other life and that the force of mortality is a function only of age and is independent of any forces or influences causing a life to enter the investigation or to leave for a non-death reason.

Let us define the following symbols to represent various (sub) sets of the lives involved in an investigation to determine the mortality rate q_x for a certain age:

L is the subset of lives who entered the investigation at age x

I is the subset of lives who entered the investigation at age $x+s_i$ for any s_i such that $0 < s_i < 1$

D is the subset of lives who left the investigation by death

W is the subset of lives who left the investigation by withdrawal

S is the subset of lives who left the investigation by survival to age x+1

N is the set of all lives who are involved in the investigation in any capacity at some point.

When the context is appropriate, let L, I, D, W, S and N also represent the number of lives in each (sub) set.

We can immediately note that:

$$N = L + I = W + D + S \tag{1.1}$$

1.4 The "actuarial estimator"

Traditionally, given the data described, British and North American actuaries have calculated q_x using formulae based on "exposed-to-risk" techniques. As any past or present student of exposed-to-risk would be able to confirm, an appropriate formula using the data described would be:

$$q_x = \frac{D}{\sum_{SD}(1 - s_i) + \sum_{W}(t_i - s_i)} \tag{1.2}$$

In this expression for q_x, it can be seen that the divisor (known as the "exposed-to-risk") can be "interpreted" in terms of exposure time. Thus the interpretation could be made that survivors and withdrawals are "exposed" for the amount of time from the points at which they entered the year of age up to their points of exit, $\sum_{S}(1 - s_i)$ and $\sum_{W}(t_i - s_i)$ respectively, and that deaths are "exposed" for the amount of time from their points of entry up to the end of the year of age ($\sum_{D}(1 - s_i)$).

There are many texts giving an exposition of the techniques of exposed-to-risk including Gershenson (1961), Benjamin and Haycocks (1970), Batten (1978), Benjamin and Pollard (1980) and Puzey (1986).

Traditionally however, it would have been unusual for exact values of s_i and t_i to be used in an exposed-to-risk formula of this type because, firstly, the information was unlikely to be collected in this detail and, secondly, if it had been available, its processing as precise information would very probably have been far too labour intensive to be contemplated. And so, if the grouping assumptions involved appeared satisfactory, it is likely that equation (1.2) would have been modified to:

$$q_x = \frac{D}{L + \frac{1}{2}I - \frac{1}{2}W} \tag{1.3}$$

Viewed from the broader academic perspective, it is a little disconcerting that actuaries do not appear to have felt any need to create a name for this form of estimator of q_x.

However non-actuarial users of the estimator have noted the long history of use of this method of calculation within the actuarial profession and, in one form or another, the estimator has been referred to in recent decades by non-actuaries as the "actuarial estimator" or the method of estimation as the "actuarial method". The description "life table estimator" has also been used. Seal (1977) attributes the name "actuarial method" to the clinical researchers Berkson and Gage (1950).

Generally, by the names "actuarial method" or "actuarial estimator" etc, non-actuarial users, usually working in the fields of clinical, biological or reliability research, will be referring to a grouped function of the type in expression (1.3) and, because of the nature of the experiments or observations concerned, there are commonly no individuals entering the investigation during the year of age, so that the "actuarial estimator" is frequently expressed by non-actuaries in the form:

$$q_x = \frac{D}{N - \frac{1}{2}W} \tag{1.4}$$

$$\text{where} \quad N = L + I = W + D + S$$

Presentation of the "actuarial estimator", "actuarial method" or "life table estimator" in these broader research contexts can be found in Elandt-Johnson and Johnson (1980), Nelson (1982) and Kalbfleisch and Prentice (1980).

1.5 The Cantelli rationale of the "actuarial estimator"

Actuaries have been using formulae of the "actuarial estimator" type for a very long time, and it appears clear that this very successful method has existed for much longer than its most commonly accepted rationale.

As Seal (1954, 1961) reports, the first complete exposition of this rationale seems to have been given by Cantelli (1914) and therefore, for convenience, we will refer to the rationale as the "Cantelli rationale". This is not a description in general use.

The Cantelli rationale for deriving the "actuarial estimator" in the form of equation (1.2) will now be described. As will be seen, it involves two important steps.

Let us consider the mortality investigation. The number of deaths expected between age x and x+1 from the lives entering the investigation is:

$$\sum_{LI} {}_{1-s_i}q_{x+s_i} \tag{1.5}$$

where the summation is taken over those lives who are members of either the subset L or the subset I (all the lives in fact).

However some lives withdraw during the year of age and the number of deaths that would have been expected to occur after withdrawal and before age x+1 in respect of these withdrawals is:

$$\sum_{W} {}_{1-t_i}q_{x+t_i} \tag{1.6}$$

The first important step in calculating the conventional actuarial estimator is to equate the observed number of deaths D to:

$$\sum_{LI} {}_{1-s_i}q_{x+s_i} - \sum_{W} {}_{1-t_i}q_{x+t_i} \tag{1.7}$$

This first step clearly has the potential for controversy since at first sight it appears to be an attempt to apply the "method of moments" to the distribution of the number of deaths in the investigation, namely by equating first moments:

$$\text{expected deaths} = \text{actual deaths} \quad ,$$

whereas a few moments' thought will make it clear that expected deaths are not being

determined in accordance with conventional principles of calculating expected values, because the number of deaths expected to be lost from observation due to lives having withdrawn is being calculated as a function of the actual withdrawals which occur, and not as purely a function of the probability distributions involved.

This potentially controversial step appears to have been generally accepted in the actuarial profession although it has met strong and consistent criticism from Seal (1954, 1961, 1981b) and was the root of the paper by Hoem (1984), dramatically entitled "A flaw in actuarial exposed-to-risk theory". In Chapter 2 of this thesis, it will be argued that the method used to calculate expected deaths in the Cantelli rationale forms part of a satisfactory method of estimation in its own right, and the simulation results reported in Chapter 5 appear to confirm this.

The second important step in the Cantelli rationale is to develop the relationship:

$$\sum_{LI} {}_{1\text{-}s_i}q_{x+s_i} - \sum_{W} {}_{1\text{-}t_i}q_{x+t_i} = D \tag{1.8}$$

with the introduction of a mortality assumption, by expressing the probabilities of the form ${}_{1\text{-}r}q_{x+r}$ as a function of q_x and r. In the Cantelli rationale, the particular formula adopted for ${}_{1\text{-}r}q_{x+r}$ is:

$${}_{1\text{-}r}q_{x+r} = (1 - r)*q_x \tag{1.9}$$

This expression is known as the Balducci hypothesis or assumption, a name which it appears to have acquired as a result of a letter written by Balducci (1921) to the Journal of the Institute of Actuaries, in which, among other things, he demonstrated that the conventional actuarial method for calculating q_x is obtained when the step summarised in equation (1.8) was performed and followed by the assumption of the relationship (1.9).

As already implied, Balducci's letter was not the first exposition of the relationship (1.9) in this context, the complete rationale having already been set out of course by Cantelli (1914) and also, as London (1988) reports, having already been discussed by Balducci himself (1917).

The implication of the Balducci assumption is that mortality during the year of age from x to x+1 follows the following law:

$$\mu_{x+t} = \frac{q_x}{1 - (1 - t)*q_x} \quad , \quad 0 \leq t \leq 1 \tag{1.10}$$

It can be seen that this mortality law implies that μ_{x+t} falls over the year of age as t increases. Usually this is unrealistic but has been tolerated because of the very convenient formulae to which the assumption leads and because the effect of using the unrealistic assumption has not been regarded as having any seriously deleterious effect, in practical terms, in estimating q_x.

Obviously it is the unreality of the Balducci assumption that is the main objection raised by critics of the second step in the rationale.

Thus, applying the Balducci assumption to complete the derivation of the "full data actuarial estimator" (to use the description coined in Broffitt (1984)), we have:

$$D = q_x \sum_{LI} (1 - s_i) - q_x \sum_{W} (1 - t_i) \tag{1.11}$$

$$\Rightarrow \quad q_x = \frac{D}{\sum_{LI}(1 - s_i) - \sum_{W}(1 - t_i)}$$

$$= \frac{D}{\sum_{SD}(1 - s_i) + \sum_{W}(t_i - s_i)} \tag{1.12}$$

The Cantelli rationale appears to have become well established among British and North American actuaries by at least the 1940's. Expositions of the Cantelli rationale are in effect given in the papers by Wolfenden (1942), Beers (1943), Marshall (1945) and Bailey and Haycocks (1947), and in the texts by Gershenson (1961), Benjamin and Haycocks (1971), Batten (1978), Benjamin and Pollard (1980) and Puzey (1986).

1.6 The contribution of Wittstein (1862)

In fact Seal (1977) reports that the equating of observed deaths to expected deaths, with expected deaths being calculated on similar principles to those subsequently employed in the Cantelli rationale, had been described by Wittstein (1862).

As Seal (1977) reports, Wittstein (1862) considers a year of age running from age x to age x+1. He assumes that A lives start the investigation at exact age x, that B lives enter the investigation during the year of age and that C lives "escape from observation" during the year of age. It is assumed that d deaths occur during the year of age to this changing group of lives.

As Seal (1954) confirms, Wittstein (1862) aggregates deterministic and random exits from observation.

Seal (1977) describes further how Wittstein assumes that the two components of the difference (B – C) are each distributed uniformly over the year of age, so that (B – C) δt net exits are assumed to occur in the time element δt at age x+t (0<t<1). Wittstein gives an expression for the expected number of lives remaining under observation at age x+1 and equates this to the actual number of lives present at age x+1:

$$A(1 - q_x) + (B - C)\int_0^1 (1 - {}_{1-t}q_{x+t})\,dt = A + B - C - d \qquad (1.13)$$

This is of course equivalent to:

$$A\,q_x + (B - C)\int_0^1 {}_{1-t}q_{x+t}\,dt = d \qquad (1.14)$$

Thus it can be seen that Wittstein has determined expected deaths using observed non-death movements, and equated this expression to actual deaths applying similar principles to those used subsequently in the Cantelli rationale.

As Seal (1977) comments, Wittstein uses his equation to estimate q_x, having first expressed ${}_{1-t}q_{x+t}$ (0<t<1) in terms of q_x.

Seal (1977) reports that Wittstein chose two alternatives:

$${}_{1-t}q_{x+t} = \frac{q_x\,(1 - t)}{1 - t\,q_x} \qquad (1.15)$$

$${}_{1-t}q_{x+t} = 1 - (1 - q_x)^{1-t} \qquad (1.16)$$

It can be seen that equation (1.15) assumes the uniform distribution of deaths over the year of age, and equation (1.16) assumes a constant force of mortality over the year of age.

Seal (1977) further reports that, if either expression (1.15) or (1.16) is substituted in equation (1.13) and if the "log" item which arises in either integration is developed as a series, the following expression is obtained as a first approximation, as may be readily verified:

$$q_x \simeq \frac{d}{A + \frac{1}{2}(B - C)} \qquad (1.17)$$

Further Wittstein pointed out that the first neglected term is:

$$-\tfrac{1}{6}(B-C)\frac{d^2}{\{A+\tfrac{1}{2}(B-C)\}^3} \tag{1.18}$$

when equation (1.15) is used and that the first neglected term is half of this if equation (1.16) is used.

As Seal (1977) comments, in actuarial practice the value of expression (1.18) would be very small.

Thus Wittstein (1862) has derived a form of the actuarial estimator, namely expression (1.17), for the scenario he considers, but his expression arises as an approximate solution, reflecting the fact that he has not used the Balducci assumption.

Hoem (1984) reports that, in a paper entitled "The German and Italian contributions to exposed-to-risk: a historical review" then expected to appear, Seal had reported that Wittstein (1862) had first suggested the Balducci assumption, although the precise context is not specified. However the expected paper by Seal does not appear to have been published. In his published papers, Seal (1954, 1961, 1977, 1981a) does not appear to associate the Balducci assumption with Wittstein (1862), and this thesis will rely on the accounts given in those sources.

1.7 Seal's criticism of the Cantelli rationale, and his alternative approach

Seal (1961) regards the Cantelli rationale as incorrect because it does not apply the method of moments principle to the number of deaths in the investigation and he comments in particular on the exposure which is given to deaths among "prospective existings"; this refers to deaths occurring to lives who have been scheduled to leave the year of age before reaching age x+1, as for example in the case of lives who would have been enders before age x+1, if they had not died first.

It will be seen that in equation (1.2), which is of course consistent with the Cantelli rationale, a death which had been a "prospective existing" will receive "exposure" until the end of the year of age, notwithstanding the fact that, had he lived, the life could only have remained at risk of dying until his scheduled exit date, before the end of the year of age.

Seal plainly regards as unreasonable this exposure which is given to deaths among "prospective existings" as a consequence of the Cantelli rationale.

A contrary view, shared by the author of this thesis, is that the apparent exposure times arise fortuitously from the method of estimation concerned and are of no significance for individual lives, simply being convenient figures that arise at an intermediate stage in the calculation of the estimator, having an apparent but only partial interpretation in terms of "exposure" time. Batten (1978), for example, cautions his readers not to search for a logical interpretation of the result, advising that "the tendency of students to think of the result as illogical must be tempered with the realization that it is merely an automatic mathematical consequence of an assumption as to the pattern of mortality", although of course an equally essential factor is the statistical criterion used in estimating the mortality rate.

Seal (1954, 1961) argues that in a single decrement environment, an "unbiased" estimate of q_x is obtained by calculating:

$$\frac{D}{\sum_{N} (u_i - s_i)} \tag{1.19}$$

where u_i is the scheduled exit age of the i^{th} life $(0<i\leq 1)$.

This approach implies that the "exposures per life", ie the exposure times allocated to each individual life, are precisely those implied under the Cantelli rationale, except that a "prospective existing" which dies before the scheduled exit date will only be given exposure up to the scheduled exit date.

Unfortunately, the derivation of this estimator, using the method of moments approach, equating expected deaths to actual deaths, requires the relationship:

$$\sum_{N} u_i\text{-}s_i q_{x+s_i} = D \tag{1.20}$$

to be modified to:

$$q_x \sum_{N} (u_i - s_i) = D \tag{1.21}$$

which involves the purported relationship:

$$u_i\text{-}s_i q_{x+s_i} = (u_i - s_i)*q_x \tag{1.22}$$

As Broffitt and Klugman (1983) observe and Broffitt (1984) again states, there is no mortality distribution that satisfies this relationship. Indeed for general values of s_i and u_i,

it is a relationship which is self-contradictory; for example, consider a demonstration given by Slawski (1991):

$$u_i\text{-}s_i q_{x+s_i} = r_i\text{-}s_i q_{x+s_i} + r_i\text{-}s_i p_{x+s_i} * u_i\text{-}r_i q_{x+r_i} \tag{1.23}$$

Substitution from equation (1.22) gives:

$$u_i\text{-}s_i q_{x+s_i} = (r_i - s_i)\, q_x + (1 - (r_i - s_i)\, q_x)\,(u_i - r_i)\, q_x \tag{1.24}$$

$$\Rightarrow \quad u_i\text{-}s_i q_{x+s_i} = (u_i - s_i)\, q_x + (r_i - s_i)\,(u_i - r_i)\,(q_x)^2 \tag{1.25}$$

which contradicts equation (1.22) (unless $q_x = 0$).

However if $s_i = 0$ for all i, the relationship (1.22) is then true if the uniform distribution of deaths applies, while if $u_i = 1$ for all i, the relationship (1.22) is then true if the Balducci assumption applies. If both $s_i = 0$ and $u_i = 1$ for all i, the relationship (1.22) is then trivially true, but we are then considering a simple binomial distribution of deaths. However for general values of s_i and u_i, the relationship (1.22) appears never to be true (unless $q_x = 0$).

Seal (1954, 1961) describes his proposed estimator as "unbiased" but as, London (1988) states, it is in fact only "unbiased" under the approximation (1.22) used to derive it, and it is actually biased to the extent that the expression (1.22) deviates from the expression applicable under the mortality distribution to which the sample is actually subject.

When several forces of decrement operate, Seal (1954) suggests that a similar format of estimator be used to estimate the dependent rates of decrement; then the numerator is equal to the number of exits by the particular mode of decrement concerned and the exit ages on which the denominator is based are those scheduled to occur if none of the modes of decrement have operated.

In this application, the relationship (1.22) is imposed on the dependent rates, eg

$$u_i\text{-}s_i (aq)^d_{x+s_i} \simeq (u_i - s_i) * (aq)^d_x \tag{1.26}$$

By a letter written initially to the Society of Actuaries newsletter "The Actuary", Seal (1981b, 1984) stimulated a brief debate in the pages of ARCH concerning the Cantelli rationale and in particular the treatment of deaths among "prospective existings", but there does not appear to have been very much enthusiasm for Seal's position among the small

number of correspondents, Batten (1983), Beekman (1983), Broffitt and Klugman (1983), Edwards (1983) and Sohn (1983), to whom Seal (1984) responded in a further published letter. However, in giving a lucid discussion of method of moments procedures and of the criticisms of the Cantelli rationale for not using the method of moments, London (1988) is sympathetic to Seal's approach. It is a sympathy not shared in this thesis, which does not regard the non-use of the method of moments procedure by the Cantelli rationale as a matter for criticism.

Basically the situation appears to be that the concept of exposure time does not arise naturally from the application of the method of moments to the number of deaths in the investigation, and in order to create quantities interpretable, at least in part, as exposure time, it is necessary either to introduce an approximation which in general will never be correct for any mortality distribution, as in Seal's approach, or to adopt an alternative to the method of moments as in Cantelli's rationale.

In referring to the method of moments, the wry thought occurs that it is q_x that we are seeking to estimate and yet it is the first moment of another variable, the number of deaths in the investigation, that we apparently regard as so central to our approach, and which leads to some methods of estimating q_x being designated as "method of moments". There does not appear to be a tenable approach actually based on the first moment of q_x itself.

1.8 Other mortality assumptions: Greville (1978)

Batten (1978) indicated that the equations (1.27) and (1.28), which follow, arise from the Cantelli rationale if the Balducci assumption is replaced by either the assumption of a uniform distribution of deaths (equation (1.27)) or the assumption of a constant force of mortality (equation (1.28)). The expression relating to the uniform distribution of deaths had also been indicated by Gershenson (1961). Equations (1.27) and (1.28) are also of course closely related to the equations which Wittstein (1862) developed by substituting equations (1.15) and (1.16) respectively into equation (1.13).

$$L q_x + \sum_I \frac{(1 - s_i)\, q_x}{1 - s_i q_x} - \sum_W \frac{(1 - t_i)\, q_x}{1 - t_i q_x} = D \qquad (1.27)$$

$$L q_x + \sum_I \{1 - (1 - q_x)^{1-s_i}\} - \sum_W \{1 - (1 - q_x)^{1-t_i}\} = D \qquad (1.28)$$

(L denotes the number of lives who start the year of age at age x exact, as was defined in

Section 1.3).

As is apparent, expressions (1.27) and (1.28) both provide equations in q_x which in general can only be solved by numerical methods and there is no evident possibility of formulating a set of "exposures-per-life" which could be used to calculate a quantity which on division into the number of observed deaths would give an estimate of q_x. This again reflects the experience of Wittstein who produced approximate solutions.

Greville (1978) sought modifications of the "actuarial method" in which the generally unrealistic Balducci assumption was replaced by either the uniform distribution of deaths assumption or the "constant μ" assumption but with the system of "exposures-per-life" still retained in a suitably modified form, thereby keeping the convenience of calculating an exposed-to-risk in order to evaluate q_x.

He reported two different sets of possible "exposures-per-life" for the uniform distribution of deaths assumption, one of which was unfortunately impracticable in application (as discussed in Section 2.3 of this thesis) though the other, proposed by D Schuette, was certainly practicable (as also discussed in Section 2.3 of this thesis), and in addition a set for the "constant μ" assumption that provided an exposed-to-risk to estimate μ, in fact the familiar "central" exposed-to-risk.

Unfortunately, it is probably fair to say that the derivation of all of these alternative sets of "exposures-per-life" owed more to the ingenuity of the algebraic manipulation or to the creative interpretation of algebraic expressions than to consistent adherence to a statistical criterion, and the precise statistical criterion by which each procedure estimated q_x was not apparent from the derivation, nor established in the paper.

The starting point of all of the new derivations was to equate actual deaths with expected deaths, the latter being determined as in the Cantelli rationale, but subject to the revised mortality assumption. However in each case the Cantelli rationale is not maintained due to the subsequent algebraic manipulation or to the way in which relevant expressions are subsequently interpreted.

The reader is referred to Greville (1978) for the full details of these derivations, although an indication of the points of departure from the Cantelli rationale is briefly given below.

In the case where the "uniform distribution of deaths" assumption leads to the impractical set of "exposures per life" (version (a) in Section 2.3 of this thesis), the following sequence of development is applied to the deaths between ages x+t and x+1, associated with lives entering/exiting at age x+t:

$$\text{“expected” deaths} = \text{actual deaths} \tag{1.29}$$

$$\Rightarrow \quad (\text{“expected” deaths})*(1 - {}_tq_x) = (\text{actual deaths})*(1 - {}_tq_x) \tag{1.30}$$

$$\Rightarrow \quad (\text{“expected” deaths})*(1 - {}_tq_x) + (\text{actual deaths})*{}_tq_x = \text{actual deaths} \tag{1.31}$$

At this point, the “uniform distribution of deaths” mortality assumption is introduced and Greville shows that the left-hand side of equation (1.31) can then be re-expressed in the form:

$$\text{“exposure”}*q_x \tag{1.32}$$

By interpreting the expression for “exposure”, Greville obtains a set of suggested exposures per life. However the transfer of the “(actual deaths)$*{}_tq_x$” item in equation (1.30) to the left-hand side, to give equation (1.31), means that the expression implied for expected deaths on the left-hand side of equation (1.31) will no longer conform to the original Cantelli definition when exposures relating to different values of t are added.

In the case where the “uniform distribution of deaths” assumption is applied in the method proposed by D Schuette (version (b) in Section 2.3 of this thesis), the method commences with the following representation of the Cantelli principle:

$$D = \int_0^1 h(x + t)\, \mu_{x+t}\, dt \tag{1.33}$$

where h(x+t) denotes the number of persons under observation at exact age x+t.

With the introduction of the “uniform distribution of deaths” mortality assumption, the following expression for E_x in “$E_x*q_x = D$” is obtained:

$$E_x = \int_0^1 h(x + t)\, dt + \int_0^1 t\, h(x + t)\, \mu_{x+t}\, dt \tag{1.34}$$

In obtaining sets of “exposures per life” from this approach, Greville (1978) interprets the second integral in terms of the “exposure per life” to be associated with *actual* deaths whereas it is actually an expression relating to the exposure of lives *expected* to die. This means that the original determination of “expected” deaths on Cantelli principles has been modified by this interpretation of the exposure.

In the case where the “constant μ” assumption is used, Greville departs from Cantelli

principles in his interpretation of the "expected" number of deaths per life after age x+t associated with lives entering/exiting at age x+t, namely in his interpretation of the expression:

$$\int_0^{1-t} {}_sp_{x+t}\, \mu_{x+t+s}\, ds = \mu \int_0^{1-t} {}_sp_{x+t}\, ds \qquad (1.35)$$

Greville interprets the right-hand side in terms of "μ times *actual* exposure", ie in terms of the alleged effect on the quantity $\mu\, E_x^c$, after age x+t, of these lives who enter/exit at age x+t. Thus a quantity relating to the *expected* exposure of lives is interpreted in terms of the *actual* exposure of lives and again the original determination of "expected" deaths on Cantelli principles has been modified by the way in which the exposure is interpreted.

Thus these new methods of estimation were not on the same statistical criteria as the Cantelli rationale used for the original Balducci based "actuarial method", and it also explains how it was possible for Greville to obtain two different sets of "exposures-per-life" when using the uniform distribution of deaths assumption. The original Cantelli principle had been modified in two different ways, so as to produce estimation calculations which conformed to two different statistical criteria. Greville discusses the difference in terms of the mechanics of the calculations, but does not refer to this more fundamental aspect.

With regard to the central exposed-to-risk when used to estimate μ, assumed constant, and hence to estimate q_x, it can be readily shown, as in Section 2.22 of this thesis, that this arises from the combination of the criterion of "maximum likelihood" with the "constant μ" assumption and it is apparent from equation (1.28) that the same estimator is not obtained by correctly combining the statistical principle in the Cantelli rationale with the "constant μ" mortality assumption.

Further discussion of the "exposures-per-life" derived in Greville (1978) will be given in Chapter 2 of this thesis (Sections 2.3–2.4).

Greville (1978) also gives a description of the product limit estimator.

1.9 Hoem's criticism of the "actuarial estimator"

Hoem (1980, 1984) responded to Greville (1978) in a letter to ARCH, published in 1980, and subsequently expanded his comments in his 1984 paper.

In effect Hoem (1980, 1984) pointed out that the established derivation of the conventional actuarial estimator of q_x did not conform to the method of moments applied to the number

of deaths in the investigation, and he concluded that the derivation of this estimator uses a faulty argument, stating the fault to be that entries and exits had been incorrectly treated symmetrically in that entries and (non-death) exits were treated as contributing expected deaths conditionally on being respectively entries and exits, whereas for correct expectations, expected deaths not observed after exits should be conditional on lives being entries, not exits.

In this regard of course, Hoem (1984) makes essentially similar points as in Seal (1954, 1961).

Hoem is uncompromising in rejecting the "faulty argument" and concludes that: "correct reasoning leads to much more complicated formulas, which makes the conventional procedures lose their appeal". He suggests the use of the central exposed-to-risk to estimate μ under the assumption that the force of mortality is constant over the year of age, this procedure being derived by maximum likelihood and having the attractions being "a classical and simple alternative".

Hoem (1980, 1984) also gives "correct moment relations" for the uniform distribution of deaths assumption and the Balducci assumption but, in order to do this, he has to assume that associated with every life in the mortality investigation there is an age $x + \tau_i$ at which the life is predestined to withdraw if he does not die first. Of course for many lives τ_i may well be 1. The age $x+\tau_i$ is thus the maximum age at which the i^{th} life can exit from the investigation.

Of course, if lives are subject to random withdrawals, the values of τ_i in respect of deaths are not known, and those for withdrawals are only available by observation during the investigation.

For the uniform distribution of deaths and Balducci assumptions respectively, the "correct moment relations" are:

$$\sum_N \frac{\tau_i - s_i}{1 - s_i\, q_x}\, q_x = D \tag{1.36}$$

$$\sum_N \frac{\tau_i - s_i}{1 - (1 - \tau_i)\, q_x}\, q_x = D \tag{1.37}$$

Thus the values of q_x solving these equations are the correct "method of moments" estimators under the respective assumptions.

It can be seen that in both these cases, the moment estimator given in Seal (1954, 1961) for q_x, if there is no force of withdrawal present, ie all withdrawals are scheduled, namely:

$$q_x = \frac{D}{\sum_N (\tau_i - s_i)} \quad , \tag{1.38}$$

will be positively biased relative to the correct "method of moments" estimator (assuming the population mortality distribution is as assumed).

Hoem proceeds to develop his "correct moment relations" by making the approximation that:

$$\tau_i = t_i + (1 - t_i)\, D_i \tag{1.39}$$

where:

$D_i = 0$ if the i^{th} life is not an exit by death

$D_i = 1$ if the i^{th} life is an exit by death

It can be seen that equation (1.39) provides the correct value of τ_i if $D_i = 0$, but always gives $\tau_i = 1$ if $D_i = 1$, which will not, in general, always be correct.

As a consequence of this development, Hoem presents the following approximate "operational moment relations" for the uniform distribution of deaths and Balducci assumptions respectively:

$$\sum_N \frac{(t_i - s_i) + (1 - t_i)\, D_i}{1 - s_i\, q_x}\, q_x = D \tag{1.40}$$

$$\sum_N \frac{(t_i - s_i) + (1 - t_i)\, D_i}{1 - (1 - t_i)\,(1 - D_i)\, q_x}\, q_x = D \tag{1.41}$$

The approximation used by Hoem appeared clearly unsatisfactory to the author of this thesis, since some deaths would surely have withdrawn earlier than age $x + 1$, had they not died, and therefore the expression for "expected deaths" for a given q_x is overstated; therefore, in order to achieve equality when this expression for "expected deaths" is equated to actual deaths, the implied value of q_x is lower than that which would have been applicable without the distortion to "expected deaths".

It therefore appears that the approximation used in the "operational moment relations"

given in Hoem (1984) will introduce a negative bias, and the estimates of q_x obtained using this estimator in the simulation studies reported in Chapter 5 of this thesis (see Section 5.20) do indeed display a pronounced negative bias when the mortality distribution to which the simulated lives are subjected is the same as that assumed in the estimator.

In Section 2.9 of this thesis, Bayes Theorem will be applied to show that Hoem's approximation implies that:

$$\tau_i - s_i q_{x+s_i} = 0 \qquad \text{if } \tau_i < 1$$

which can also be deduced intuitively.

Slawski (1991) has also argued that these estimators are unsatisfactory as her analysis shows that the average maximum age of deaths, ie the average value of $x+\tau_i$ for deaths, which Hoem effectively assumes to be x+1, should be less than x+1.

Hoem (1984) also gives equations defining the maximum likelihood estimators of q_x for the three mortality assumptions of uniform distribution of deaths, Balducci and "constant μ", and it is clear that, for the first two of these, q_x can in general only be determined by numerical methods, whereas for the assumption of "constant μ", q_x is obtained from:

$$q_x = 1 - e^{-\mu} \tag{1.42}$$

where:

$$\mu = \frac{D}{\sum_N (t_i - s_i)} \tag{1.43}$$

ie in this case, μ is obtained using the central exposed-to-risk.

The derivation of equation (1.43) is given in Section 2.22 of this thesis. Section 2.22 also quotes the formulae for the maximum likelihood estimators of q_x using the uniform distribution of deaths assumption and the Balducci assumption (equations (2.73) and (2.74) respectively).

Hoem (1984) comments that the equations defining the maximum likelihood estimators of q_x for the uniform distribution of deaths and Balducci assumptions appear "reminiscent" of his earlier approximate "operational moment relations" but do not "coincide" with them.

One feature which Hoem (1984) fails to observe is that, after rearrangement, his equation (12) defining the maximum likelihood estimator of q_x under the uniform distribution of deaths assumption is identical with his equation (3A) defining the conventional actuarial

estimator based on the uniform distribution of deaths assumption, an estimator which he has uncompromisingly rejected for using the Cantelli expected deaths principle!

Hoem's equation (3A):

$$m(0)\,\tilde{q}_x + \sum_t m(t)\,\frac{(1-t)\,\tilde{q}_x}{1-t\,\tilde{q}_x} = D \qquad (1.44)$$

Hoem's equation (12):

$$\sum_i \frac{(1-D_i)\,t_i\,\hat{q}_x}{1-t_i\,\hat{q}_x} - \sum_i \frac{s_i\,\hat{q}_x}{1-s_i\,\hat{q}_x} = D \qquad (1.45)$$

[In Hoem's notation, m(t) is the net number of lives entering the year of age at duration t (net entries = entries minus non-death exits), $\tilde{q}_x$ is the value of the conventional estimator, D_i is a variable taking the value 0 if the i^{th} life becomes a non-death exit and the value 1 if the i^{th} life exits by death, $\hat{q}_x$ is the value of the maximum likelihood estimator and s_i, t_i, D have similar interpretation as in this thesis.]

The fact that $\tilde{q}_x$ and $\hat{q}_x$ in the above equations are identical will be demonstrated in Section 2.23 of this thesis.

No reference has been found in the literature in which the fact has been recognised that the conventional and maximum likelihood estimators under the uniform distribution of deaths assumption are identical. This identity will be demonstrated in this thesis by three different analyses (see Sections 2.23, 3.12 and 4.7); it arises most neatly as a trivial implication of the theory developed in Chapter 4, as demonstrated in Section 4.7.

As indicated earlier, it will be argued in Chapter 2 of this thesis that the method used to calculate expected deaths in the Cantelli rationale represents part of a satisfactory method of estimation in its own right.

1.10 Method of moments derivation of the conventional actuarial (Balducci) exposure formula: Broffitt and Klugman (1983)

Broffitt and Klugman (1983) provide a derivation of the conventional actuarial estimator which takes as its starting point the application of the method of moments principle to the deaths in the investigation. Necessarily a modification is introduced during the development. The argument put forward by Broffitt and Klugman follows the lines set out

below.

Applying the method of moments definition of "expected deaths" to the i^{th} life:

$$E(D_i) = {}_{\tau_i - s_i}q_{x+s_i} \tag{1.46}$$

where D_i, τ_i, s_i are as defined in Section 1.9.

$$\Rightarrow \quad E(D_i) = {}_{1-s_i}q_{x+s_i} - {}_{\tau_i - s_i}p_{x+s_i} * {}_{1-\tau_i}q_{x+\tau_i} \tag{1.47}$$

$$= (1 - s_i)\, q_x - E(W_i)\,(1 - \tau_i)\, q_x \tag{1.48}$$

applying the Balducci assumption and where $W_i = 1 - D_i$.

For all lives:

$$\text{Expected deaths} = \left[\sum_N (1 - s_i) - \sum_N \{E(W_i)\,(1 - \tau_i)\} \right] q_x \tag{1.49}$$

As Broffitt and Klugman (1983) state, the modification that produces the usual estimator is to replace $E(W_i)$ by W_i, so that:

$$\text{"Expected deaths"} = \left[\sum_N (1 - s_i) - \sum_W (1 - t_i) \right] q_x \tag{1.50}$$

It will be noted that, for withdrawals, $t_i = \tau_i$ where t_i is the observed duration at exit.

Broffitt (1984) also gives this argument.

Slawski (1991) applies a similar argument to produce the corresponding result for a general mortality distribution and, on the basis of this, argues that Hoem (1984) is wrong in asserting that actuarial exposed-to-risk theory is flawed.

In Chapter 2 of this thesis, an alternative rationale for the actuarial estimator will be deduced which does not depend on using a modified method of moments argument.

1.11 The product limit estimator

The product limit estimator is mainly attributed to Kaplan and Meier (1958) although

earlier it had been proposed by Böhmer (1912), with similar proposals being made subsequently by Linder (1935), as Seal (1981) reports, and by Meier (1953), and the Böhmer proposal had been discussed by Seal (1954).

In order to define the product limit estimator, let us suppose that there are n+2 durations, during the year of age from age x to x+1, at which non-death movements occur, comprising durations 0 and 1, and n intermediate durations at which lives enter or make non-death exits. Note that more than one person may be involved in entering or exiting at any of the durations. Let the n+2 durations be labelled from r = 0 to r = n+1.

Let P_r^2 be the total population of lives present at the r^{th} duration immediately before the movement(s) occur, and let P_{r+1}^1 be the total population of lives present immediately after the movement(s) at the r^{th} duration. If any deaths occur exactly at the r^{th} duration ($1 \leq r \leq n+1$), these deaths will be considered to have occurred before the population P_r^2 is counted.

Then the product limit estimator of q_x is given by:

$$q_x = 1 - \prod_{r=1}^{n+1} \frac{P_r^2}{P_r^1} \tag{1.51}$$

An alternative but equivalent method of calculation is given by:

$$q_x = 1 - \prod_{D} \frac{P_j - 1}{P_j} \tag{1.52}$$

where P_j is the population existing in the year of age immediately before the j^{th} death occurs and it is assumed that no deaths occur simultaneously. Should d' deaths occur simultaneously, one term in the product, of the form:

$$\frac{P' - d'}{P'} \quad ,$$

would deal with the d' lives where P' is the population existing in the year of age immediately before the deaths of the d' lives occur.

It will be noted that the product limit estimator does not require the use of a mortality assumption expressed in the form of a formula involving one or more parameters which have to be estimated.

Instead it is effectively assumed that the behaviour of a life when unobserved can be represented by the average behaviour, at the corresponding points of the year of age, of the lives which are observable.

The price for this is that there must always be appropriate data available for every point of the year of age to define the average behaviour of lives. This means that, if there are no surviving lives present at a point of the year of age, there must have been at least one life previously present in the year of age and the most recent exit of a life must have been an exit by death.

This means that, in theory at least, the product limit estimator is not always defined and cannot always be calculated.

Mortality assumptions based on parametric equations do not suffer this restriction since data available from just part of the year of age can be used to fit a formula representing the force of mortality to the whole of the year of age.

Kaplan and Meier (1958) explain that their choice of the name "product limit" arises because "this estimate is a limiting case of the actuarial estimates", ie the product limit estimator is a limiting case of the use of the principle of the actuarial estimator.

It can be seen that the product limit estimator can be interpreted as applying the principle of the actuarial estimator to each period between non-death movements to estimate the probabilities of death and survival during these periods, the probabilities then being combined to provide estimates of the probabilities of death and survival during the whole period covered by the product limit estimator. Because, by definition, there are no non-death movements during the periods between non-death movements, no mortality assumption is needed to determine the actuarial estimates.

1.12 Bias of the product limit estimator

Kaplan and Meier (1958) present an apparent demonstration that the product limit estimator is supposedly unbiased but then point out that the demonstration is flawed since it ignores the fact that the product limit estimator may not always be defined.

The exclusion of certain mortality experiences, because this has resulted in the estimator being undefined, will generally mean that those cases where the estimator can be defined represent a biased selection from all possible mortality experiences.

Admittedly, as Kaplan and Meier indicate, the probability of a situation occurring in which the product limit estimator is not defined is generally very small. But since the possibility exists, however remotely, Kaplan and Meier do not present the product limit estimator as unbiased, unlike one or two subsequent writers, eg Broffitt (1984), London (1988).

The following very simple example demonstrates how bias can arise.

Consider a species of animal which is such that an individual which survives to age x then has probability of 0.9 of surviving to age $x+\frac{1}{2}$, and an individual which survives to age $x+\frac{1}{2}$ then has probability of 0.9 of surviving to age x+1.

Suppose that we have two such individuals A and B each aged x and that we will observe both animals up to age $x+\frac{1}{2}$ and that we will then observe animal B only to age x+1, perhaps because animal A is scheduled for a terminal appointment with the researcher's scalpel at age $x+\frac{1}{2}$.

Table 1.1 summarises all the possible outcomes that would arise, if animal A would have continued to be observed through period 2 (age $x+\frac{1}{2}$ to age x+1), if it had survived through period 1 (age x to age $x+\frac{1}{2}$).

Table 1.1 Product limit estimator:
Summary of possible outcomes in animal A and B example

Out-come	Deaths in Period 1	Deaths in Period 2	Probability of outcome	Value of q_x according to the PL estimator: A included in period 2	Value of q_x according to the PL estimator: A excluded in period 2
(1)	(2)	(3)	(4)	(5)	(6)
a	none	none	.6561	0.0	0.0
b	none	A	.0729	0.5	0.0
c	none	B	.0729	0.5	1.0
d	none	A&B	.0081	1.0	1.0
e	A&B	—	.0100	1.0	1.0
f	A	none	.0810	0.5	0.5
g	A	B	.0090	1.0	1.0
h	B	none	.0810	0.5	not defined
j	B	A	.0090	1.0	not defined
			1.0000		

Column (4) gives the probability of each outcome, column (5) gives the estimate of q_x provided by the product limit estimator for each outcome assuming A would continue to be

observed through period 2 if A had survived period 1, while column (6) gives the estimate of q_x provided by the product limit estimator assuming A would not continue to be observed through period 2 if A had survived period 1.

It will be noted that if A dies in period 1 (outcomes *e*, *f* and *g*), the estimate of q_x provided by the product limit estimator is the same whether or not A would have continued to be observed in period 2 in event of its survival.

Where B dies in period 1 but A survives (outcomes *h* and *j*), the product limit estimator is undefined if A is not to be observed in period 2.

Where A survives period 1 and the other life does as well (outcomes *a*, *b*, *c* and *d*), the expected value of the product limit estimator conditional on this joint survival of period 1 is the same, whether A is observed during period 2 or not, since we have at least one life to observe during period 2 and the expected rate of death during period 2 will be the same irrespective of the number of lives studied.

When A is assumed to be observed in period 2 if A survives period 1, the expected value of the estimate of q_x provided by the product limit estimator is:

$$\begin{aligned} E(\mathring{q}_x) &= 0.0*.6561 + 0.5*(.0729 + .0729 + .0810 + .0810) \\ &\quad + 1.0*(.0081 + .0100 + .0090 + .0090) \\ &= 0.19 \end{aligned}$$

This is obviously the appropriate result since the probability of an individual animal dying between age x and x+1 is:

$$1 - (1 - 0.10)^2$$

If we now consider the situation where A is not observed in period 2 even if A survives period 1, the expected value of the estimate of q_x provided by the product limit estimator, conditional upon the product limit estimator being defined, is:

$E(\mathring{q}_x|\text{PLE is defined}) =$

$$\frac{\{0.0*.6561 + 0.5*.0810 + 1.0*(.0729 + .0081 + .0100 + .0090)\}}{(1 - .0810 - .0090)} = 0.1544$$

Clearly in this extremely simple example, there is a severe negative bias in the estimate of q_x provided by the product limit estimator.

In the example, it can be seen that the relevant effect of excluding those outcomes where the product limit estimator is not defined (outcomes *h* and *j*) is to exclude outcomes in which the period 1 experience had one life dying out of two, when the probability of a life dying was only 0.1, ie in calculating our expected value of the product limit estimator conditional upon the product limit estimator being defined, we excluded some experience that was heavier than that expected on the basis of the population mortality rates. Hence we obtain a negatively biased expected value of q_x.

It can be seen that if the probability of a life dying in period 1 had been greater than 0.5, we would have been excluding experience which is lighter than that expected on the basis of the population mortality rates and so in this case we would obtain a positively biased expected value of q_x. Thus it appears that the product limit estimator can be either negatively or positively biased.

Broffitt (1984) gives a purported proof of unbiasedness of the product limit estimator that appears to run along very similar lines to the demonstration given by Kaplan and Meier which they explain is flawed.

His argument seeks to show the unbiasedness of the expected value of the estimate of q_x conditional on a given set of ages at withdrawal, entry and forced withdrawal, and assumes firstly that, given this set of ages, the year of age will be split into the same periods between the non-death movements for all realisations and that secondly all realisations in earlier periods can be allowed, for the given set of ages, whereas in fact realisations in earlier periods cannot be allowed if they result in the product limit estimator being undefined, through there being no surviving lives left to carry on after a non-death exit.

That the first of these assumptions is wrong is illustrated by outcome *e* in the simple example, where the product limit estimator would be based on one period covering the year of age, whereas Broffitt's method of proof would seem to assume in the simple example that the split into period 1 and period 2 is immutable.

That the second of these assumptions is wrong is illustrated by outcomes *h* and *j* which cannot be allowed as the product limit estimator is then undefined.

Working backwards through the year of age, the Broffitt proof argues for each period in turn that the proportion surviving the period is independent of the proportions surviving in earlier periods, which appears reasonable if the proportion is defined, but also argues that the expected value of the proportion surviving the period is unbiased, which is unlikely to be true if some realisations of the proportion surviving have to be excluded to ensure that the product limit estimator is defined over the entire year of age.

In fairness, it should again be emphasised that for all but the very smallest experiences, the probability of the product limit estimator being undefined is normally very tiny, so that in the very great majority of mortality investigations the product limit estimator can be treated as effectively unbiased.

London (1988) also states without qualification that the product limit estimator is unbiased, but does not offer any argument in support of this.

1.13 Maximum likelihood estimators

Estimators which use the maximum likelihood criterion to estimate parameters of distributions have an important role in the theory of statistical estimation.

As summarised for example by Wonnacott and Wonnacott (1977), under mild conditions a maximum likelihood estimator has the following properties:

(a) Asymptotic unbiasedness and variance tending to zero as sample size increases. Therefore a maximum likelihood estimator also has the weaker property of consistency.

(b) An asymptotic distribution which is normal.

(c) Asymptotic efficiency, ie among the class of consistent estimators that have normal asymptotic distributions, there is none that has a variance smaller than that of the maximum likelihood estimator when the sample size is large.

Larson (1982) defines consistency as follows:

> "Let Γ be an estimator for γ, based on a random sample of size n. If
>
> $$\lim_{n \to \infty} \text{Prob}\,(|\Gamma - \gamma| \geq \epsilon) = 0 \qquad \text{for any } \epsilon > 0,$$
>
> then Γ is a consistent estimator for γ."

It should be emphasised that in general maximum likelihood estimators are biased, notwithstanding the property of asymptotic unbiasedness.

Broffitt (1984) presents a unified treatment of maximum likelihood estimators for q_x, derived from models which make allowance for withdrawals. As Broffitt states, the major

reason for considering maximum likelihood estimators is that they are asymptotically efficient under mild conditions.

Broffitt presents maximum likelihood estimators for the "full data" case which is the situation considered in this thesis, and also for the "partial data" case in which only the number of withdrawals and deaths during the year of age are known and not the exact ages at exit. Broffitt considers two withdrawal models reflecting two types of assumption about withdrawals: a random withdrawal model in which unforced withdrawals occur at durations which are random variables, and a fixed withdrawal model in which unforced withdrawals occur at durations which are fixed but unknown. ("Forced" withdrawals refer to withdrawals scheduled to occur at known fixed times, such as enders.)

For the full data situation, Broffitt finds the likelihood to be the same under the fixed withdrawal model as under the random withdrawal model, so that for a particular mortality assumption, the two models yield the same maximum likelihood estimator. He shows derivations of maximum likelihood estimators in these scenarios for the "constant μ" mortality assumption and the uniform distribution of deaths mortality assumption. The derivations for these mortality assumptions in the case of the full data random withdrawal model are also given in Sections 2.22 and 2.23 of this thesis.

Broffitt reports that most of the maximum likelihood estimators he presents have been previously derived by other writers, for example: Steelman (1968), Elveback (1958), Chiang (1961, 1968) and Elandt-Johnson and Johnson (1980).

Broffit also discusses, but does not derive, the product limit estimator and also compares four estimators by means of their asymptotic properties and the use of simulation. The four estimators are the maximum likelihood estimator for the "constant μ" assumption and full data, the product limit estimator and two versions of the actuarial estimator (for full data and for partial data).

A possibility discussed by one or two writers is to estimate more than one parameter relating to a mortality distribution using maximum likelihood.

Grenander (1956) considers, among other things, the use of the method of maximum likelihood to estimate the three parameters A,B and c in the Makeham formula:

$$\mu_x = A + Bc^x \tag{1.53}$$

Powell (1984) applies the method of maximum likelihood firstly to obtain estimators for the parameters c_r ($r = 1, 2, \ldots k$) when the force of mortality is given by:

$$\mu_x = c_1 + c_2 x + ... + c_k x^{k-1} \qquad (1.54)$$

and secondly to obtain estimators for the parameters α and λ when the Weibull distribution applies:

$$\mu_x = \alpha \lambda x^{\alpha-1} \qquad (1.55)$$

In both cases, Powell takes the partial differential of the log-likelihood with respect to each parameter and, setting each derivative to zero, obtains a system of simultaneous equations to be solved for the estimate of each parameter. Powell suggests possible methods of solution in sampling situations for the polynomial mortality law (1.54) and gives an iterative procedure for the Weibull law (1.55). Powell tests the iterative procedure for the Weibull distribution using simulation and the method is found to perform satisfactorily.

London (1988) presents the method of maximum likelihood as one of several possible methods for estimating both parameters in two parameter mortality laws, and illustrates this for the Weibull law. Slawski (1991) differentiates the log-likelihood in the full data situation when the Gompertz law $\mu_x = Bc^x$ applies, to obtain two simultaneous equations in the estimates of the parameters B and c.

1.14 Maximum likelihood derivation of the product limit estimator

There appear to be conflicting interpretations as to whether the product limit estimator is a maximum likelihood estimator.

Kaplan and Meier (1958) apply the principle of maximum likelihood in order to select from the class of admissible distributions the population distribution of ages at death and non-death movement which best fits the observed data and they show that this leads to the product limit estimator.

Broffitt (1984) does not give a derivation of the product limit estimator but states that the product limit estimator is the full data maximum likelihood estimator of q_x in the random withdrawal model if the distributions of the random times to death and withdrawal are discrete, or in the fixed withdrawal model if the distribution of the random time to death is discrete.

London (1988) interprets the product limit estimator of q_x as the product of a sequence of maximum likelihood estimators, but states categorically that the product limit estimator itself is not a maximum likelihood estimator. Elandt-Johnson and Johnson (1980) also

show the derivation of the product limit estimator as a product of maximum likelihood estimators, each relating to a very short time element.

Kalbfleisch and Prentice (1980) recognise that the Kaplan and Meier approach represents a generalisation of the usual concept of maximum likelihood used in parametric models and refer to the product limit estimator as a "non-parametric maximum likelihood estimator", which also reflects comments in Kaplan and Meier (1958).

1.15 Bias and consistency of the "actuarial estimator" and of other estimators of q_x

Breslow and Crowley (1974) have shown that the actuarial estimator in the form:

$$q_x = \frac{D}{N - \frac{1}{2}W} \tag{1.56}$$

is generally inconsistent. They assume a random withdrawal model which does not admit the possibility that lives may enter observation after the beginning of the interval over which q_x is measured (ie after the beginning of the year of age in actuarial applications).

They show that the estimator (1.56) is consistent if and only if it is consistent when all individuals are due for withdrawal before the end of the year of age (or its non-actuarial equivalent), and this leads to their Theorem 1 which gives a general form for the mortality/failure distribution that must apply if the estimator is to be consistent. This distribution is a function of the distribution of the random variable denoting the durations at which withdrawals are due (the "censoring distribution").

If the censoring distribution is uniform, the required mortality distribution for consistency of the estimator (1.56) is one in which, among other things, the force of mortality decreases with increasing age. Breslow and Crowley (1974) quote results obtained by Crowley (1970) concerning the asymptotic bias of the estimator (1.56) when the censoring distribution is uniform, firstly when the mortality assumption is "constant μ", and secondly when the mortality assumption is the uniform distribution of deaths. In both cases the asymptotic bias of the estimator is negative, the bias being greater when the uniform distribution of deaths assumption applies.

At least two writers, Elandt-Johnson and Johnson (1980) and London (1988) state without qualification that the actuarial estimator is negatively biased. Elandt-Johnson and Johnson (1980 page 157) appear to base their statement on Breslow and Crowley (1974) while London (1988 page 129) refers specifically to Breslow and Crowley (1974) and Broffitt

(1984) while also implying that there are other unspecified confirmatory references.

Broffitt (1984) conducts simulations, which include the actuarial estimator, assuming either that the mortality distribution and the censoring distribution are both uniform or that both are exponential (ie constant forces of decrement). Again the model does not admit the possibility that lives may enter observation after the beginning of the year of age. Broffitt's results are consistent with the view that the estimator (1.56) is negatively biased for the mortality distribution and censoring distribution considered.

The evidence does not appear to rule out however the possibility that the actuarial estimator (1.56) could be positively biased for other appropriate mortality and censoring distributions. For example, the results quoted in Breslow and Crowley (1974) suggest that, when the censoring distribution is uniform, the most plausible guess is that the estimator (1.56) would be positively biased for suitable mortality distributions in which the force of mortality decreases more rapidly with increasing age than in the mortality distribution indicated by their Theorem 1 as giving the estimator (1.56) the property of consistency.

In general, it does not appear satisfactory merely to specify that an estimator is unbiased, or positively biased, or negatively biased, without specifying the assumptions for which these results are believed to apply. The case of the "unbiased" method of moments estimator proposed by Seal (1954, 1961) is a further example of this arguably misleading practice.

Two likely factors contributing to bias in the actuarial estimator (1.56) can be identified.

Firstly it will be noted that the actuarial estimator in the form:

$$q_x = \frac{D}{N - \frac{1}{2}W} \tag{1.57}$$

is an approximation (with no entries into observation during the year of age) to the full data actuarial estimator, which is the description coined in Broffitt (1984) for:

$$q_x = \frac{D}{\sum_{SD}(1 - s_i) + \sum_{W}(t_i - s_i)} \tag{1.58}$$

$$= \frac{D}{\sum_{N}(t_i - s_i) + \sum_{D}(1 - t_i)} \tag{1.59}$$

$$= \frac{D}{\sum_{N}(1 - s_i) - \sum_{W}(1 - t_i)} \tag{1.60}$$

The full data actuarial estimator can be derived using the Cantelli rationale incorporating the Balducci mortality assumption. It follows from a result to be shown in Section 4.13 of this thesis that the full data actuarial estimator is asymptotically unbiased when applied to data from a population subject to the Balducci mortality assumption, and that more generally any estimator derived using the Cantelli rationale, but incorporating a different mortality assumption, will be asymptotically unbiased if used with a population subject to the same mortality assumption.

It would hardly be surprising if the introduction of an approximation into the formula were thereby to introduce asymptotic bias.

It is to be noted that if a similar approximation were made for example in evaluating Seal's proposed moment estimator, one might anticipate that a similar effect might occur in that estimator also.

A second likely source of asymptotic bias in the actuarial estimator is its use with populations which are not subject to the Balducci assumption. Plainly when we apply an estimator which has been derived assuming a particular mortality assumption to data from a population subject to another mortality assumption, we are in effect applying an estimator designed for one statistical distribution to data from another statistical distribution, and it would hardly be surprising if this produces an asymptotically biased result.

Clearly if we consider an alternative estimator to the actuarial estimator, the alternative may also suffer asymptotic bias for precisely similar reasons as in the actuarial estimator. In particular, when we consider maximum likelihood estimators, and are especially attracted by their asymptotic properties, we have to bear in mind that their attractive properties will only be obtained if the assumptions underlying the maximum likelihood estimator are realised in its application, for example only if a maximum likelihood estimator which assumes a particular mortality distribution is applied to a population subject to the distribution.

Indeed, Breslow and Crowley (1974) have pointed out that "while large sample properties for such estimates may be derived from the corresponding likelihoods, these can only be expected to hold under the assumed model", and Elandt-Johnson and Johnson (1980) have commented that "these properties depend on the model being a sufficiently accurate presentation of reality". Elandt-Johnson and Johnson (1980) have also pointed out that "even if the model is valid, the desirable properties are *asymptotic* — they apply when the volume of data is sufficiently large, and it is not always clear what is "sufficiently large"".

The fact that the actuarial estimator has a uniquely long history of use doubtless reflects its

ease of calculation and its apparently acceptable performance. Generally most maximum likelihood estimators of mortality parameters appear to be difficult to calculate without the use of numerical methods and computer facilities, although the estimator of μ which assumes a constant force of mortality is an obvious exception; however even in this latter example, the required central exposed-to-risk is more demanding to calculate than the initial exposed-to-risk for the full data actuarial estimator, because the exposure of the deaths must be calculated precisely, and not merely taken to the end of the year of age.

And if one were to calculate the central exposed-to-risk under the same circumstances in which the initial exposed-to-risk has in the past been approximated by the introduction of the "$\frac{1}{2}$" factors, the same approximation would obviously be made to the central exposed-to-risk, doubtless with similar apparent adverse consequences for the estimator's asymptotic unbiasedness.

Apart from maximum likelihood alternatives to the actuarial estimator, there is also of course the product limit estimator. As already discussed, this is effectively unbiased for all but the very smallest experiences, and this unbiasedness is not subject to any assumptions about the mortality distribution. However it is only with the advent of computerised data manipulation that the calculation of the product limit estimator has become a practicable proposition for any data volume beyond the smallest experiences.

At this point, it is of interest to note that, in the simulations discussed in Section 5.26, the full data actuarial estimator (or "Balducci" conventional estimator) appears to be positively biased for all population mortality distributions in which the force of mortality has a more positive gradient than in the Balducci mortality assumption, the amount of bias decreasing as the Balducci assumption is approached. When the Balducci mortality assumption applies in the population, any bias which might be present appears too small to be distinguished in the simulation results from the random fluctuations.

As already commented, the apparent bias must be considered, among other things, as a function of all the parameters of the investigation. Doubtless, some would be surprised that a negative bias is not manifested. However none of the writers who comment on the bias of the actuarial estimator in the form (1.56) appear to consider the possible effect, among other things, on an appropriately generalised form of the estimator of allowing lives to enter observation after the beginning of the year of age.

Roberts (1987) considered theoretically the bias involved in estimating q_x using the full data actuarial estimator when the mortality law applicable in the population is different from the Balducci mortality assumption. He similarly considered the bias involved in estimating m_x using the "constant μ" maximum likelihood estimator of μ when the

mortality law applicable in the population is different from "constant μ"; here the estimator of m_x is taken as the expression which we earlier identified as the maximum likelihood estimator of μ when the "constant μ" mortality law applies (Section 1.9), and this is of course correct if the "constant μ" mortality law applies:

$$m_x = \frac{D}{\sum_N (t_i - s_i)} \tag{1.61}$$

However in order to facilitate his analysis, Roberts assumes that the number of lives exposed to risk of dying during any element of the year of age is non-random and that, in addition, the expected value of the full data actuarial estimator of q_x can be approximated satisfactorily as the expected value of the number of deaths observed in the investigation divided by the expected value of the initial exposed-to-risk (which depends on the number and timing of deaths occurring as well as on the number of lives exposed to risk in any element of the year of age).

These are obviously important assumptions which may affect the levels of bias apparently detected and analyzed, although Roberts comments that the assumptions are adequate provided the number of decrements is not too large relative to the number of lives in the experience, and he refers the reader to Roberts (1986) for further justification.

Given these important assumptions, Roberts' analysis leads to the following conclusions:

(a) When the Balducci mortality assumption holds in the population, the full data actuarial estimator is unbiased.

(b) When the "constant μ" assumption holds in the population, the "constant μ" maximum likelihood estimator provides an unbiased estimate of m_x.

(c) When the uniform distribution of deaths assumption holds in the population, the proportional bias (ie bias as a proportion of the true q_x or m_x value) in the full data actuarial estimator of q_x is about twice the proportional bias in the "constant μ" maximum likelihood estimator of m_x).

(d) If the force of mortality does not fall over the year of age, the full data actuarial estimator will be subject to greater bias than m_x.

(e) The proportional bias in both estimators are about the same for extremely concave or convex survival functions (l_x curves).

Plainly, some or all of these conclusions may be subject to modification if the approximations inherent in Roberts' assumptions are taken into account. A result obtained in Section 4.13 of this thesis indicates that the above conclusions (a) and (b) are asymptotically exact.

Forfar, McCutcheon and Wilkie (1988) report that, in constructing the new mortality tables based on the 1979–82 CMI experience, the Executive Committee of the Continuous Mortality Investigation Bureau decided that the "constant μ" maximum likelihood estimator should be used to estimate the force of mortality. This was a break from the previous practice when q_x was estimated assuming the theory of the full data actuarial estimator. (It should be noted, however, that in both cases the required exposed-to-risks were determined approximately using a census method).

Among the arguments advanced for this change were the views put forward by Hoem (1984) and the analysis of Roberts (1987). As has been commented, Hoem's criticisms of the full data actuarial estimator are based on theoretical considerations whose validity will be argued against in this thesis, and Roberts' conclusions are subject to important assumptions which are likely to introduce approximation. However the simulation studies reported in Chapter 5 of this thesis do suggest that the "constant μ" maximum likelihood estimator may be subject to less bias than the full data actuarial estimator when the mortality law in the population is different from that assumed in the estimator, for most mortality laws likely to be encountered in practice in the population (see Section 5.26).

Forfar et al (1988) also appear to demonstrate that the "constant μ" maximum likelihood estimator is unbiased if the "constant μ" assumption applies in the population but, as in Roberts (1987), this is achieved because the central exposed-to-risk is taken as non-random; for, according to equation (2.4.14) in Forfar et al, the expected value of μ^*, the estimator of μ, is derived as follows:

$$E[\mu^*] = E[A/R] = E[A]/R = \mu R/R = \mu$$

where R represents the central exposed-to-risk and A represents the actual number of deaths.

This author is not aware of any other work, apart from these approximate analyses of Roberts (1987) and Forfar et al (1988), that indicates that the "constant μ" maximum likelihood estimator is unbiased for finite sample sizes when applied to a population in which the "constant μ" mortality law applies.

1.16 Terminology and notation

The discussion in this thesis is presented from the point of view of an actuary concerned with the evaluation of q_x relating to human life, and terminology and notation familiar to actuaries is generally used. However it will be obvious that much of the material discussed is likely to be equally relevant to biostatisticians, whether concerned with animal or human mortality, and to engineering reliability scientists, concerned with failure rates of components, machines and engineering systems in general.

While the general principles underlying the estimation of mortality/failure rates will be common to all fields of research, there are differences in the methodology, terminology and notation which has come into use.

For example there are differences in the mortality/failure laws which are appropriate in the different fields, there are differences in the measures conventionally used to express the phenomenon of mortality/failure/survival, and there are differences in the nature of the data typically gathered.

With regard to the last of these points, the actuary typically observes a human being over only a relatively small fraction of that person's lifetime and typically has to contend with significant numbers of people entering observation during the year of age, or rate year, and with significant numbers of people exiting for non-death reasons during the year of age, or rate year.

In contrast, the reliability scientist or biostatistician may be able to observe systems/components/animals for their entire lifetimes, may not suffer the entry of any lives into observation equivalent to the actuary's "new entrants" or "beginners" and might conduct investigations in which observations are terminated at a point determined by the experience, for example when the observed number of deaths/failures equals a pre-specified number.

Those who are interested in gaining familiarity with methodology, terminology and notation used by non-actuaries will find appropriate accounts in Elandt-Johnson and Johnson (1980), which has an especially strong human biostatistical perspective, Nelson (1982), where the perspective is strongly from the point of view of the reliability scientist, and Kalbfleisch and Prentice (1980), where the intention is to serve as a text both in the analysis of failure data and in biostatistics and statistics. Lee (1992) also deals with the analysis of biostatistical data and consciously emphasises applications over rigorous mathematics. London (1988) gives an account that is written primarily for actuaries, but which also seeks to be of interest to a broader audience and includes consideration of study designs encountered by

clinical statisticians and reliability engineers.

1.17 Censored/truncated data

Actuaries are very used to dealing with data in which there are significant numbers of lives entering, or exiting for non-death reasons, during the year of age; indeed, it would probably be regarded as rather a novelty to have data in which one or both features were absent. Perhaps because it is very much the norm, British actuaries have not evolved any general technical terms to describe such features, other than the description of the particular lives as beginners, new entrants, withdrawals or enders.

As intimated in Section 1.16, practitioners in other fields may be more likely to encounter data without such features, but they may also meet a wider variety of formats of data in which lives are absent for part of the time from observation for non-death or non-failure reasons. The terms "censored" and/or "truncated" are used by practitioners in other fields, to describe such loss of observation, generally qualified by the use of further descriptive words reflecting different forms or mechanisms of loss of observation. The terminology/usage may differ slightly between different fields, and even between different authorities.

Thus, data where survivors are not observed beyond a certain point appear to be generally described as "censored on the right", as for example in Nelson (1982). Thus in the actuarial context, "enders" and "withdrawals" represent such data in the calculation of q_x.

However Elandt-Johnson and Johnson (1980) would use "censored" to refer only to data where observation ceases when a preassigned number of deaths has occurred, and would use "truncated" to refer to data where observation ceases at a predetermined time.

The expression "censored on the left" appears to be generally used to refer to the situation where it is only known that an individual has already died/failed before a certain time, ie before observation commenced, as for example in Nelson (1982) and Cox and Oakes (1984).

Cox and Oakes (1984) use the term "left-truncation" to describe the situation where individuals come under observation only some known time after the natural time origin of the phenomenon under study. As they explain, had the individual failed before the truncation time in question, that individual would not have been recorded. Thus in the actuarial context, "beginners" and "new entrants" represent left-truncated data in the calculation of q_x.

CHAPTER II

Aspects of some mortality estimators and their rationales

2.1 The "actuarial estimator" again

As we have seen in Section 1.5, the estimator for q_x given by traditional exposed-to-risk theory in the form described by Broffitt (1984) as the "full data actuarial estimator", is:

$$q_x = \frac{D}{\sum_{SD}(1 - s_i) + \sum_{W}(t_i - s_i)} \tag{2.1}$$

$$= \frac{D}{\sum_{N}(t_i - s_i) + \sum_{D}(1 - t_i)} \tag{2.2}$$

$$= \frac{D}{\sum_{N}(1 - s_i) - \sum_{W}(1 - t_i)} \tag{2.3}$$

As previously commented, it can be seen that the divisor, known as the "exposed-to-risk", can be presented in terms of exposure time. Survivors and withdrawals are "exposed" for the amount of time from their points of entry into the year of age up to their points of exit, $\sum_{S}(1 - s_i)$ and $\sum_{W}(t_i - s_i)$ respectively, while deaths are "exposed" for the amount of time from their points of entry up to the end of the year of age, $\sum_{D}(1 - s_i)$.

This very convenient interpretation of the "exposed-to-risk" as the summation of so much exposure time per life, where the amount of time per life depends on the subset of lives to which the life belongs, is seen as a major advantage of adopting the generally unrealistic Balducci mortality assumption in deriving the "actuarial estimator".

However it perhaps carries the risk that the user may be blinded to the fact that these rations of exposure time per life do not represent any sort of fundamental truth but are simply a consequence of the method of equating the number of observed deaths to the expression based on "expected" deaths, together with the assumption made about the behaviour of μ_{x+t} over the year of age.

We are simply considering a method of estimation and this thesis supports the view, already set out during the discussion in Section 1.7, that the apparent exposure times arise fortuitously from the method of estimation concerned and are of no significance for individual lives, simply being convenient figures that arise at an intermediate stage in the calculation of the estimator.

2.2 The conventional estimator

The "actuarial estimator" is derived by applying what we have termed for convenience the "Cantelli rationale". In Section 1.8, we considered the effect of replacing the Balducci mortality assumption in the Cantelli rationale by alternatives, namely the uniform distribution of deaths or a constant force of mortality, and equations (1.27) and (1.28) were obtained.

Henceforth in this thesis we will refer to an estimator derived using the method of the Cantelli rationale, but incorporating any mortality assumption, as a "conventional estimator", the characteristic of a conventional estimator thus being that it uses the statistical criterion of the Cantelli rationale in equating actual deaths to an expression for "expected deaths" in which the "expected" loss of deaths from observation after non-death exit is calculated using the numbers of actual non-death exits.

Thus the term "conventional estimator" will be used to refer to all estimators produced from the relationship:

$$D = \sum_{LI} {}_{1-s_i}q_{x+s_i} - \sum_{W} {}_{1-t_i}q_{x+t_i} \qquad (2.4)$$

no matter what formula is assumed to express ${}_{1-r}q_{x+r}$ in terms of q_x and r, ie no matter what mortality assumption is made.

2.3 Other sets of "exposures per life"

As described in Section 1.8, Greville (1978) sought modifications of the "actuarial method" in which the generally unrealistic Balducci assumption was replaced by either the uniform distribution of deaths assumption or the "constant μ" assumption but the system of "exposures-per-life" still retained in a suitably modified form, thereby keeping the convenience of calculating an exposed-to-risk in order to evaluate q_x.

He reported two different sets of possible "exposures-per-life" for the uniform distribution of deaths assumption, one of which was unfortunately impractible in application though the other, proposed by D Schuette, was certainly practicable, and a set for the "constant μ" assumption.

In deriving these sets of "exposures-per-life", the Cantelli rationale (subject to the modified mortality assumption) was not maintained meaning that none of the estimators involved are conventional estimators.

For the "constant μ" assumption, the set of "exposures-per-life" given in Greville (1978) defines the central exposed-to-risk and, when μ is constant, the central exposed-to-risk corresponds to the maximum likelihood estimator of μ, as is readily shown, as for example in London (1988). Then μ is estimated by:

$$\mu_x = \frac{D}{\sum_N (t_i - s_i)} \tag{2.5}$$

ie, to evaluate this estimator, the "exposure per life" for every life in the investigation is $(t_i - s_i)$.

We will now consider the two sets of exposures per life presented in Greville (1978) for the uniform distribution of deaths assumption (hereafter called the "level deaths" assumption). The second set of exposures per life arose from the method of derivation proposed by D Schuette.

The two sets of exposures per life are summarised below.

(a) "Level deaths" assumption: Exposures per life - Version (a)

(1) Any life who does not die during the investigation, and also does not subsequently die between age $x + t_i$ and age $x + 1$, receives an exposure per life equal to $(t_i - s_i)$ which includes the cases where $s_i = 0$ and/or $t_i = 1$.

(2) Any life who dies during the investigation receives an exposure of 1

(3) Any life who dies after leaving the investigation at age $x + t_i$ but before age $x + 1$ receives an exposure of nil.

(b) "Level deaths" assumption: Exposures per life - Version (b)

(1) Any life who does not die during the investigation receives an exposure per life equal to $(t_i - s_i)$ which includes the cases where $s_i = 0$ and/or $t_i = 1$.

(2) Any life who dies during the investigation receives an exposure per life of $(t_i - s_i) + t_i = 2t_i - s_i$.

As has already been suggested in Sections 1.7 and 2.1, in connection with the "actuarial estimator" (the Balducci conventional estimator), "exposures per life" are simply a convenient means of calculating the observed value of the estimator and again it is of no relevance to seek to place any form of rationalisation on the actual "exposures per life" applicable. (It will be noted for example that in version (b), category (2), the "exposure per life" can take values approaching 2).

As previously commented, the two sets of "exposures per life" differ because different estimators are concerned in the two versions.

It will be noted that version (a) of the "exposures per life" for the "level deaths" assumption is of limited practical use since it requires knowledge of whether a life who withdraws goes on subsequently to die before age x + 1. On the other hand, there are not any practical limitations to the application of version (b) of the exposures per life.

It is perhaps arguable whether the estimator which version (a) calculates is actually valid as an estimator, since it requires information which we do not apparently regard ourselves as having. It should perhaps be a prerequisite of an estimator that it uses information that is available!

If the information concerning whether or not withdrawn lives survive to age x+1 is in fact always available, "withdrawal" seems a quite pointless and redundant concept in version (a); it appears to this author that all lives who do not die before age x+1 could be regarded as remaining in the investigation until age x+1, receiving an exposure per life of $(1 - s_i)$ according to rule (1) of version (a), while those who die between age $x+s_i$ and age x+1 could be given an exposure per life of one year according to rule (2) of version (a). As no lives would now be regarded as withdrawals, rule (3) of version (a) would be redundant. In calculating the mortality rate, the numerator would now of course consist of all the deaths occurring between age $x+s_i$ and age x+1.

Basically, version (a) is a technique that cannot cope with a normal withdrawal scenario.

One conclusion that may be drawn from this is that, whatever method of estimation version (a) represents, it is not one of the well-known methods of estimation such as conventional, method of maximum likelihood or product limit, nor one of the new estimators developed in this thesis, since none of these have any difficulty in coping with a normal withdrawal scenario.

In Section 4.9 of this thesis, version (b) will be seen to be an example of a "time-count estimator", a type of estimator which will be identified using a new analytical approach.

2.4 "Level deaths" assumption: reconciliation of total "exposure" contributed by the deaths under version (a) and version (b) of the "exposures per life"

It is interesting to note that the total amounts of "exposure" expected to be contributed by the deaths, under version (a) and under version (b) of the "exposures per life", is the same if the "level deaths" assumption does indeed apply. (In calculating the "expected" exposure, it will be assumed that every life has a predestined age of non-death exit).

From the set of lives who enter the investigation at age $x + s$ and who die between the ages of $x + s$ and $x + 1$ including those who had already left the investigation before death, let us consider the subset of these lives who withdrew at duration t', or who would have done if they had not died first. In accordance with the "level deaths" mortality assumption, we will assume that the deaths of these lives are uniformly spread between ages $x + s$ and $x + 1$.

Then let:

$$k*(t' - s) \;=\; \text{the number of deaths occurring between age } x + s \text{ and } x + t'$$

$$k*(1 - t') \;=\; \text{the number of deaths occurring between age } x + t' \text{ and } x + 1$$

Therefore under version (a) of the "exposures per life", the total "exposure" contributed by these deaths is:

$$k\,(t' - s)*1 = k\,(t' - s).$$

And under version (b) of the set of "exposures per life", the total "exposure" contributed by these lives is:

$$\int_s^{t'} (2r - s)\,k\,dr + k\,(1 - t')*(t' - s)$$

where the integral is again based on the "level deaths" mortality assumption and recognises that the $k*\delta r$ deaths occurring in the segment $(r, r+\delta r)$, $s \leq r \leq t'$, each contribute an "exposure per life" of $(2r - s)$.

On evaluation, the expression for version (b) also gives the value $k*(t' - s)$ so that both sets of "exposures per life" lead to the same expected total contribution of "exposure" from this subset of lives.

Thus the expected total amount of exposure contributed to the investigation from lives who die between entering the year of age and age $x + 1$ is the same under both version (a) and version (b) of the "exposures per life". Further the exposure contributed to the investigation by lives who have entered the investigation and are still alive at age $x + 1$ (whether or not they have already left the investigation before age $x + 1$) is measured identically under both versions. Thus the expected total amount of exposure from all lives is the same under version (a) and version (b).

Of course the fact that the two versions of "exposures per life" give the same expected total amount of exposure does not give any indication that the expected values of the two estimators are the same.

2.5 "Exposed-to-risk" is a function of q_x

When we use "exposed-to-risk" methods to estimate q_x, we use an expression of the form:

$$q_x = \frac{D}{E_x} \tag{2.6}$$

where E_x is the "exposed-to-risk".

Alternatively, these formulae can be expressed in a form in which actual deaths are equated to an item of the form E_x*q_x.

It is important to realise that the item E_x generally depends, among other things, on q_x itself, so that potentially we might appear to have a "chicken and egg" situation. We require E_x to calculate q_x, but E_x is a function of q_x, which is a quantity we do not know.

The "exposures per life" methods deal with this apparent conundrum very neatly by reflecting the number, and possibly the timing, of the observed deaths in the calculation of E_x. Thus the observed deaths are a reflection of q_x (admittedly an imprecise reflection) and these are used in the calculation of E_x, thus bringing the influence of q_x into the

calculation of E_x. The fact that different mortality assumptions, or different methods of obtaining the estimator, lead to different sets of "exposures per life" is therefore reassuring since E_x is a different function of q_x for different mortality assumptions or different methods of obtaining the estimator.

2.6 A simple example illustrating the contention that E_x is generally a function of q_x

The assertion that E_x is a function of q_x will now be illustrated for a simple example.

Suppose N lives all enter an investigation at age $x + s$ and that each life will exit at age $x + t$ if he is still alive. $(0 \leq s < t \leq 1)$.

Note that this is a very special case in that we know the point at which the lives who die would have exited if they had not died. Generally we do not know this. This limited situation, which excludes new entrants and withdrawals at random durations, is being considered for simplicity.

Now, our conventional estimator is given by

$$N *_{1-s}q_{x+s} - (N - D) *_{1-t}q_{x+t} = D \tag{2.7}$$

where D is the observed number of deaths.

$$\Rightarrow \quad N\,({}_{1-s}q_{x+s} - {}_{1-t}q_{x+t}) = D\,(1 - {}_{1-t}q_{x+t}) \tag{2.8}$$

$$\Rightarrow \quad N\left(\frac{{}_{1-t}p_{x+t} - {}_{1-s}p_{x+s}}{{}_{1-t}p_{x+t}}\right) = D \tag{2.9}$$

$$\Rightarrow \quad N\left(1 - \frac{{}_{1-s}p_{x+s}}{{}_{1-t}p_{x+t}}\right) = D \tag{2.10}$$

$$\Rightarrow \quad N\,(1 - {}_{t-s}p_{x+s}) = D \tag{2.11}$$

$$\Rightarrow \quad N *_{t-s}q_{x+s} = D \tag{2.12}$$

So, in this special case, the criterion giving the conventional estimator is the same as the criterion giving the method of moments estimator. This is not generally the case.

In Section 2.10 of this thesis, an analysis will be presented which confirms that the

conventional estimator and the method of moments estimator will always give the same value if all lives are predestined to withdraw at the same point in the year of age if they do not die first.

Now $$N*_{t-s}q_{x+s} = D = E_x*q_x \tag{2.13}$$

However, for convenience in subsequent algebraic development, we will write this in the form:

$$N\left(1 - \frac{{}_{1-s}p_{x+s}}{{}_{1-t}p_{x+t}}\right) = D = E_x*q_x \tag{2.14}$$

Line (2.10) demonstrates that this form is correct.

Let us assume that the Balducci assumption applies.

Then $$N\left(1 - \frac{1 - (1 - s)q_x}{1 - (1 - t)q_x}\right) = \text{expected deaths}$$

$$\Rightarrow \quad \frac{N\,(t - s)q_x}{1 - (1 - t)q_x} = E_x*q_x \tag{2.15}$$

Thus $$E_x = \frac{N\,(t - s)}{1 - (1 - t)q_x} \tag{2.16}$$

Obviously E_x is a function of q_x.

If it is the case that E_x is a function of q_x when we have new entrants and withdrawals only entering or leaving the investigation each at a fixed point in the year of age, it seems unlikely that E_x would not remain a function of q_x in the more general scenario of new entrants and withdrawals occurring at random points in the year of age.

Note that in our scenario, we seem to have an "exposure per life" of:

$$\frac{(t - s)}{1 - (1 - t)q_x} \tag{2.17}$$

irrespective of whether the life exits as a death or not. However, it explicitly depends on q_x, which we do not know. And of course the purpose of evaluating E_x is so that we can evaluate q_x!

However from:

$$\text{Expected deaths} = N*_{t-s}q_{x+s} = \frac{N\,(t - s)\,q_x}{1 - (1 - t)\,q_x}\,, \tag{2.18}$$

we can write:

$$N*_{t-s}q_{x+s} - N*_{t-s}q_{x+s}\,(1 - t)\,q_x = N\,(t - s)\,q_x \tag{2.19}$$

$$\Rightarrow \qquad N*_{t-s}q_{x+s} = (N\,(t - s) + N*_{t-s}q_{x+s}\,(1 - t))\,q_x \tag{2.20}$$

$$\text{ie} \qquad E_x = N\,(t - s) + N*_{t-s}q_{x+s}\,(1 - t) \tag{2.21}$$

ie E_x can be calculated giving exposure per life of $(t - s)$ to all lives, plus additional exposure per life of $(1 - t)$ for the $N*_{t-s}q_{x+s}$ lives expected to die. Or, alternatively, we can say that E_x can be calculated using a total exposure per life of $(1 - s)$ for the $N*_{t-s}q_{x+s}$ lives expected to die, and exposure per life of $(t - s)$ for the rest.

So one practical way of evaluating E_x would appear to be to give exposure of $(1 - s)$ to the D lives who actually die, rather than to the $N*_{t-s}q_{x+s}$ lives expected to die, and exposure of $(t - s)$ to the rest.

This latter procedure is an estimation procedure, and arises from using actual deaths in place of expected deaths in expression (2.21). It is this step in association with the earlier mortality assumption and initial statistical criterion that creates the "exposures per life" of $(t - s)$ for survivors and $(1 - s)$ for deaths. These "exposures per life" are only relevant while we are using this estimation procedure and mortality assumption.

2.7 Exposures per life: some parting comments

We have seen that exposed-to-risk should be regarded as a function of q_x and, in formulating sets of "exposures per life" for calculating the exposed-to-risk in an investigation, we effectively replace expressions for exposures which are functions of q_x by alternative sets of exposures which reflect the dependence on q_x by requiring different exposures to be ascribed to lives that die and to lives that do not.

These alternative sets of "exposures per life", for the calculation of E_x, will be such quantities as are appropriate to ensure that the figure reached for the *total* exposure will be that appropriate for the method of estimation concerned. There is no need for a mechanism that ensures that the exposure apparently ascribed to an *individual* is reasonable and there is therefore no reason to expect that such a mechanism exists.

And the evidence indicates that generally there is no mechanism to ensure that the exposure apparently ascribed to an individual is reasonable. Thus, for example, when the Cantelli

rationale of the Balducci conventional estimator is expressed in terms of "exposures per life", we obtain the exposure ascribed to "prospective existings" which, as discussed in Section 1.7, Seal (1954, 1961, 1981b, 1984) found so unsatisfactory and, when we consider version (b) of the "exposures per life" for the "level deaths" mortality assumption given in Greville (1978) and discussed in Section 2.3, we see that deaths can receive an "exposure per life" of as much as nearly 2 years.

It should be clear that systems of "exposures per life" simply represent rules of thumb which happen to be conveniently available for calculating particular estimators and that the existence of this convenient method of calculation says nothing about the quality of the estimator concerned. They do carry the danger however that the user may be beguiled into thinking that there is a rational interpretation of the amounts of "exposure per life" and that, in some way, these are fundamental and absolute quantities.

2.8 The alleged flaw in the conventional estimator

Hoem (1984) contends that the conventional estimator for q_x is flawed because "expected deaths" is calculated taking account of the expected loss of observed deaths occurring to the lives who actually withdraw. He points out that this is not the statistical estimation method known as the "method of moments". Under the "method of moments" approach, "expected deaths" would be determined using a probability distribution which embraces withdrawals, as well as deaths, so that "expected deaths" would be determined using predictions of the withdrawals, and not the actual withdrawals.

Clearly there can be little argument that the conventional estimator is not the method of moments estimator. However, this author would dispute whether the conclusion drawn in Hoem (1984), that the conventional estimator is not a satisfactory estimator, is correct. In the view of this author, the arguments put forward in Hoem (1984) to criticise the theoretical basis of the conventional estimator are simply not relevant, because they apply the requirements of the "method of moments", as interpreted in Hoem (1984), to an estimator which is not a "method of moments" estimator.

The fact that an estimator would be acceptable if it is a method of moments estimator does not of course mean that an estimator would be acceptable only if it is a method of moments estimator.

In Sections 2.17 and 2.18 of this chapter, an interpretation of the conventional estimator will be presented which, in the opinion of the author, gives the conventional estimator a very rational theoretical basis (and one which does not depend on being a flawed version of

some other theoretical basis).

In addition, extensive simulation experiments have been conducted which, as reported in Chapter 5, appear to support strongly the view that the conventional estimator is very satisfactory. (The simulation results for the conventional estimator are discussed for example in Sections 5.19, 5.23 and 5.27).

2.9 Use of Bayes Theorem to show the theoretical inconsistency in the derivation of Hoem's suggested "operational moment relations"

In Section 1.9, an account has been given of the "operational moment relations", suggested by Hoem (1984), which rely on the approximation of assuming that all the lives who die would otherwise have continued in the investigation until age $x + 1$, ie would have been at risk of dying until age $x + 1$.

It was argued that this approximation was clearly unsatisfactory since some deaths would surely have withdrawn earlier than age $x + 1$, had they not died, and the argument lead on to the conclusion that the approximation creates a negative bias in the suggested estimators, a conclusion confirmed by simulation studies.

We will now see that Bayes Theorem can be invoked to show that it is unsatisfactory to assume that all lives dying would otherwise have continued in the investigation to age $x + 1$.

Consider the i^{th} life. Suppose that this life will leave the investigation at age $x+\tau_i$ $(0<\tau_i\leq 1)$ if he does not die first.

Let D_i be a function such that $D_i = 0$ if the i^{th} life does not die before age $x+1$, and let $D_i = 1$ if he does.

Then, in deriving his suggested "operational moment relations", Hoem (1984) assumed:

$$p(\tau_i=1|D_i=1) = 1$$

which gives:

$$p(\tau_i<1|D_i=1) = 0$$

Now, with this assumption, Bayes Theorem tells us:

$$p(D_i=0|\tau_i<1) = \frac{p(\tau_i<1|D_i=0)\ p(D_i=0)}{p(\tau_i<1|D_i=0)\ p(D_i=0)\ +\ p(\tau_i<1|D_i=1)\ p(D_i=1)}$$

$$= 1 \qquad \text{(noting that the second term in the divisor equals zero).}$$

$$\Rightarrow \qquad \tau_i - s_i q_{x+s_i} = 0 \qquad \text{if } \tau_i < 1$$

where the life enters the investigation at age $x+s_i$.

Quite apart from the obvious unreality of this, it also directly contradicts the mortality assumption on which the estimator is purportedly based, whatever form this mortality assumption takes.

2.10 The link between the conventional estimator and the method of moments estimator

An interesting feature of the simulation experiments reported in Chapter 5 of this thesis is that the conventional estimator and the method of moments estimator appear to give very similar values when the mortality assumption is correct, and in fact it can be seen theoretically that the values of the two estimators are likely to be very similar. (The similarity of the values of the conventional estimator and the method of moments estimator in the simulation studies is discussed in Sections 5.21 and 5.27).

Let us consider a mortality investigation in which we observe lives for all or part of the year from age x to age x+1. Let the typical life be observed from age $x+s_i$ $(0 \le s_i \le 1)$ up to age $x+t_i$ $(0 \le t_i \le 1)$.

Let us suppose for the purpose of analysis that the typical life will withdraw at age $x+\tau_i$ $(0 \le \tau_i \le 1)$, if the life has not died already. Thus, if the life exits by a cause other than death, we have $t_i = \tau_i$ but, if the life exits by death, we have $t_i \le \tau_i$.

Then the conventional estimator for q_x is the value of q_x which, in association with the assumed mortality law, solves the equation:

$$\sum_N {}_{1-s_i}q_{x+s_i} - \sum_W {}_{1-t_i}q_{x+t_i} = D \qquad (2.22)$$

which, since $t_i = \tau_i$ for all lives which exit by a cause other than death, can be re-expressed as:

$$\sum_{N} {}_{1-s_i}q_{x+s_i} - \sum_{W} {}_{1-\tau_i}q_{x+\tau_i} = D \tag{2.23}$$

The assumed mortality law will have the form:

$$\mu_{x+t} = f(\phi,t) \quad \text{where} \quad q_x = q(\phi)$$

Most plausible mortality laws are likely to be expressible in the form:

$$\mu_{x+t} = f(q_x,t)$$

and for simplicity of argument, we will assume that this is the case here, although similar conclusions, to those which follow here, would be reached in the more general scenario. (It is worth noting that ϕ could, possibly, be taken as m_x, μ_x or $\mu_{x+\frac{1}{2}}$).

We will rearrange equation (2.23) as follows:

$$\sum_{N} {}_{1-s_i}q_{x+s_i} - \sum_{N} {}_{1-\tau_i}q_{x+\tau_i} = \sum_{D} (1 - {}_{1-\tau_i}q_{x+\tau_i}) \tag{2.24}$$

$$\Rightarrow \quad \sum_{N} ({}_{1-\tau_i}p_{x+\tau_i} - {}_{1-s_i}p_{x+s_i}) = \sum_{D} {}_{1-\tau_i}p_{x+\tau_i} \tag{2.25}$$

$$\Rightarrow \quad \sum_{N} (1 - \frac{{}_{1-s_i}p_{x+s_i}}{{}_{1-\tau_i}p_{x+\tau_i}}) ({}_{1-\tau_i}p_{x+\tau_i}) = \sum_{D} {}_{1-\tau_i}p_{x+\tau_i} \tag{2.26}$$

$$\Rightarrow \quad \sum_{N} (1 - {}_{\tau_i-s_i}p_{x+s_i}) ({}_{1-\tau_i}p_{x+\tau_i}) = \sum_{D} {}_{1-\tau_i}p_{x+\tau_i} \tag{2.27}$$

$$\Rightarrow \quad \sum_{N} ({}_{\tau_i-s_i}q_{x+s_i}) ({}_{1-\tau_i}p_{x+\tau_i}) = \sum_{D} {}_{1-\tau_i}p_{x+\tau_i} \tag{2.28}$$

Now the method of moments estimator of q_x is the value of q_x which, in association with the assumed mortality law, solves the equation:

$$\sum_{N} {}_{\tau_i-s_i}q_{x+s_i} = D \tag{2.29}$$

ie

$$\sum_{N} {}_{\tau_i-s_i}q_{x+s_i} = \sum_{D} 1 \tag{2.30}$$

Thus the equation (2.28) which defines the conventional estimator differs from equation (2.30) which defines the method of moments estimator in that the contributions from the i^{th} life on either side of the equation (and note that the contribution on the right-hand side is either 0 or 1) are weighted by the factor ${}_{1-\tau_i}p_{x+\tau_i}$. It will now be argued that the modified method of moments equation given by equation (2.28) still provides an estimate of q_x.

Suppose that we had divided the year of age into a series of segments of age bounded by ages x, $x+r_1$, $x+r_2$, ... $x+r_n$, $x+1$ where obviously $0<r_1<r_2....<r_n<1$. Let us associate each life in the investigation with the segment in which his value of $x+\tau_i$ falls. Now the lives associated with a particular segment can be used to provide a self-contained sample to estimate q_x, since we can apply the method of moments principle to just these lives based on their experience during the whole investigation. Thus in respect of the experience of these lives, we write:

$$\text{Expected deaths} = \text{Actual deaths}$$

It will be noted that, since $x+\tau_i$ represents the latest age at which the i^{th} life will exit from the investigation, the contribution of expected deaths and actual deaths by lives associated with a segment can only relate to the period from entry into the year of age up to the segment, and the lives will contribute no experience relating to the year of age after the segment.

Nevertheless, even if we are using only the experience of the lives associated with just one segment of $x+\tau_i$ values, we are still able in theory to estimate q_x, which relates to the whole of the year of age, because we have assumed a law of mortality which in effect relates μ_{x+t} at any point in the year of age to q_x for the whole year of age.

We can create a bigger sample than that provided by a single segment by combining the data of many segments together to give combined values for "expected deaths" and "actual deaths", and these combined segments should provide a better estimator of q_x than individual segments, because of the increased sample size.

Since the data of any segment on its own can provide an estimate of q_x, we can give the data from different segments different weightings in the process of combination, in calculating expected deaths and actual deaths, and still have a combined sample which gives an estimate of q_x.

We can take this process to the limits of considering each segment as of elemental length, with a different weighting factor for each element, and of combining all elements of the year

of age together in this way to provide a single combined calculation of q_x based on all the data.

And what is more, this argument has not referred to the way in which the weighting factors vary over the year of age, ie to the relative size of the weights at different points in the year of age.

Now, in fact, we know that, in most mortality investigations, the weights ${}_{1-\tau_i}p_{x+\tau_i}$ will be very close to unity and will change very little as τ_i takes values from 0 to 1.

Because of this small variation in ${}_{1-\tau_i}p_{x+\tau_i}$ as τ_i varies, the estimate of q_x given by equation (2.28) is likely to be very similar to that given by the method of moments as defined by equation (2.30). (This assumes that there is a reasonable number of lives involved, so that any one individual life does not have a disproportionally large effect in the calculations). This conclusion appears to be borne out by the simulation studies.

It will however be noted that, when all lives in the investigation have the same value of τ_i, equation (2.28) simplifies to give equation (2.30), as the factor of ${}_{1-\tau_i}p_{x+\tau_i}$ for the single value of τ_i will cancel from both sides of the equation. In other words the conventional estimator and the method of moments estimator will then give the same value, as was observed to be the case in Section 2.10 in the example used to illustrate that E_x is a function of q_x.

In the view of this author, the preceding analysis gives strong evidence that the conventional estimator is very soundly based. And of course if the Balducci assumption in particular is accepted, the conventional estimator is very readily applied in practice, unlike in general the method of moments estimator.

Also, the method of moments generally requires a force of withdrawal to be assumed at every point of the investigation which, given the complex, changeable and often very unpredictable nature of the factors determining withdrawal rates (eg the abolition of life assurance premium tax relief), appears potentially very difficult, whereas the conventional estimator does not require any such assumption.

2.11 A search for an alternative to the conventional estimator

This author was initially persuaded by the arguments in Hoem (1984) that the conventional estimator was indeed unsatisfactory and set out to design an alternative approach which was not subject to the apparent objection.

Eventually the search brought the author back to the conventional estimator and to the strong conviction that this estimator was in fact very sound.

However, before this stage was reached, the author investigated two possible designs for estimators for q_x, which will be referred to as:

(1) the whole-year estimator
(2) the implication-B estimator

It was subsequently realised that the "whole-year" estimator was identical with the "product limit" estimator.

2.12 The whole-year estimator

The idea here was that the mortality rate should be based primarily on those lives who go through an entire year of age from x to x + 1, or who would have done if they had not died first, these lives being termed "whole-yearers". Where a death occurred, it was proposed that this be proportioned between the population of whole-yearers and the rest of the lives. Then the mortality rate would be obtained by dividing the sum of the proportions of deaths credited to whole-yearers by the number of whole-yearers.

In removing a death from the investigation, it was assumed that the withdrawal experience lost subsequently for that individual would have been exactly typical of the average subsequent withdrawal experience of the lives who remained in the investigation at the moment of that death, ie the life dying was assumed to be an exactly typical representative in terms of potential withdrawal behaviour of the body of lives carrying on.

In practice, the procedure would be as follows:

(1) Let ${}^{W}P$ be the number of whole-yearers surviving to age x+1, and let ${}^{T}P$ be the total number of all lives surviving to age x+1.

(2) Starting at age x+1, work backwards in time until the first new entrant, withdrawal or death is encountered:

(a) If it is a new entrant, reduce ${}^{T}P$ by deducting 1.

(b) If it is a withdrawal, increase ${}^{T}P$ by adding 1.

(c) If it is a death, increase ${}^{W}P$ by adding $\frac{{}^{W}P}{{}^{T}P}$ and increase ${}^{T}P$ by adding 1.

(3) Continue working back in time until another new entrant, withdrawal or death is encountered and repeat the adjustment set out in (2) using the current values of ${}^{W}P$ and ${}^{T}P$, and so on until age x is reached.

Then if the original value of ${}^{W}P$ is ${}^{W}P'$ and the final value of ${}^{W}P$ is ${}^{W}P''$, the deaths allocated to the whole-yearers is $({}^{W}P'' - {}^{W}P')$ and the estimate of q_x is

$$\frac{{}^{W}P'' - {}^{W}P'}{{}^{W}P''} = 1 - \frac{{}^{W}P'}{{}^{W}P''} \tag{2.31}$$

Obviously $\frac{{}^{W}P'}{{}^{W}P''}$ is an estimate of p_x.

Numerical experiments using this procedure produced very encouraging results. However, it was then noticed that the method always produced results identical with those produced by the product limit estimator!

A subsequent algebraic investigation revealed that the whole-year estimator was in fact the very same thing as the product limit estimator.

2.13 Demonstration that the whole-year estimator is identical with the product limit estimator

Let there be n+2 durations, during the year from age x to x + 1, at which non-death movements occur, comprising durations 0 and 1, and n durations at which new entrants enter or withdrawals exit. Note that more than one person may be involved in entering or exiting at any of the durations. Let the n+2 durations be labelled from r = 0 to r = n+1.

Let ${}^{T}P^{2}_{r}$ be the total population of all lives present at the r^{th} duration immediately before the movement(s) occur, and let ${}^{T}P^{1}_{r+1}$ be the total population of all lives present immediately after the movement(s) at the r^{th} duration. If any deaths occur exactly at the r^{th} duration ($1 \leq r \leq n+1$), it will be considered that these deaths have occurred before the population ${}^{T}P^{2}_{r}$ is counted. Let ${}^{W}P^{2}_{r}$ and ${}^{W}P^{1}_{r+1}$ be the corresponding populations of whole-yearers. Let ${}^{T}P^{1}_{1}$ and ${}^{W}P^{1}_{1}$ be respectively the populations of all lives and of whole-yearers at the beginning of the year of age, and let ${}^{T}P^{2}_{n+1}$ and ${}^{W}P^{2}_{n+1}$ be respectively the populations of all lives and of whole-yearers at the end of the year of age.

It will be noted that ${}^{W}P^{2}_{r}$ equals ${}^{W}P^{1}_{r+1}$ ($1 \leq r \leq n$) whereas of course ${}^{T}P^{2}_{r}$ does not normally equal ${}^{T}P^{1}_{r+1}$.

Then the product limit estimator gives the following estimate of q_x:

$$q_x = 1 - \prod_{r=1}^{n+1} \frac{{}^{\top}P_r^2}{{}^{\top}P_r^1} \tag{2.32}$$

Turning to the whole-year estimator, we have the following relationship linking ${}^{w}P_r^2$ and ${}^{w}P_{r+1}^2$:

$${}^{w}P_r^2 = ({}^{\top}P_{r+1}^1 - {}^{\top}P_{r+1}^2) * \frac{{}^{w}P_{r+1}^2}{{}^{\top}P_{r+1}^2} + {}^{w}P_{r+1}^2 , \qquad 1 \leq r \leq n \tag{2.33}$$

(Note that, if several deaths occur during a segment between non-death movements, the proportion of each death allocated to the population of whole-yearers is always effectively:

$$\frac{{}^{w}P_{r+1}^2}{{}^{\top}P_{r+1}^2} ,$$

where the deaths occur in the segment following the r^{th} non-death movement).

The relationship (2.33) simplifies to give:

$${}^{w}P_r^2 = {}^{w}P_{r+1}^2 * \frac{{}^{\top}P_{r+1}^1}{{}^{\top}P_{r+1}^2} \tag{2.34}$$

so that we can deduce that:

$${}^{w}P_1^2 = {}^{w}P_{n+1}^2 * \prod_{r=2}^{n+1} \frac{{}^{\top}P_r^1}{{}^{\top}P_r^2} \tag{2.35}$$

and so:

$${}^{w}P_1^1 = {}^{w}P_{n+1}^2 * \prod_{r=1}^{n+1} \frac{{}^{\top}P_r^1}{{}^{\top}P_r^2} \tag{2.36}$$

Thus the whole-year estimator for q_x is given by:

$$q_x = \frac{{}^{w}P_1^1 - {}^{w}P_{n+1}^2}{{}^{w}P_1^1}$$

$$= 1 - \frac{{}^{w}P_{n+1}^2}{{}^{w}P_1^1}$$

$$= 1 - \frac{{}^{w}P_{n+1}^2}{{}^{w}P_{n+1}^2 * \prod_{r=1}^{n+1} \frac{{}^{\top}P_r^1}{{}^{\top}P_r^2}}$$

$$= 1 - \prod_{r=1}^{n+1} \frac{{}_{\top}P_r^2}{{}_{\top}P_r^1} \tag{2.37}$$

which is identical with the product limit estimator.

Although it is disappointing that the whole-year estimator only represented a re-invention of the product limit estimator, it is interesting to see how a link is provided between an estimator whose rationale is to follow lives through the year of age, and adjust for the effects of non-death entries and exits, and the seemingly different product limit estimator which apparently just considers the year of age as a series of separate and distinct intervals whose experience is simply combined together without any reference to the continuity of individual lives.

2.14 The implication-B estimator

(This estimator was originally called simply the "implication estimator", but in order to avoid potential ambiguities arising as a result of subsequent developments, it was relabelled the "implication-B estimator").

The rationale behind the implication-B estimator is that we know the details of the lives exiting by withdrawal and survival, and assuming a law of mortality, we can construct an expression to estimate the number of deaths that could be expected to correspond to this withdrawal/survival experience. This expression can then be equated to the observed number of deaths and a value for q_x derived.

This was viewed as being an interesting line of research since it had no pretensions to being a "method of moments" estimator but simply took the final position reached at the end of the investigation and attempted to work backwards to infer a value of q_x from the finishing position.

For each life exiting the investigation as a withdrawal or survivor, the number of deaths implied was taken to be:

$$\frac{{}_{t_i-s_i}q_{x+s_i}}{{}_{t_i-s_i}p_{x+s_i}}$$

where the life entered at age $x+s_i$, $0 \leq s_i < 1$ and exited at age $x+t_i$, $0 < t_i \leq 1$.

Thus the number of deaths implied is given by:

$$\sum_{SW} \frac{{}_{t_i-s_i}q_{x+s_i}}{{}_{t_i-s_i}p_{x+s_i}}$$

$$= \sum_{SW} \left(\frac{1}{{}_{t_i-s_i}p_{x+s_i}} - 1\right)$$

Equating this to the observed number of deaths leads to:

$$D + W + S = \sum_{SW} \frac{1}{{}_{t_i-s_i}p_{x+s_i}} \tag{2.38}$$

Thus, the total number of lives in the investigation is given by:

$$N = \sum_{SW} \frac{{}_{s_i}p_x}{{}_{t_i}p_x} \tag{2.39}$$

The probabilities in this equation would be expressed in terms of q_x by means of the assumed mortality law. An iterative method of solution will commonly be needed in order to obtain the value for q_x from the equation.

2.15 The implication-B criterion

Thus the rationale of the implication-B estimator can be re-expressed as determining an expression for the number of lives implied by the withdrawals and survivors as entering the investigation, and then equating this expression to the actual number of lives entering the investigation, to obtain the estimate of q_x which is the solution of the resulting equation. (The assumption of a mortality law is necessary in order to express probabilities of the form ${}_{s_i}p_x$ and ${}_{t_i}p_x$ in terms of q_x).

2.16 The implication-B estimator for some mortality assumptions

The following forms of the equation defining the implication-B estimator can be derived for various mortality assumptions:

(a) "Level deaths" assumption

$$N = \sum_{SW} \frac{1 - {}_{s_i}q_x}{1 - {}_{t_i}q_x} \tag{2.40}$$

(b) "Constant μ" assumption

$$N = \sum_{SW} \frac{(1 - q_x)^{s_i}}{(1 - q_x)^{t_i}} \tag{2.41}$$

(c) Balducci assumption

$$N = \sum_{SW} \frac{1 - (1 - t_i)q_x}{1 - (1 - s_i)q_x} \tag{2.42}$$

Numerical experiments indicated that the implication-B estimator produced reasonable results, and this has subsequently been confirmed by the simulation studies reported in Chapter 5 of this thesis. (The simulation results for the implication-B estimator are discussed for example in Sections 5.22, 5.23 and 5.27).

During the numerical experiments, it was found that generally the implication-B estimator and the conventional estimator gave slightly different estimates of q_x, but that if all lives entered the investigation at the same age x + s, the two estimators gave identical results.

This latter effect can be shown algebraically.

If all lives enter the investigation at age x + s, the implication-B estimator gives us:

$$D + W + S = \sum_{SW} \frac{{}_sp_x}{{}_{t_i}p_x} \tag{2.43}$$

$$\Rightarrow \quad (D + W + S) * \frac{1}{{}_sp_x} = \sum_{SW} \frac{1}{{}_{t_i}p_x} \tag{2.44}$$

$$\Rightarrow \quad (D + W + S) * \frac{{}_{1-s}p_{x+s}}{p_x} = \sum_{SW} \frac{{}_{1-t_i}p_{x+t_i}}{p_x} \tag{2.45}$$

$$\Rightarrow \quad (D + W + S)\,(1 - {}_{1-s}q_{x+s}) = \sum_{SW} (1 - {}_{1-t_i}q_{x+t_i}) \tag{2.46}$$

$$\Rightarrow \quad (D + W + S) = N * {}_{1-s}q_{x+s} + S + W - \sum_{SW} {}_{1-t_i}q_{x+t_i} \tag{2.47}$$

$$\Rightarrow \quad D = N * {}_{1-s}q_{x+s} - \sum_{W} {}_{1-t_i}q_{x+t_i} \tag{2.48}$$

Equation (2.48) defines the conventional estimator.

2.17 The conventional estimator revisited

The link between the implication-B estimator and the conventional estimator, when all lives had a common entry age, led the author to seek a re-interpretation of the conventional estimator as an implication estimator.

Starting from the familiar rationale for the conventional estimator, the following algebraic manipulation was made:

$$D = \sum_{N} {}_{1\text{-}s_i}q_{x+s_i} - \sum_{W} {}_{1\text{-}t_i}q_{x+t_i} \tag{2.49}$$

$$\Rightarrow \quad D = \sum_{N} (1 - {}_{1\text{-}s_i}p_{x+s_i}) - \sum_{WS} (1 - {}_{1\text{-}t_i}p_{x+t_i}) \tag{2.50}$$

$$\Rightarrow \quad D = (D + W + S) - \sum_{N} \frac{p_x}{{}_{s_i}p_x} - (W + S) + \sum_{WS} \frac{p_x}{{}_{t_i}p_x} \tag{2.51}$$

$$\Rightarrow \quad \sum_{N} \frac{1}{{}_{s_i}p_x} = \sum_{WS} \frac{1}{{}_{t_i}p_x}\,, \tag{2.52}$$

remembering that: $N = D + W + S = L + I$

2.18 The implication-A criterion

The above equation (2.52) gives an entirely fresh perspective to the rationale for the conventional estimator. The left-hand side of the equation gives the number of lives implied as being present at age x in order to provide the requisite number of lives surviving under mortality to enter the investigation for whatever age $x + s_i$ at which they enter, while the right-hand side gives the number of lives implied as being present at the beginning of the year of age to provide the requisite number of lives surviving under mortality to exit the investigation as non-deaths, for whatever age $x + t_i$ at which they exit.

The estimator for q_x is that value for q_x which, in association with the assumed mortality law, ensures that the number of lives implied as present at the beginning of the year of age, to provide the lives entering the investigation, equals those implied as present at the

beginning of the year of age, to provide the lives exiting as non-deaths from the investigation.

The author gave this criterion the name "implication-A criterion"; as we have seen it is closely related to the experimental "implication-B estimator", but will be seen to have a more fundamentally satisfying basis.

A feature of the implication-A criterion which is particularly pleasing is that the treatment of every life involved in the investigation involves reference back to the beginning of the year of age, even for those lives who enter the investigation after age x. We are, after all, seeking to use the experience of every life to determine the rate of mortality over the entire year from age x to age $x + 1$ and, also, to be an entrant at age $x + s_i$ does imply that the life was alive at age x, which is a piece of mortality data about that life in the year of age concerned.

It will be noticed that no knowledge of any probability distribution for withdrawals, nor new entrants, is required at any stage. This is viewed by the author as a particularly important feature and strength of this estimation criterion (and also of the implication-B criterion), given the complex, changeable and often very unpredictable nature of the factors determining withdrawal rates, or new entrance rates.

Thus it is contended that the conventional estimator has an acceptable, and intuitively attractive, theoretical basis giving results which, according to the analysis in Section 2.10, would be similar to those given by a method of moments estimator, if it could actually be calculated, when the correct mortality assumption is made.

Subsequently it will be shown, in Section 2.20, that the calculation of the conventional estimator according to the Implication-A criterion is analogous to the calculation of a money-weighted rate of return in a financial transaction, further enhancing the intuitive attraction of the criterion.

Further the simulation studies reported in Chapter 5 appear to confirm that the performance of the conventional estimator is satisfactory and is not compromised by alleged theoretical flaws as suggested by Hoem (1984). The performance of the conventional estimator in the simulations is discussed in particular in Sections 5.19, 5.21, 5.23, 5.26 and 5.27. The simulation studies also suggest that, even when the wrong mortality assumption is made, the results given by the conventional estimator are just marginally more biased than those that would be given by a method of moments estimator (see Section 5.27).

2.19 The product limit estimator also conforms to the implication-A criterion

It is a further pleasing feature of the implication-A criterion, applicable for the conventional estimator, that the product limit estimator can also be shown to conform to this criterion.

In the case of the product limit estimator, the probabilities used in the equation:

$$\sum_{LI} \frac{1}{{}_{s_i}p_x} = \sum_{WS} \frac{1}{{}_{t_i}p_x} \tag{2.53}$$

are not based on the assumption of a mortality law such as "level deaths" or Balducci, as in the conventional implication-A method, but instead, if the year of age is split into intervals bounded by the points at which lives have entered or left the investigation for reasons other than death, then the proportion of lives observed to survive across an interval is taken as the underlying probability of surviving across the interval concerned. The product limit estimator for q_x is obviously determined by deducting from unity the amalgamation of the survival rates for the fractional periods represented by the intervals.

It is found that these survival probabilities satisfy the implication-A criterion and so, therefore, does the product limit estimator of q_x.

This is easily shown. Let there be n+2 durations, during the year from age x to x + 1, at which non-death movements occur, comprising durations 0 and 1, and n durations at which new entrants enter or withdrawals exit. Note that more than one person may be involved in entering or exiting at any of the durations. Let the n+2 durations be labelled from t = 0 to t = n+1.

Let P_t^2 be the population present at the t^{th} duration immediately before the movement(s) occur and let P_{t+1}^1 be the population present immediately after the movement(s) at the t^{th} duration. Further let P_1^1 and P_{n+1}^2 be the populations at the beginning and end of the year of age.

Also let n_t and w_t be respectively the numbers of new entrants and withdrawals at the t^{th} duration, and let $x+r_t$ be the age at this duration.

Then from the mortality assumption made in the product limit estimator:

$$P_{t+1}^1 = \frac{P_{t+1}^2}{{}_{r_{t+1}-r_t}p_{x+r_t}} \tag{2.54}$$

where ${}_{r_{t+1}-r_t}p_{x+r_t}$ is the probability that a life aged $x+r_t$ will die within time $(r_{t+1} - r_t)$.

We also have:

$$P_t^2 + n_t - w_t = P_{t+1}^1 \tag{2.55}$$

so that:

$$\frac{P_t^2}{{}_{r_t}p_x} + \frac{n_t}{{}_{r_t}p_x} = \frac{P_{t+1}^1}{{}_{r_t}p_x} + \frac{w_t}{{}_{r_t}p_x} \tag{2.56}$$

$$= \frac{P_{t+1}^2}{{}_{r_{t+1}}p_x} + \frac{w_t}{{}_{r_t}p_x} \tag{2.57}$$

noting that: $${}_{r_t}p_x*({}_{r_{t+1}}p_{x+r_t}) = {}_{r_{t+1}}p_x \quad . \tag{2.58}$$

Summing from $r_t = 1$ to $r_t = n$, and cancelling common terms on either side of the equation, gives:

$$\frac{P_1^2}{{}_{r_1}p_x} + \sum_{r_t=1}^{n} \frac{n_t}{{}_{r_t}p_x} = \frac{P_{n+1}^2}{p_x} + \sum_{r_t=1}^{n} \frac{w_t}{{}_{r_t}p_x} \tag{2.59}$$

ie $$P_1^1 + \sum_{r_t=1}^{n} \frac{n_t}{{}_{r_t}p_x} = \frac{P_{n+1}^2}{p_x} + \sum_{r_t=1}^{n} \frac{w_t}{{}_{r_t}p_x} \tag{2.60}$$

which gives the criterion for the implication-A estimator.

In fact, it can be shown that the product limit estimator satisfies the implication-A criterion over any section of the year of age, if lives present at the beginning and end of the section are treated respectively as entering and exiting at these points.

Thus the implication-A criterion provides a means of unifying the product limit estimator with the conventional estimator, the difference between them lying in the nature of the mortality assumption.

2.20 A comparison of the use of the implication-A criterion to calculate the rate of mortality with the technique of equating present values to calculate the rate of return in a financial transaction

At a seminar on 7th May 1991, the author presented these results concerning the implication-A criterion to colleagues, and Professor Steven Haberman (1991) pointed out to him that the concept of equating expressions for the number of lives implied as present at the beginning of the year of age in order to evaluate the mortality rate has a resemblance to the concept of equating present values, as encountered in financial mathematics, in order to

evaluate a financial rate of return. This analogy will now be discussed.

Let us consider a financial scenario in which we have a sum of money in an interest bearing account which is having interest continuously added. Let us also think of the account-holder adding sums of money to the account and withdrawing sums of money from time to time.

If we study the account over a period of time, we know that we can equate the money in the account at the beginning of the period, plus the sums of money added to the account during the period, to the money which is in the account at the end of the period, together with the monies withdrawn during the period, so long as we adjust the various sums for the effect of interest.

A common calculation would be to work out the present values of the sums of money to be "equated", by discounting their values back to the beginning of the period using the force of interest. (Commonly we are able to work with the more convenient rate of interest, rather than with the force of interest).

Then if the correct force of interest is used and interest has been correctly credited to the account, the sum of the present values of the monies "in-coming" equals the sum of the present values of the monies "out-going". It is of course elementary that the interest additions are not regarded as movements of money whose present values are also to be included in these sums of present values.

If we now turn to the mortality scenario studied in this thesis, the year of age is analogous to the period for which we considered the interest bearing account. The number of lives present at any moment corresponds to the money in the account at any moment (after addition of the continuous interest). The lives starting, or entering during, the year of age correspond to the monies starting the period in the account or subsequently paid in by the account-holder during the period. The lives surviving the year or withdrawing during the year correspond to the money in the account at the end of the period or withdrawn during the period. The lives dying during the year, and hence removed from the population, correspond to the continuous interest added to the money in the account.

It is here that we see an important difference in the comparison of the two scenarios, namely that one involves the positively acting force of interest while the other involves the negatively acting force of mortality. However this does not prevent us from drawing a close analogy between the interest bearing account and the mortality bearing population, and just as we can discount, say, a sum of money withdrawn at time t' by a factor of the form:

$$v^{t'} = \exp\left[- \int_0^{t'} \delta_t \, dt \right] \tag{2.61}$$

where δ_t is the force of interest at time t, so similarly we can "discount" a group of lives withdrawing at time t' using a factor of the form:

$$\frac{1}{{}_{t'}p_x} = \exp\left[- \int_0^{t'} (- \mu_{x+t}) \, dt \right] \tag{2.62}$$

where μ_{x+t} is the force of mortality at time t.

So for example, in the financial scenario, we can calculate the sum of money implied at duration 0 as corresponding to a sum of money withdrawn at time t', ie the sum that will grow under interest to the amount withdrawn, and similarly in the mortality scenario, we can calculate the number of lives implied at duration 0 as corresponding to a number of lives withdrawing at time t', ie the number of lives that will decrease under mortality to the number of lives withdrawing.

Then just as we can equate the present values of the monies moving in and out of the account, so we can equate the implied numbers of people at duration 0 corresponding to the numbers of people moving in and out of the population.

Again it is elementary that the deaths themselves are not regarded as movements of lives to be "discounted" and included in the sum of implied numbers, just as the additions of interest are not regarded as movements of money to be discounted and included in the sums of present values.

Also, just as the financial present values can be calculated and equated at any chosen point in time, so similarly can the implied numbers of lives be calculated and equated at any chosen point in time. However the beginning of the year of age is a convenient point at which to make the calculation, and one which is intuitively helpful in understanding the procedure.

There is no theoretical difficulty implied by the fact that deaths occur as a random process and in units of one. In fact both these features have analogies in the financial scenario, in that the force of interest can vary as a random variable and money is itself expressed in units of currency which are ultimately indivisible, and these features do not give rise to difficulty in the financial scenario.

In the financial scenario, there are two important ways in which we can use the discounting technique. Either we can use the force of interest as actually credited, taking any changes in

the force of interest into account in making the calculations, in which case the present values will automatically balance out, or we can seek to calculate the "internal rate of return", which is the rate of interest which, if applicable unchanged throughout the period, would also result in the present values balancing.

In our mortality scenario, we also have two choices, more or less corresponding to the two financial alternatives. We can either use the force of mortality, as observed in the intervals between non-death movements, to reconcile the numbers of lives moving in or out, or we can seek the value of a mortality parameter which, in association with a mortality law dependent on this single parameter, will ensure that the numbers of lives at duration 0 implied by the incoming and outgoing lives balance.

The first approach is the basis of the product limit estimator which uses the mortality experience between each adjacent pair of non-death entries or exits to determine the mortality rate observed to apply during the segment of the year of age concerned, and then combines the rates from each such segment to give a mortality rate for the whole year of age.

The second approach is the basis of the conventional estimator. It is of interest to note that the method is more sophisticated than the corresponding calculation of an internal rate of return. In the case of the conventional estimator, the force of mortality is assumed to vary according to a mortality law, the general level of the force of mortality being governed by a single mortality parameter, which is to be determined by the calculation. This mortality parameter is either q_x or some other parameter which will allow q_x to be determined.

In contrast, the calculation of the internal rate of return simply assumes that the force of interest is constant during the period of the scenario, and in calculating the internal rate of return, we effectively determine this force of interest (though in practice it is the rate of interest that is generally calculated).

An interesting feature that becomes apparent from the analogy is that the calculation of the mortality parameter determining the value of the conventional estimator is "lives-weighted". In the financial scenario, the force of interest experienced at the time when the balance of money in the account is high will have a greater influence on the value calculated for the internal rate of return than the force of interest experienced at the time when the balance in the account is low, all other things being equal. The internal rate of return thus calculated is said to be a "money-weighted" rate of return.

Similarly the force of mortality experienced when the number of lives present is high will have a greater influence on the value calculated for the mortality parameter than the force

of mortality experienced when the number of lives present is low, all other things being equal.

In contrast, the product limit estimator is not "lives-weighted" but is "time-weighted" since the mortality rate experienced in each segment is applied for the time covered by the segment in the calculation of the product limit estimator, and the number of lives involved is not reflected in combining the observed rates for each segment.

The mortality rate determined by the product limit estimator has its counterpart in the financial scenario in the single interest rate which if applied to a sum of money over the whole period of the financial scenario, without any withdrawals or additions of money, will produce the same closing balance as the interest rates actually experienced over the various intervals between money movements in the original scenario. It is the rate of return given by the administrators of the account on an undisturbed sum of money over the period of the financial scenario. Such a rate of return is said to be a "time-weighted" rate of return. Adams (1989) gives a concise discussion of "money-weighted" and "time-weighted" rates of return.

An implication of the fact that the product limit estimator is "time-weighted" whereas the conventional estimator is "lives-weighted" may be that the product limit estimator may generally have a greater standard deviation than the conventional estimator because the importance given to the data at each point of the year of age is not weighted to reflect the amount of data involved, unlike the approach used in the conventional estimator. The extent to which this apparent implication is borne out will depend on the suitability of the weighting given in the conventional estimator. In the simulations reported in Chapter 5, it is found that in most cases, but not all, the product limit estimator does have a larger standard deviation than the conventional estimator (see Section 5.23).

Thus there appears to be a very strong resemblance between the method of calculating the conventional estimator of q_x, which involves the application of the implication-A criterion, and the method of calculating the internal rate of return in a financial transaction; further there also appears to be a very strong resemblance between the method of calculating the product limit estimator and the method of calculating a time-weighted rate of return.

2.21 The method of moments: some parting observations

In general, the method of moments can be seen to be highly impractical for application to a mortality investigation, both in terms of the formulae and calculations that would be involved and in terms of making accurate assumptions about the distribution of

withdrawals, and if appropriate about the distribution of new entries.

If we look at a proposed mortality investigation with the intention of applying the method of moments to estimate q_x, a number of observations can be made.

Firstly, the experiment extends over finite time (unlike, say, a coin tossing experiment which can be thought of as taking place in an instant).

Secondly, the experiment consists of a sequence of events, or potential events, the occurrence or potential occurrence of which depends on earlier events in the experiment. Since the whole experiment occupies finite time, we might take the view that we have a sequence of an infinite number of potential events, each of which individually requires just an instant to occur (eg withdrawal/non-withdrawal, death/non-death).

Thirdly, the question arises of what exactly constitutes the starting position of the experiment. When does the experiment start? If a life is a new entrant at duration one month into the year of age say, does the experiment start at that point for that life, notwithstanding that other lives have already been involved at an earlier point of the year of age? If we accept this point of view, the starting position consists of knowing, before the experiment, the precise number and age at entry of all the lives who will enter the experiment. This is the point of view adopted for example in Hoem (1984).

Alternatively, one might take the view that the starting point of the experiment for all lives is at age x since we are studying mortality over the year of age from age x exact to age x+1 exact; on this view we cannot take an event occurring at age x+f ($0<f<1$), such as entry at age x+f, as part of the starting position. There must exist some mechanism operating from age x, for lives defined as existing at age x, whereby entries of some of these lives occur at subsequent ages. The entry of a life at age x+f ($0<f<1$) will occur if the life is still alive at age x+f and if at that point he becomes an entrant. Clearly survival under mortality is involved in the required mechanism; several possibilities concerning occurrence of entry suggest themselves, including the following:

(1) At age x, a life is earmarked to be an entrant at a particular age x+f if he survives to age x+f.

(2) At age x, a life is earmarked as an entrant at a particular age x+f if he is still alive at age x+f and if a random variable subject to a defined probability distribution takes an appropriate value.

(3) At age x, a life is earmarked as an entrant at any age x+f ($0<f<1$) if a random

variable subject to a defined probability distribution takes the value f and the life is still alive at age x+f.

Thus arguably, it appears that there is not a unique theoretical approach for the application of the method of moments to the mortality investigation scenario, so that it may not be enough simply to talk without qualification about applying the method of moments in this scenario.

An important factor giving rise to this ambiguity seems to be the fact that the experiment extends over finite time, so that we have to define at what time the experiment begins for different individuals. As already noted, when we are applying the method of moments, it more usually seems to be in scenarios where the experiment can be thought of as occurring instantaneously, so that this issue does not arise.

There is also the consideration that survival from age x up to entry involves mortality, the very phenomenon that the experiment is designed to investigate.

In this thesis, it has been assumed that the force of mortality is not a function of calendar time. If this could not be assumed, the "starting position" would also have to specify the point of calendar time at which each life attains exact age x (or an equivalent piece of information).

In addition, there seems to be a further arbitrary factor in any proposed application of the method of moments to a mortality investigation, namely what random variable is the method of moments to be applied to? Of course in practice, it is the first moment of the number of deaths during the appropriate year of age that we use, but there seems no fundamental theoretical reason for selecting this particular random variable, above any other, the justification appearing to be that it is the least impractical thing to do.

This discussion of the theoretical ambiguities draws attention to the fact that decisions have been made, and are taken for granted, in the application of the method of moments to estimate q_x, as discussed for example in Hoem (1984).

A further observation concerning application of the method of moments to the mortality investigation experiment is the need to assume the general form of a probability distribution for withdrawals, and possibly new entrants. As already commented this may be difficult, given the complex, changeable and often very unpredictable nature of the factors determining withdrawal rates, or new entry rates.

2.22 The derivation of maximum likelihood estimators for q_x

The derivation of maximum likelihood estimators for q_x has been discussed by a number of writers, including Broffitt (1984). The general procedure is to create a likelihood function of the form:

$$L = \prod_{N} (1 - {}_{t_i-s_i}q_{x+s_i}) (1 - {}_{t_i-s_i}r_{x+s_i}) \prod_{D} \mu_{x+t_i} \prod_{W^*} \nu_{x+t_i} \qquad (2.63)$$

where ${}_{t_i-s_i}r_{x+s_i}$ is the independent rate of unscheduled withdrawal analogous to the independent rate of mortality ${}_{t_i-s_i}q_{x+s_i}$, ν_{x+t_i} represents the force of unscheduled withdrawal analogous to the force of mortality μ_{x+t_i} and W^* represents those withdrawals not occurring at durations fixed in advance.

It should be commented that, in order to formulate the likelihood, it is assumed that we know whether a withdrawal was scheduled to occur or was a random unscheduled event, and that we know the force of withdrawal, governing unscheduled withdrawals, at every point of the investigation. The latter information in particular might be difficult to establish in practice, if the details were actually to be required, given the complex, changeable and often very unpredictable nature of the factors determining unscheduled withdrawals (eg the abolition of life assurance premium tax relief), as previously commented (in Section 2.10). However, it can be subsequently seen that the information concerning withdrawals, needed to formulate the likelihood, is not actually used in the evaluation of the maximum likelihood estimator of q_x.

Generally a mortality assumption is made which is equivalent to the form:

$$\mu_{x+t} = f(q_x,t) , \quad (0<t\leq 1) \qquad (2.64)$$

and L modified accordingly.

Then, in the most common approach, we differentiate L (or more conveniently log L) with respect to q_x and equate the derivative to 0.

This gives an equation which can be solved to give the estimator for q_x.

The most convenient result comes when "$\mu_{x+t} = f(q_x,t)$" is taken as:

$$\mu_{x+t} = \text{constant} , \quad (0<t\leq 1) \qquad (2.65)$$

Then we obtain:

$$q_x = 1 - e^{-\mu} \tag{2.66}$$

where:

$$\mu = \frac{D}{\sum_N (t_i - s_i)} \tag{2.67}$$

This is easily shown. The log-likelihood function is:

$$\log L = \sum_D \log \mu_{x+t_i} + \sum_N \log {}_{t_i}p_x - \sum_N \log {}_{s_i}p_x + \text{terms independent of mortality}$$

$$= \sum_D \log \mu + \sum_N (-t_i * \mu) - \sum_N (-s_i * \mu) + \text{terms independent of mortality} \tag{2.68}$$

where: $$\mu_{x+t} = \mu \quad , \quad (0 < t \leq 1) \tag{2.69}$$

Here, it is more convenient to determine the maximum likelihood estimator of μ rather than the maximum likelihood estimator of q_x. Then, by the invariance property of maximum likelihood estimators (see for example Larson (1982)), the maximum likelihood estimator of q_x will be the value of q_x that occurs when μ in equation (2.66) takes the value given by the maximum likelihood estimator of μ.

So: $$\frac{\partial \log L}{\partial \mu} = \frac{D}{\mu} - \sum_N (t_i - s_i) \tag{2.70}$$

Equating $\frac{\partial \log L}{\partial \mu}$ to zero gives:

$$\mu = \frac{D}{\sum_N (t_i - s_i)} \tag{2.71}$$

By considering:

$$\frac{\partial^2 \log L}{\partial \mu^2} = -\frac{D}{\mu^2} \ , \tag{2.72}$$

we confirm that the log-likelihood is maximised by the value given by expression (2.71), so that we confirm that the maximum likelihood estimator of μ is given by expression (2.71),

from which the maximum likelihood estimator of q_x can be determined using equation (2.66).

If, alternatively we consider the maximum likelihood estimator of q_x when the "level deaths" assumption applies, we obtain, as demonstrated for example in Hoem (1984), Broffitt (1984) or in Section 2.23 of this thesis, the following equation defining the estimator for q_x:

$$\frac{D}{q_x} + \sum_{N} \frac{s_i}{1 - s_i * q_x} - \sum_{SW} \frac{t_i}{1 - t_i * q_x} = 0 \qquad (2.73)$$

Obviously this can generally only be solved by an iterative method.

If, as a further alternative, we consider the maximum likelihood estimator of q_x when the Balducci assumption applies, we can obtain after some simplification the following equation defining the estimator for q_x:

$$\sum_{N} \frac{1}{1 - (1 - s_i) * q_x} = \sum_{DN} \frac{1}{1 - (1 - t_i) * q_x} \qquad (2.74)$$

Again, this can generally only be solved by an iterative method.

2.23 Demonstration that, when the "level deaths" assumption applies, the maximum likelihood estimator is identical with the conventional estimator

Before proceeding to demonstrate that the maximum likelihood estimator is identical with the conventional estimator when the "level deaths" assumption applies, we will derive equation (2.73), quoted in the previous section, which defines the maximum likelihood estimator for this mortality assumption.

The log-likelihood function is:

$$\log L = \sum_{D} \log \mu_{x+t_i} + \sum_{N} \log {}_{t_i}p_x - \sum_{N} \log {}_{s_i}p_x + \text{terms independent of mortality}$$

$$= \sum_{D} \log \left(\frac{q_x}{1 - t_i * q_x}\right) + \sum_{N} \log (1 - t_i * q_x) - \sum_{N} \log (1 - s_i * q_x)$$

$$+ \text{terms independent of mortality}$$

$$= \sum_{D} \log q_x - \sum_{D} \log (1 - t_i * q_x) + \sum_{N} \log (1 - t_i * q_x) - \sum_{N} \log (1 - s_i * q_x)$$

$$+ \text{ terms independent of mortality}$$

$$= \sum_{D} \log q_x + \sum_{SW} \log (1 - t_i * q_x) - \sum_{N} \log (1 - s_i * q_x)$$

$$+ \text{ terms independent of mortality} \qquad (2.75)$$

$$\Rightarrow \qquad \frac{\partial \log L}{\partial q_x} = \frac{D}{q_x} + \sum_{N} \frac{s_i}{1 - s_i * q_x} - \sum_{SW} \frac{t_i}{1 - t_i * q_x} \qquad (2.76)$$

Equating $\frac{\partial \log L}{\partial q_x}$ to zero gives:

$$\frac{D}{q_x} + \sum_{N} \frac{s_i}{1 - s_i * q_x} - \sum_{SW} \frac{t_i}{1 - t_i * q_x} = 0 \qquad (2.77)$$

which is the equation defining the maximum likelihood estimator. This was quoted earlier as equation (2.73).

It can be seen that this equation is the same as equation (1.45) which set out equation (12) of Hoem (1984).

We will now proceed to develop this equation into a format which defines the conventional estimator.

From the equation (2.77) we have:

$$\frac{D}{q_x} = \sum_{S} \frac{1}{1 - q_x} + \sum_{W} \frac{t_i}{1 - t_i * q_x} - \sum_{N} \frac{s_i}{1 - s_i * q_x} \qquad (2.78)$$

Then multiplying through by $(1 - q_x)$ and remembering that $N = D + W + S$, we have:

$$D * \frac{(1 - q_x)}{q_x} = N - W - D + \sum_{W} \frac{(1 - q_x) t_i}{1 - t_i * q_x} - \sum_{N} \frac{(1 - q_x) s_i}{1 - s_i * q_x} \qquad (2.79)$$

Gathering together the terms relating to the (sub)sets N, W and D, we have:

$$\frac{D}{q_x} = \sum_N \frac{(1 - s_i{*}q_x) - (1 - q_x)s_i}{1 - s_i{*}q_x} - \sum_W \frac{(1 - t_i{*}q_x) - (1 - q_x)t_i}{1 - t_i{*}q_x} \qquad (2.80)$$

$$\Rightarrow \qquad D = q_x \left[\sum_N \frac{1 - s_i}{1 - s_i{*}q_x} - \sum_W \frac{1 - t_i}{1 - t_i{*}q_x} \right] \qquad (2.81)$$

$$\Rightarrow \qquad D = \sum_N {}_{1\text{-}s_i}q_{x+s_i} - \sum_W {}_{1\text{-}t_i}q_{x+t_i} \qquad (2.82)$$

because under the "level deaths" assumption:

$${}_{1\text{-}s}q_{x+s} = \frac{(1 - s)q_x}{1 - s{*}q_x} \quad \text{etc.}$$

Equation (2.82) is of course the familiar equation solved by the value of q_x given by the conventional estimator. It can also be seen to be the same equation as equation (1.44) which set out equation (3A) of Hoem (1984).

Thus when the "level deaths" mortality assumption applies, the maximum likelihood and conventional estimators are identical.

This author is not aware of this general co-incidence of the conventional and maximum likelihood estimators under the "level deaths" assumption having been previously noted in the literature, although coincidences in less general situations have been noted; certainly Hoem (1984) did not refer to the co-incidence when making unfavourable comments on conventional estimators and favourable comments on maximum likelihood estimators, and did not note that his equations (3A) and (12), defining respectively the conventional and maximum likelihood estimators of q_x under the "level deaths" assumption, are identical when expressed in a common notation and rearranged to a common format (as demonstrated in this section).

Broffitt (1984) observes that if all lives enter the year of age at age x exact, and that half the withdrawals occur at age x and the other half at age x+1, then the value given by the maximum likelihood estimator assuming "level deaths", defined by equation (2.77), is the same as that given by the actuarial estimator:

$$q_x = \frac{D}{N - \frac{1}{2}W} \qquad (2.83)$$

The actuarial estimator is of course based on the full data conventional estimator using the

Balducci assumption but, in the situation considered by Broffitt, there are no lives making non-death movements during the year of age, and this means that the conventional estimator will be the same for all mortality assumptions. Consequently, the maximum likelihood estimator using the "level deaths" assumption will give the same value as the full data conventional estimator using any mortality assumption. Here, it also equals the actuarial estimator, as the equal split of the withdrawals between the beginning and end of the year of age accommodates the approximated "$\frac{1}{2}$W" term in the divisor of the actuarial estimator.

Slawski (1991) shows that the maximum likelihood estimator and conventional estimator for full data using the "level deaths" mortality assumption are *asymptotically* equal.

It is interesting to note that equation (2.77), which defines the maximum likelihood estimator of q_x when the "level deaths" mortality assumption applies, can be simplified to:

$$\sum_{N} \frac{1}{1 - s_i * q_x} = \sum_{SW} \frac{1}{1 - t_i * q_x} \tag{2.84}$$

and that this then does suggest that the maximum likelihood and conventional estimators of q_x are identical when the "level deaths" assumption is made; because the "level deaths" mortality assumption applies, equation (2.84) can be written as:

$$\sum_{N} \frac{1}{s_i p_x} = \sum_{WS} \frac{1}{t_i p_x} \tag{2.85}$$

and, from equation (2.52), this defines the conventional estimator.

2.24 An alternative criterion generally producing the same estimator as the method of maximum likelihood

We will now consider the general form of the equation for the estimator of a general mortality parameter ϕ, which could be q_x, given by the maximum likelihood approach just discussed, and we will then identify an alternative criterion which gives the same estimator without involving a notional withdrawal distribution. Starting from the general likelihood function set out earlier in equation (2.63):

$$L = \prod_{N} (1 - {}_{t_i - s_i}q_{x+s_i})(1 - {}_{t_i - s_i}r_{x+s_i}) \prod_{D} \mu_{x+t_i} \prod_{W^*} \nu_{x+t_i}$$

$$= \prod_{N} \frac{{}_{t_i}p_x}{{}_{s_i}p_x} \prod_{D} \mu_{x+t_i} \prod_{N} (1 - {}_{t_i-s_i}r_{x+s_i}) \prod_{W^*} \nu_{x+t_i} \tag{2.86}$$

$$\Rightarrow \quad \log L = \sum_{D} \log \mu_{x+t_i} + \sum_{N} \log {}_{t_i}p_x - \sum_{N} \log {}_{s_i}p_x$$

$$+ \text{ terms independent of mortality} \tag{2.87}$$

$$\Rightarrow \quad \frac{\partial \log L}{\partial \phi} = \sum_{D} \frac{\frac{\partial \mu_{x+t_i}}{\partial \phi}}{\mu_{x+t_i}} + \sum_{N} \frac{\frac{\partial {}_{t_i}p_x}{\partial \phi}}{{}_{t_i}p_x} - \sum_{N} \frac{\frac{\partial {}_{s_i}p_x}{\partial \phi}}{{}_{s_i}p_x} \tag{2.88}$$

Equating to zero leads to:

$$\sum_{D} \frac{\frac{\partial \mu_{x+t_i}}{\partial \phi}}{\mu_{x+t_i}} = \sum_{N} \frac{\frac{\partial {}_{s_i}p_x}{\partial \phi}}{{}_{s_i}p_x} - \sum_{N} \frac{\frac{\partial {}_{t_i}p_x}{\partial \phi}}{{}_{t_i}p_x} \tag{2.89}$$

Further manipulation leads to:

$$\sum_{D} \frac{\frac{\partial ({}_{t_i}p_x \, \mu_{x+t_i})}{\partial \phi}}{{}_{t_i}p_x \, \mu_{x+t_i}} = \sum_{N} \frac{\frac{\partial {}_{s_i}p_x}{\partial \phi}}{{}_{s_i}p_x} - \sum_{SW} \frac{\frac{\partial {}_{t_i}p_x}{\partial \phi}}{{}_{t_i}p_x} \tag{2.90}$$

Alternatively we have:

$$\sum_{N} \frac{\frac{\partial {}_{s_i}p_x}{\partial \phi}}{{}_{s_i}p_x} = \sum_{D} \frac{\frac{\partial ({}_{t_i}p_x \, \mu_{x+t_i})}{\partial \phi}}{{}_{t_i}p_x \, \mu_{x+t_i}} + \sum_{SW} \frac{\frac{\partial {}_{t_i}p_x}{\partial \phi}}{{}_{t_i}p_x} \tag{2.91}$$

Let us look closely at this last expression. It has an interesting and exciting interpretation.

The expression inside the summation on the left-hand side is the rate of proportionate change, as ϕ varies, in the number of lives surviving from age x to be entrants at age $x+s_i$, and this is applied to each of the actual entrants for the appropriate values of $x+s_i$ to give, after summing, the rate of change as ϕ varies of the number of those entering.

The expression inside the first summation on the right-hand side is the rate of proportionate change, as ϕ varies, in the number of lives dying at age $x+t_i$, and this is applied to each of

the actual deaths for the appropriate values of $x+t_i$ to give, after summing, the rate of change as ϕ varies of the number of those dying.

The expression inside the second summation on the right-hand side is the rate of proportionate change, as ϕ varies, in the number of lives surviving from age x to be non-death exits at age $x+t_i$, and this is applied to each of the actual non-deaths for the appropriate values of $x+t_i$ to give, after summing, the rate of change as ϕ varies of the number of those exiting other than by death.

Thus equation (2.91) equates the rate of change, as ϕ varies, of the number of those entering the investigation to the rate of change, as ϕ varies, of the number of those exiting the investigation.

It is important to note that in each of the three summation expressions, we are considering the lives surviving under mortality from age x, the beginning of the year of age, up to entry and exit. The period from age x up to the point of entry, if this is after age x, thus plays an essential role in this analysis. This is pleasing from the philosophical point of view since we are attempting to estimate ϕ, a parameter related to the probability of dying in the year commencing at exact age x, and to be an entrant at age $x+s_i$, a life must survive from age x.

It is also pleasing that this type of estimator can be seen to arise from considering the survival under mortality from age x exact of both entrants and exits, because the conventional estimator was also seen to arise from a consideration of the survival under mortality from age x exact of both entrants and exits, a pleasing common feature.

Thus, by considering only mortality aspects of the mortality investigation scenario, we are able to reproduce the equation defining the estimator of a general mortality parameter which was previously obtained by using the technique of maximum likelihood.

This is a very interesting result, and it is also interesting that the new scenario-based derivation does not at any stage assume knowledge of the nature of withdrawals (ie whether scheduled or unscheduled) or of the force of withdrawal governing unscheduled withdrawals. The method of maximum likelihood assumes initially that such knowledge is available, although it generally become irrelevant in the subsequent mathematical development.

CHAPTER III

Properties and applications of the rectangular hyperbolic and Gompertz mortality distributions

3.1 Three common mortality assumptions

Three particular mortality assumptions have been introduced very frequently in the literature when exposed-to-risk methods and the derivation of mortality rates have been discussed. They are also three assumptions to which frequent reference has also been made already in this thesis, namely:

A — uniform distribution of deaths ("level deaths")

B — Balducci assumption

C — constant force of mortality ("constant μ")

The notation A, B and C appears to have been first used by Batten (1978) and has been followed by a number of subsequent authors, for example Greville (1978), Hoem (1980, 1984) and Broffitt (1984). However it should be noted that the assumptions do not form a logical sequence in the order A, B, C, as Batten himself recognised.

It is easily shown, as demonstrated in Section A1.1 of Appendix 1, that these mortality assumptions are special cases of a more general mortality law, namely:

$$\mu_{x+t} = \frac{1}{a - bt}, \qquad (0 \leq t \leq 1) \tag{3.1}$$

As further demonstrated in Section A1.1 of Appendix 1,

$b = -1$ gives assumption B, "Balducci"

$b = 0$ gives assumption C, "constant μ"

b = 1 gives assumption A, "level deaths"

It will be seen that the three assumptions fall into the natural sequence B, C, A or A, C, B.

3.2 The rectangular hyperbolic mortality distribution

Under the mortality distribution defined by the equation:

$$\mu_{x+t} = \frac{1}{a - bt}, \qquad (0 \leq t \leq 1), \tag{3.2}$$

the force of mortality follows the mathematical form known as the rectangular hyperbola, and therefore it appears appropriate to call this distribution, "the rectangular hyperbolic mortality distribution".

It can be seen that the constant a determines μ_x, the value of the force of mortality at the beginning of the year of age, and in fact μ_x equals the reciprocal of a, while the constant b determines how the force of mortality develops over the year of age from the value set at exact age x by the constant a.

As shown in Section A1.4 of Appendix 1,

$$\text{if } b \neq 0, \qquad a = \frac{b}{1 - (1 - q_x)^b} \tag{3.3}$$

$$\text{if } b = 0, \qquad a = \frac{-1}{\log (1 - q_x)} \tag{3.4}$$

Thus μ_{x+t} can be expressed in the range $(0 \leq t \leq 1)$ as a function of q_x and b, where b is the parameter determining the particular mortality distribution.

The constant b can be expressed in terms of μ_x and μ_{x+1} as follows:

$$b = \frac{1}{\mu_x} - \frac{1}{\mu_{x+1}} \tag{3.5}$$

and this reflects the fact that, once it is decided that the rectangular hyperbolic distribution is applicable, there is only one possible curve that can represent μ_{x+t} if its values at $t = 0$ and $t = 1$ are already determined, ie the distribution is then fully defined.

Further expressions which arise are:

$$q_x = 1 - (1 - \frac{b}{a})^{\frac{1}{b}} = 1 - (1 - b\mu_x)^{\frac{1}{b}} \qquad \text{if } b \neq 0 \tag{3.6}$$

or
$$q_x = 1 - e^{\frac{-1}{a}} = 1 - e^{-\mu} \qquad \text{if } b = 0 \tag{3.7}$$

Differentiation of the expression:

$$\mu_{x+t} = \frac{1}{a - bt}, \qquad (0 \leq t \leq 1), \tag{3.8}$$

with respect to t leads to the results:

$$\frac{d\mu_{x+t}}{dt} < 0 \qquad \text{for } b < 0 \tag{3.9}$$

$$\frac{d\mu_{x+t}}{dt} > 0 \qquad \text{for } b > 0 \tag{3.10}$$

These show that μ_{x+t} decreases or increases with decreasing t according to whether b is less than or greater than zero, which is consistent with the fact that $b = 0$ corresponds to "constant μ".

As also shown in Section A1.6 of Appendix 1, we have the further results:

$$\frac{d^2 l_{x+t}}{dt^2} > 0 \qquad \text{for } b < 1 \tag{3.11}$$

$$\frac{d^2 l_{x+t}}{dt^2} < 0 \qquad \text{for } b > 1 \tag{3.12}$$

These expressions show that the life table curve l_{x+t} is convex downwards or upwards according to whether b is less than or greater than one. This implies that a transition from $b < 1$ to $b > 1$, or vice versa, indicates the presence of a point of inflection in l_{x+t}, which is consistent with $b = 1$ corresponding to the uniform distribution of deaths, for which l_{x+t} will be a straight line.

Thus, given a table of μ_x for successive integral ages x, it is easy to detect the approximate location of points of inflection in the l_x curve by calculating:

$$b = \frac{1}{\mu_x} - \frac{1}{\mu_{x+1}} \tag{3.13}$$

for successive x and looking for the ages at which b moves either up or down past the value $b = 1$ as x increases.

Table 3.1 shows some values of b, calculated using equation (3.13), for a selection of

mortality tables. It will be seen that the progress of b as age increases is broadly similar in the five tables considered, the value of b declining from values of the order 50–100 for ages in the late 30's, through values of the order 5–10 around age 60, to values of the order 0.1–0.2 around age 100. The decline in b appears to be generally delayed for mortality tables with lighter mortality.

Table 3.1 Some values of b calculated using the formula

$$b = \frac{1}{\mu_x} - \frac{1}{\mu_{x+1}}$$

Age	A1967-70 ultimate	ELT 14 males	ELT 14 females	a(90) ult males	a(90) ult females
20	-63.311	-80.183	79.365		
25	-53.635	15.056	64.102		
30	28.933	38.314	73.992		
35	99.658	62.730	101.351		
40	81.242	59.249	81.454		
45	46.109	37.003	49.735		
50	24.372	19.445	27.925		
55	13.072	10.022	15.297		
60	7.247	5.268	9.072	6.928	10.989
65	4.148	3.149	5.784	4.336	7.202
70	2.438	1.971	4.106	2.628	4.500
75	1.462	1.192	2.563	1.568	2.676
80	0.890	0.716	1.546	0.925	1.563
85	0.548	0.427	0.853	0.544	0.897
90	0.341	0.242	0.398	0.319	0.511
95	0.214	0.167	0.193	0.188	0.290
100	0.135	0.165	0.204	0.110	0.163
105	0.087				

Some further important results derived in Sections A1.7 and A1.8 of Appendix 1 are:

For $b \neq 0$:
$$_{t-s}p_{x+s} = \left(\frac{a - bt}{a - bs}\right)^{\frac{1}{b}} = \left(\frac{\mu_{x+s}}{\mu_{x+t}}\right)^{\frac{1}{b}} \qquad (3.14)$$

For $b = 0$:
$$_{t-s}p_{x+s} = e^{\frac{-(t-s)}{a}} = e^{-(t-s)\mu} = (p_x)^{t-s} \qquad (3.15)$$

And:

For $b \neq 0$:
$$l_{x+r} \propto (\frac{1}{\mu_{x+r}})^{\frac{1}{b}} \tag{3.16}$$

where x is a given integer and $0 \leq r \leq 1$.

For $b = 0$:
$$l_{x+r} \propto e^{-\mu r} \tag{3.17}$$

where x is a given integer and $0 \leq r \leq 1$.

It will be noted that, when $b = 1$ ("level deaths" assumption), we have:

$$l_{x+r} * \mu_{x+r} = \text{a constant}, \tag{3.18}$$

which is a familiar result from life contingencies, and that when $b = -1$ (Balducci assumption), we have:

$$l_{x+r} = \mu_{x+r} * \text{constant}, \tag{3.19}$$

so that both l_{x+r} and μ_{x+r} have the same downward sloping, convex downwards, shape.

Using the mortality law that

$$\mu_{x+t} = \frac{1}{a - bt}, \qquad (0 \leq t \leq 1), \tag{3.20}$$

it is possible to derive a number of interesting life contingencies relationships and to create some possibly useful approximations for application when the law is not strictly true. Perhaps these might be thought of as enhancements of approximations based on the common "level deaths" assumption, since b is now no longer assumed to take the value unity, but is estimated from available tabulated items.

Some interesting results are the following expressions for p_x, ${}_{t-s}p_{x+s}$ and m_x, when μ is not constant, requiring only values of μ_x and μ_{x+1} for evaluation:

$$p_x = (\frac{\mu_x}{\mu_{x+1}})^{\frac{\mu_x \mu_{x+1}}{\mu_{x+1} - \mu_x}} \tag{3.21}$$

$${}_{t-s}p_{x+s} = (\frac{t\mu_x + (1-t)\mu_{x+1}}{s\mu_x + (1-s)\mu_{x+1}})^{\frac{\mu_x \mu_{x+1}}{\mu_{x+1} - \mu_x}} \tag{3.22}$$

$$m_x = \frac{1 - \left(\frac{\mu_x}{\mu_{x+1}}\right)^{\frac{\mu_x \mu_{x+1}}{\mu_{x+1} - \mu_x}}}{1 - \left(\frac{\mu_x}{\mu_{x+1}}\right)^{\left(\frac{\mu_x \mu_{x+1}}{\mu_{x+1} - \mu_x} + 1\right)}} * \left(1 + \mu_x - \frac{\mu_x}{\mu_{x+1}}\right) \tag{3.23}$$

The expressions for p_x and ${}_{t-s}p_{x+s}$ follow from the earlier result (3.14):

$${}_{t-s}p_{x+s} = \left(\frac{\mu_{x+s}}{\mu_{x+t}}\right)^{\frac{1}{b}} \tag{3.24}$$

by firstly expressing the right-hand in terms of a and b, and then expressing a and b in terms of μ_x and μ_{x+1}.

The derivation of the expression for m_x is summarised in Section A1.9 of Appendix 1.

Many of the results just developed for the rectangular hyperbolic mortality distribution will be applied in the subsequent development of ideas relating to the determination of q_x.

It is of course a major aspect of the rectangular hyperbolic mortality distribution that it involves two constants in order to define the mortality assumption concerned; another mortality distribution also involving two constants is of course the Gompertz distribution, and this distribution will also be applied in the subsequent work. Although the Gompertz distribution is very well known, some results based on it will be used in forms which may not be immediately familiar. These will be derived next.

3.3 The Gompertz mortality distribution

The form in which "Gompertz's Law" is traditionally quoted is:

$$\mu_x = B\, c^x \tag{3.25}$$

where the law is typically taken to apply over a large range of age, perhaps as originally from a young age up to the limiting age ω. However in most of our applications, we will only be concerned with the behaviour of μ_{x+t} as t varies in the range $0 \leq t \leq 1$, with x being fixed. Therefore we will consider the Gompertz mortality distribution in the form:

$$\mu_{x+t} = B'\, c^t \qquad (0 \leq t \leq 1) \tag{3.26}$$

Now we will proceed to derive some results applicable under this mortality law.

If $c \neq 1$,

$$
\begin{aligned}
{}_tp_x &= \exp\left(-\int_0^t \mu_{x+r}\, dr\right) \\
&= \exp\left(-\int_0^t B' c^r\, dr\right) \\
&= \exp\left(-\left[\frac{B'}{\log c} c^r\right]_0^t\right) \\
&= \exp\left(-\frac{B'}{\log c}(c^t - 1)\right) \\
&= h^{(c^t - 1)} \qquad (3.27)
\end{aligned}
$$

$$
\text{where } h = \exp\left(-\frac{B'}{\log c}\right) \qquad (3.28)
$$

$$
\Rightarrow \quad {}_{t-s}p_{x+s} = \frac{{}_tp_x}{{}_sp_x} = h^{(c^t - c^s)} \qquad (3.29)
$$

$$
\Rightarrow \quad p_x = h^{c-1} \qquad (3.30)
$$

$$
\Rightarrow \quad {}_{t-s}p_{x+s} = p_x^{\left(\frac{c^t - c^s}{c-1}\right)} \qquad (3.31)
$$

An interesting form is:

$$
{}_{t-s}p_{x+s} = p_x^{\left(\frac{\mu_{x+t} - \mu_{x+s}}{\mu_{x+1} - \mu_x}\right)} \qquad (3.32)
$$

When $c = 1$, we have the "constant μ" assumption again. Bearing in mind equation (3.15) applying to the rectangular hyperbolic distribution when $b = 0$, and observing that $\mu_x = B'$ here, the following results can be seen to apply:

For $c = 1$:
$$
{}_{t-s}p_{x+s} = e^{-(t-s)\mu} = e^{-(t-s)B'} = (p_x)^{t-s} \qquad (3.33)
$$

It is worth noting that the situation where both distributions give the "constant μ" assumption is the only occasion on which the rectangular hyperbolic mortality distribution and the Gompertz distribution give the same distribution, for appropriate values of the distribution parameters.

We will recall that in the case of the rectangular hyperbolic mortality distribution, we noted that one parameter, a, determined μ_x, the value of the force of mortality at the beginning of the year of age, while the other parameter, b, determined how the force of mortality developed over the year of age from the value set at exact age x by the parameter a.

It is interesting to note that a similar situation applies over the year of age in the case of the

Gompertz distribution: the parameter B' determines μ_x (and in fact equals μ_x) while the parameter c determines how the force of mortality develops over the year of age from the value set at exact age x by the parameter B'.

3.4 The shape of the rectangular hyperbolic mortality distribution

In Sections 3.19 to 3.27 of this chapter, the shapes of the rectangular hyperbolic and Gompertz mortality distributions are compared in some detail.

It is found in Section 3.20 that both curves are monotonically increasing or decreasing, and that both have a second differential coefficient which is always positive.

However the curvature of the rectangular hyperbolic curve will be greater than that of the Gompertz curve and, in particular, the vertical displacement of the rectangular hyperbolic curve at the age $x+\frac{1}{2}$ from the straight line joining the given values of μ_x and μ_{x+1} will be about twice as great as that of the Gompertz curve (as shown in Section 3.22).

Although the rectangular hyperbolic curve would appear typically to exhibit greater curvature than the Gompertz curve over a year of age, it is not so great that it appears in any way calamitous. In fact the curve seems to provide a useful alternative to the Gompertz curve for experimentation and investigations over a year of age.

A useful benefit of fitting the rectangular hyperbolic curve to μ_{x+t} over a year of age is the convenient algebraic development which it permits, when other mortality functions are evaluated. The curve is arguably more co-operative in terms of algebraic simplicity than the Gompertz curve.

However, as also discussed in Section 3.27, the shape of the rectangular hyperbolic curve is unlikely to be suitable for fitting over a wide age span to μ_{x+t} for human data.

3.5 Applications of the rectangular hyperbolic and Gompertz mortality distributions

We will now re-express the equations defining the conventional and implication-B estimators in terms of the parameters defining:

(a) the rectangular hyperbolic mortality distribution

(b) the Gompertz mortality distribution

3.6 The conventional estimator for the rectangular hyperbolic mortality distribution

The conventional estimator is the value of q_x that solves:

$$\sum_{N} \frac{1}{s_i p_x} = \sum_{WS} \frac{1}{t_i p_x} \tag{3.34}$$

When the rectangular hyperbolic distribution applies (and $b \neq 0$), we have:

$$\sum_{N} \frac{1}{(a - bs_i)^{\frac{1}{b}}} = \sum_{WS} \frac{1}{(a - bt_i)^{\frac{1}{b}}} \tag{3.35}$$

or

$$\sum_{N} \frac{1}{(1 - ks_i)^{\frac{1}{b}}} = \sum_{WS} \frac{1}{(1 - kt_i)^{\frac{1}{b}}} \qquad \text{where } k = \frac{b}{a} \tag{3.36}$$

An interesting form of the equation is:

$$\sum_{N} (\mu_{x+s_i})^{\frac{1}{b}} = \sum_{WS} (\mu_{x+t_i})^{\frac{1}{b}} \tag{3.37}$$

It will be recalled that the normal use of the conventional estimator involves making a mortality assumption, and of course, commonly, the Balducci assumption is used, since this does not lead to an iterative derivation of q_x. Making a mortality assumption is equivalent to assuming a value for b in expression (3.35) or (3.36) and solving for a or k.

We then obtain q_x by applying equation (3.6):

$$q_x = 1 - (1 - \frac{b}{a})^{\frac{1}{b}} = 1 - (1 - k)^{\frac{1}{b}} \tag{3.38}$$

This procedure has been used in the simulation studies.

It will be apparent that the solution of the equation for a or k will normally involve an iterative method; however it can be seen that, if $b = -1$, the equation for k, say, simplifies to:

$$k = \frac{-D}{\sum_{WS} t_i - \sum_{N} s_i} \tag{3.39}$$

which thus avoids an iterative solution. Of course, $b = -1$ corresponds to the Balducci assumption, and the appropriate expression for q_x follows.

3.7 The conventional estimator for the Gompertz mortality distribution

Again we recall that the conventional estimator is the value of q_x that solves:

$$\sum_{N} \frac{1}{{}_{s_i}p_x} = \sum_{WS} \frac{1}{{}_{t_i}p_x} \tag{3.40}$$

When the Gompertz distribution applies (and $c \neq 1$), we have:

$$\sum_{N} \frac{1}{h^{c^{s_i}}} = \sum_{WS} \frac{1}{h^{c^{t_i}}} \tag{3.41}$$

The equivalent of assuming a value for b under the rectangular hyperbolic distribution is to assume a value of c. (Both of these parameters relate to the way the force of mortality develops over the year of age from the value of μ_x at the beginning of the year of age).

Therefore we assume a value for c and then solve the equation, almost certainly by an iterative method, to obtain a value for h.

We then obtain q_x by applying the following relationship, which follows from equation (3.30) derived for p_x for the Gompertz distribution:

$$q_x = 1 - h^{c-1} \tag{3.42}$$

Again this procedure has been used in the simulation studies.

3.8 The implication-B estimator for the rectangular hyperbolic mortality distribution

The implication-B estimator is the value of q_x that solves:

$$\sum_{WS} \frac{{}_{s_i}p_x}{{}_{t_i}p_x} = N \tag{3.43}$$

When the rectangular hyperbolic distribution applies (and $b \neq 0$), we have:

$$\sum_{WS} \left(\frac{a - bs_i}{a - bt_i}\right)^{\frac{1}{b}} = N \tag{3.44}$$

or

$$\sum_{WS} \left(\frac{1 - ks_i}{1 - kt_i}\right)^{\frac{1}{b}} = N \tag{3.45}$$

An interesting form of the equation is:

$$\sum_{WS} \left(\frac{\mu_{x+t_i}}{\mu_{x+s_i}}\right)^{\frac{1}{b}} = N \tag{3.46}$$

Following a similar procedure as for the conventional estimator, we assume a value for b, which is equivalent to choosing a mortality assumption, and solve iteratively for a (or k).

As before we then obtain q_x by applying equation (3.38):

$$q_x = 1 - (1 - \frac{b}{a})^{\frac{1}{b}} = 1 - (1 - k)^{\frac{1}{b}} \tag{3.47}$$

This procedure has also been used in the simulation studies.

3.9 The implication-B estimator for the Gompertz mortality distribution

Again we recall that the implication-B estimator is the value of q_x that solves:

$$\sum_{WS} \frac{s_i p_x}{t_i p_x} = N \tag{3.48}$$

When the Gompertz distribution applies (and $c \neq 1$), we have:

$$\sum_{WS} \frac{h^{c^{s_i}}}{h^{c^{t_i}}} = N \tag{3.49}$$

Again following a similar procedure as for the conventional estimator, we assume a value for c, which is equivalent to choosing a mortality assumption, and solve iteratively for h.

As before we then obtain q_x by applying the following relationship:

$$q_x = 1 - h^{c-1} \tag{3.50}$$

This procedure has also been used in the simulation studies.

3.10 The conventional and implication-B estimators when "constant μ" mortality assumption is made

It will have been noticed that the cases $b = 0$ and $c = 1$ have been omitted in our

consideration of the rectangular hyperbolic and Gompertz distributions respectively. It will be seen that the equations considered previously, which define the conventional and implication-B estimators in terms of the distribution parameters, cease to be defined when $b = 0$ or $c = 1$.

It is easily established that, when the "constant μ" assumption applies, the following equations can be obtained from the general equations defining the conventional and implication-B estimators:

Conventional estimator:

$$\sum_{N} \frac{1}{(p_x)^{s_i}} = \sum_{WS} \frac{1}{(p_x)^{t_i}} \tag{3.51}$$

Implication-B estimator:

$$\sum_{WS} \frac{(p_x)^{s_i}}{(p_x)^{t_i}} = N \tag{3.52}$$

These equations may be solved iteratively for p_x.

3.11 Maximum likelihood estimators

We turn now to consider the derivation of maximum likelihood estimators when the rectangular hyperbolic and Gompertz mortality distributions apply.

In Section 2.24, we saw that generally the method of maximum likelihood leads to an estimator of a mortality parameter ϕ (which could be q_x) which satisfies the equation:

$$\sum_{D} \frac{\frac{\partial({}_{t_i}p_x \, \mu_{x+t_i})}{\partial \phi}}{{}_{t_i}p_x \, \mu_{x+t_i}} = \sum_{N} \frac{\frac{\partial {}_{s_i}p_x}{\partial \phi}}{{}_{s_i}p_x} - \sum_{SW} \frac{\frac{\partial {}_{t_i}p_x}{\partial \phi}}{{}_{t_i}p_x} \tag{3.53}$$

This is obtained by differentiating the following log-likelihood function with respect to ϕ and equating the derivative to zero:

$$\log L = \sum_{D} \log \mu_{x+t_i} + \sum_{N} \log {}_{t_i}p_x - \sum_{N} \log {}_{s_i}p_x$$

$$+ \text{ terms independent of mortality} \tag{3.54}$$

The value of ϕ given by equation (3.53) will correspond with the maximum likelihood estimate of q_x, and so when we consider the situations where the rectangular hyperbolic or Gompertz mortality distributions apply, we can use the method of maximum likelihood to obtain values of the parameters corresponding to the maximum likelihood estimate of q_x.

Firstly, we will proceed as we did in the cases of the conventional and implication-B estimators, and suppose that we choose a mortality assumption, ie in the case of the rectangular hyperbolic distribution, we will choose the value of b and then obtain the value of a by applying the method of maximum likelihood, while in the case of the Gompertz distribution, we will choose the value of c and then obtain the value of B'.

Later, in Sections 3.16 and 3.17, we will consider the exciting alternative of letting the data choose the mortality assumption, by using the method of maximum likelihood to evaluate b or c.

However, firstly we consider the situation where a mortality assumption is made.

3.12 The rectangular hyperbolic mortality distribution: the maximum likelihood estimator of the parameter a when the value of parameter b is assumed

For convenience we will use the expression for the log-likelihood as our starting point, that is:

$$\log L = \sum_D \log \mu_{x+t_i} + \sum_N \log {}_{t_i}p_x - \sum_N \log {}_{s_i}p_x + \text{terms independent of mortality} \qquad (3.55)$$

When the rectangular hyperbolic distribution applies (and $b \neq 0$), this may be rewritten:

$$\log L = \sum_D \log \frac{1}{a - bt_i} + \sum_N \log \left(\frac{a - bt_i}{a}\right)^{\frac{1}{b}} - \sum_N \log \left(\frac{a - bs_i}{a}\right)^{\frac{1}{b}} + \text{etc} \qquad (3.56)$$

$$\Rightarrow \qquad \log L = -\sum_D \log(a - bt_i) + \frac{1}{b}\sum_N \log(a - bt_i) - \frac{1}{b}\sum_N \log(a - bs_i) + \text{etc} \qquad (3.57)$$

Now b is regarded as having been fixed in advance by the choice of the mortality assumption. We proceed to obtain a maximum likelihood estimate for a.

Differentiating with respect to a gives:

$$\frac{\partial \log L}{\partial a} = -\sum_{D} \frac{1}{a - bt_i} + \frac{1}{b}\sum_{N} \frac{1}{a - bt_i} - \frac{1}{b}\sum_{N} \frac{1}{a - bs_i} \tag{3.58}$$

Equating to zero gives:

$$\sum_{D} \frac{1}{a - bt_i} = \frac{1}{b}\left[\sum_{N} \frac{1}{a - bt_i} - \sum_{N} \frac{1}{a - bs_i}\right] \tag{3.59}$$

Equation (3.59) obviously ceases to be defined when $b = 0$ and appears to require an iterative solution for a when $b \neq 0$ for general data.

It is interesting to note that when $b = 1$, equation (3.59) simplifies to:

$$\sum_{N} \frac{1}{a - s_i} = \sum_{WS} \frac{1}{a - t_i} \tag{3.60}$$

which is equation (3.35) defining the conventional estimator when $b = 1$. This then provides elegant confirmation of the result in Section 2.23 that, when the "level deaths" mortality assumption applies, the maximum likelihood estimator and the "conventional" estimator are identical.

As with the equations for the conventional estimator and the implication-B estimator, the item $k = b/a$ might be introduced into the equation, giving the following expression, and the equation solved for k in this form:

$$\sum_{D} \frac{1}{1 - kt_i} = \frac{1}{b}\left[\sum_{N} \frac{1}{1 - kt_i} - \sum_{N} \frac{1}{1 - ks_i}\right] \tag{3.61}$$

An interesting form of the equation is:

$$\sum_{D} \mu_{x+t_i} = \frac{1}{b}\left[\sum_{N} \mu_{x+t_i} - \sum_{N} \mu_{x+s_i}\right] \tag{3.62}$$

As earlier, we obtain q_x by applying equation (3.38):

$$q_x = 1 - (1 - \tfrac{b}{a})^{\frac{1}{b}} = 1 - (1 - k)^{\frac{1}{b}} \tag{3.63}$$

This procedure has been used in the simulation studies.

3.13 The Gompertz mortality distribution: the maximum likelihood estimator of the parameter B' when the value of parameter c is assumed

When the Gompertz distribution applies (and $c \neq 1$), the log-likelihood may be written:

$$\log L = \sum_D \log B' c^{t_i} + \sum_N \log h^{(c^{t_i}-1)} - \sum_N \log h^{(c^{s_i}-1)} + \text{etc} \tag{3.64}$$

where it will be recalled that (equation (3.28)):

$$h = \exp\left(-\frac{B'}{\log c}\right) \tag{3.65}$$

$$\Rightarrow \qquad \log L = D \log B' + (\log c) \sum_D t_i + (\log h) \sum_N c^{t_i} - (\log h) \sum_N c^{s_i} \tag{3.66}$$

$$\Rightarrow \qquad \log L = D \log B' + (\log c) \sum_D t_i - \frac{B'}{\log c} \sum_N (c^{t_i} - c^{s_i}) \tag{3.67}$$

Now c is regarded as having been fixed in advance by the choice of the mortality assumption. We proceed to obtain a maximum likelihood estimate for B'

Differentiating with respect to B' gives:

$$\frac{\partial \log L}{\partial B'} = \frac{D}{B'} - \frac{1}{\log c} \sum_N (c^{t_i} - c^{s_i}) \tag{3.68}$$

Equating to zero gives:

$$B' = \frac{D}{\frac{1}{\log c} \sum_N (c^{t_i} - c^{s_i})} \tag{3.69}$$

By considering:

$$\frac{\partial^2 \log L}{\partial B'^2}$$

it is immediately obvious that the value of B' given by this equation corresponds to a maximum of the likelihood.

It will be seen that expression (3.69) does not define B' when $c = 1$.

Expression (3.69) is very interesting. Firstly B' can always be evaluated without resorting to an iterative method.

Secondly the format of the expression is redolent of a traditional "exposed-to-risk" style expression but with the divisor based on transformations of the times from the beginning of the year of age up to entry and up to exit, the transformation being achieved by the function:

$$f(r) = \frac{c^r}{\log c} \tag{3.70}$$

If the data is held on a computer, the expression (3.69) for B' is very easy to calculate.

The value for q_x can readily be obtained from B' and the assumed value of c, by applying equations (3.28) and (3.30):

$$q_x = 1 - h^{c-1} \quad \text{where} \quad h = \exp\left(-\frac{B'}{\log c}\right) \tag{3.71}$$

In fact, if we substitute for B' in the expression for h using equation (3.69), we see that q_x can be estimated directly using:

$$q_x = 1 - \exp\left[\frac{-D\,(c-1)}{\sum_N (c^{t_i} - c^{s_i})}\right] \tag{3.72}$$

Again this procedure has been used in the simulation studies.

It is interesting to note that the expression (3.69) giving B' can be re-expressed as:

$$D = \frac{1}{\log c} \sum_N (\mu_{x+t_i} - \mu_{x+s_i}) \tag{3.73}$$

3.14 The maximum likelihood estimator when the "constant μ" mortality assumption is made

It will have been noticed that the cases b = 0 and c = 1 have again been omitted in our consideration of the rectangular hyperbolic and Gompertz distributions respectively. It has been seen that the equations defining the parameters a and B′, respectively, cease to be defined when b = 0 or c = 1.

As shown in Section 2.22, when the "constant μ" assumption applies, the method of maximum likelihood leads to the following estimator of μ:

$$\mu = \frac{D}{\sum_{N} (t_i - s_i)} \tag{3.74}$$

3.15 Maximum likelihood estimators with no distribution parameter assumed

Now we come on to the exciting alternative of allowing the data to determine the mortality assumption used in the analysis, by using the method of maximum likelihood to evaluate b or c.

3.16 The rectangular hyperbolic mortality distribution: maximum likelihood estimators with no distribution parameter assumed

We have the following expression for the log-likelihood under the rectangular hyperbolic mortality distribution (when $b \neq 0$):

$$\log L = -\sum_{D} \log (a - bt_i) + \frac{1}{b} \sum_{N} \log (a - bt_i) - \frac{1}{b} \sum_{N} \log (a - bs_i) + \text{etc} \tag{3.75}$$

Now we are regarding both a and b as parameters to be evaluated by the method of maximum likelihood. Therefore we will determine the partial differential coefficients of the log-likelihood with respect to a and b, equate them to zero and solve the resulting simultaneous equations for a and b. We must however bear in mind that difficulties will arise if b = 0.

The simultaneous equation obtained from the partial differential coefficient with respect to a will be identical with that obtained when b was regarded as a pre-chosen constant, that is (equation (3.59)):

$$\sum_{D} \frac{1}{a - bt_i} = \frac{1}{b}\left[\sum_{N} \frac{1}{a - bt_i} - \sum_{N} \frac{1}{a - bs_i}\right] \tag{3.76}$$

When we differentiate with respect to b, we obtain:

$$\frac{\partial \log L}{\partial b} = \sum_{D} \frac{t_i}{a - bt_i} - \frac{1}{b^2}\sum_{N} \log (a - bt_i) - \frac{1}{b}\sum_{N} \frac{t_i}{a - bt_i} + \frac{1}{b^2}\sum_{N} \log (a - bs_i) + \frac{1}{b}\sum_{N} \frac{s_i}{a - bs_i} \tag{3.77}$$

Equating this to zero gives:

$$\sum_{D} \frac{t_i}{a - bt_i} = \frac{1}{b}\left[\sum_{N} \frac{t_i}{a - bt_i} - \sum_{N} \frac{s_i}{a - bs_i})\right] - \frac{1}{b^2}\left[\sum_{N} \log (a - bs_i) - \sum_{N} \log (a - bt_i)\right] \tag{3.78}$$

This is obviously a more complicated equation than we have met previously.

However if we view it as one of a pair of simultaneous equations, it is possible that application of the other equation in the pair can achieve some simplification, and this proves to be the case.

The other equation in the pair is:

$$\sum_{D} \frac{1}{a - bt_i} = \frac{1}{b}\left[\sum_{N} \frac{1}{a - bt_i} - \sum_{N} \frac{1}{a - bs_i}\right] \tag{3.79}$$

which gives:

$$\sum_{D} \frac{a}{a - bt_i} = \frac{1}{b}\left[\sum_{N}(\frac{a}{a - bt_i} - 1) - \sum_{N}(\frac{a}{a - bs_i} - 1)\right] \tag{3.80}$$

leading to:

$$\sum_{D} \frac{1}{a - bt_i} = \frac{1}{a}\left[\sum_{N} \frac{t_i}{a - bt_i} - \sum_{N} \frac{s_i}{a - bs_i}\right] \tag{3.81}$$

Thus, in the pair of simultaneous equations, equation (3.78) can be replaced by:

$$\sum_D \frac{t_i}{a - bt_i} = \frac{a}{b} \sum_D \frac{1}{a - bt_i} - \frac{1}{b^2} \left[\sum_N \log (a - bs_i) - \sum_N \log (a - bt_i) \right] \tag{3.82}$$

This equation can be rearranged to give:

$$\sum_D \frac{bt_i - a}{a - bt_i} = - \frac{1}{b} \left[\sum_N \log (a - bs_i) - \sum_N \log (a - bt_i) \right] \tag{3.83}$$

$$\Rightarrow \qquad D = \frac{1}{b} \left[\sum_N \log (a - bs_i) - \sum_N \log (a - bt_i) \right] \tag{3.84}$$

Thus the values of a and b given by the method of maximum likelihood can be obtained by solving the simultaneous equations:

$$D = \frac{1}{b} \left[\sum_N \log (a - bs_i) - \sum_N \log (a - bt_i) \right] \tag{3.85}$$

$$\sum_D \frac{1}{a - bt_i} = \frac{1}{b} \left[\sum_N \frac{1}{a - bt_i} - \sum_N \frac{1}{a - bs_i} \right] \tag{3.86}$$

As before, the equations can be expressed and solved using $k = \frac{b}{a}$ which gives:

$$D = \frac{1}{b} \left[\sum_N \log (1 - ks_i) - \sum_N \log (1 - kt_i) \right] \tag{3.87}$$

$$\sum_D \frac{1}{1 - kt_i} = \frac{1}{b} \left[\sum_N \frac{1}{1 - kt_i} - \sum_N \frac{1}{1 - ks_i} \right] \tag{3.88}$$

It will be noted that these equations are not defined when $b = 0$. In practice an iterative method of solution will almost certainly be required, and steps must be taken to ensure that the procedure can cope, should the value $b = 0$ be thrown up during the iterative process.

These equations were employed as part of the simulation studies and a practical expedient was successfully employed to circumvent the complication.

The equation (3.85) of the pair of simultaneous equations has some interesting features.

Firstly, if a mortality assumption is being made, ie a value of b assumed, this equation provides another estimator for a, and simulation studies have shown this to give very

satisfactory results. In Chapter 4 of this thesis, theory will be developed which will give a better understanding of this estimator. The author will refer to this estimator as the "log-estimator".

Secondly, equation (3.85) can be expressed in some interesting forms. From equation (3.85), we have:

$$D = \frac{1}{b} \sum_{N} \log \frac{a - bs_i}{a - bt_i}$$

$$= \sum_{N} \log \left(\frac{a - bs_i}{a - bt_i}\right)^{\frac{1}{b}} \tag{3.89}$$

which leads to the forms:

$$D = \sum_{N} \log \frac{\mu_{x+t_i}}{\mu_{x+s_i}} \tag{3.90}$$

and

$$D = \sum_{N} \log \frac{1}{t_i\text{-}s_i p_{x+s_i}} \tag{3.91}$$

Expression (3.91) is superficially reminiscent of the expression defining the implication estimator, namely:

$$\sum_{WS} \frac{1}{t_i\text{-}s_i p_{x+s_i}} = N \tag{3.92}$$

Clearly however, there are major differences in these two expressions.

Expression (3.91) can also be expressed as:

$$\prod_{N} t_i\text{-}s_i p_{x+s_i} = e^{-D} \tag{3.93}$$

which appears a quite remarkable relationship. The left-hand side is the probability that all the lives in the investigation will each survive under mortality for exactly the period for which they were actually present in the investigation.

In Section 4.8 of this thesis, a derivation of equation (3.93) will be presented that does not exclude the case $b = 0$, as here, and it can be seen that if the left-hand side is evaluated assuming the "constant μ" mortality law, the familiar maximum likelihood estimator for μ

(equation (2.67)) is obtained , namely:

$$\mu = \frac{D}{\sum_{N} (t_i - s_i)} \tag{3.94}$$

3.17 The Gompertz mortality distribution: maximum likelihood estimators with no distribution parameter assumed

We have the following expression for the log-likelihood under the Gompertz mortality distribution (when $c \neq 1$):

$$\log L = D \log B' + (\log c) \sum_{D} t_i - \frac{B'}{\log c} \sum_{N} (c^{t_i} - c^{s_i}) \tag{3.95}$$

Now we are regarding both B' and c as parameters to be evaluated by the method of maximum likelihood. Therefore we will determine the partial differential coefficients of the log-likelihood with respect to B' and c, equate them to zero and solve the resulting simultaneous equations for B' and c. We must however bear in mind that difficulties will arise if $c = 1$.

The simultaneous equation obtained from the partial differential with respect to B' will be identical with that obtained when c was regarded as a pre-chosen constant (equation (3.69)), that is:

$$B' = \frac{D}{\frac{1}{\log c} \sum_{N} (c^{t_i} - c^{s_i})} \tag{3.96}$$

When we differentiate with respect to c, we obtain:

$$\frac{\partial \log L}{\partial c} = \frac{1}{c} \sum_{D} t_i + \frac{B'}{c (\log c)^2} \sum_{N} (c^{t_i} - c^{s_i}) - \frac{B'}{c \log c} \sum_{N} (t_i c^{t_i} - s_i c^{s_i}) \tag{3.97}$$

Equating this to zero (and assuming $c \neq 1$) gives:

$$\sum_{D} t_i = \frac{B'}{\log c} \left(\sum_{N} (t_i c^{t_i} - s_i c^{s_i}) - \frac{1}{\log c} \sum_{N} (c^{t_i} - c^{s_i}) \right) \tag{3.98}$$

Again this is a complicated expression. However if we view it as one of a pair of

simultaneous equations, we are able to effect some simplification by application of the other equation in the pair of equations.

The other equation in the pair is:

$$B' = \frac{D}{\frac{1}{\log c} \sum_{N} (c^{t_i} - c^{s_i})} \tag{3.99}$$

and substituting for B' in equation (3.98) gives:

$$\sum_{D} t_i = D \left[\frac{\sum_{N} (t_i c^{t_i} - s_i c^{s_i})}{\sum_{N} (c^{t_i} - c^{s_i})} - \frac{1}{\log c} \right] \tag{3.100}$$

This equation has only one unknown, namely c, and it must be solved iteratively. Obviously the equation is not defined when $c = 1$ and steps must be taken to ensure that the iterative procedure can cope, should the value $c = 1$ be thrown up during the iteration.

Thus the values of B' and c given by the method of maximum likelihood can be obtained by solving the simultaneous equations:

$$\sum_{D} t_i = D \left[\frac{\sum_{N} (t_i c^{t_i} - s_i c^{s_i})}{\sum_{N} (c^{t_i} - c^{s_i})} - \frac{1}{\log c} \right] \tag{3.101}$$

$$B' = \frac{D}{\frac{1}{\log c} \sum_{N} (c^{t_i} - c^{s_i})} \tag{3.102}$$

As before the value of q_x can be readily obtained using the relationship:

$$q_x = 1 - h^{c-1} \quad \text{where} \quad h = \exp\left(-\frac{B'}{\log c}\right) \tag{3.103}$$

These equations have been successfully used in the simulation studies.

In fact, if we substitute for B' in the expression for h using equation (3.102), we see that q_x can be estimated directly using:

$$q_x = 1 - \exp\left[\frac{-D\,(c-1)}{\sum_N (c^{t_i} - c^{s_i})}\right] \tag{3.104}$$

and we need only to solve equation (3.101) iteratively for c in order to evaluate this.

3.18 An approximate relationship between b and c

In the simulation studies reported in Chapter 5 of this thesis, values of both b and c are estimated for the same bodies of data as part of the estimation of q_x using two-parameter maximum likelihood estimators, assuming firstly a rectangular hyperbolic mortality distribution and secondly a Gompertz mortality distribution.

It is useful to have an approximate relationship linking values of b and c fitted to the same data, in order to apply a rough check to the results. Such a formula must of necessity be approximate because, as already noted, the two mortality distributions never coincide except in the special case when μ is constant.

A simple approximate relationship can be readily found. Consider the rectangular hyperbolic mortality distribution which is such that:

$$\mu_x = \tfrac{1}{a} \quad , \quad \mu_{x+1} = \frac{1}{a-b} \quad \text{and} \quad q_x = 1 - (1 - \tfrac{b}{a})^{\frac{1}{b}} \tag{3.105}$$

Let c be the value of μ_{x+1}/μ_x in the Gompertz mortality distribution which has the same values of μ_{x+t} as the rectangular hyperbolic mortality distribution when $t = 0$ and $t = 1$.

Then it is apparent that:

$$p_x = 1 - q_x = (1 - \tfrac{b}{a})^{\frac{1}{b}} = (\tfrac{1}{c})^{\frac{1}{b}} \tag{3.106}$$

This gives:

$$c = \frac{1}{(p_x)^b} \tag{3.107}$$

or alternatively:

$$b = -\frac{\log c}{\log p_x} \tag{3.108}$$

It should be noted that p_x in the formulae (3.107) and (3.108) refers to the probability of surviving from age x to x+1 in the rectangular hyperbolic mortality distribution. The probability of surviving from age x to x+1 in the Gompertz mortality distribution will be slightly different. This reflects the fact that the two distributions do not coincide.

3.19 Comparison of the shapes of the rectangular hyperbolic and Gompertz mortality distributions over the year of age

The remainder of this chapter will be devoted to a detailed comparison of the shapes of the rectangular hyperbolic and Gompertz mortality distributions over the year of age.

3.20 Preliminary examination of the shapes

The shape of the Gompertz distribution is well-known; it is of course an exponential curve of the general shape:

$$y = k_1 e^{k_2 x} \qquad (k_1, k_2 \text{ constants}) \tag{3.109}$$

With regard to the rectangular hyperbolic curve, as t increases, μ_{x+t} travels from the value μ_x to the value μ_{x+1} along a monotonically increasing or decreasing curve which arcs below the straight line joining the values μ_x and μ_{x+1}, i.e. the curve is concave upwards.

This can be seen from the first and second derivatives of:

$$\mu_{x+t} = \frac{1}{a - bt} \tag{3.110}$$

namely:

$$\frac{d\mu_{x+t}}{dt} = \frac{b}{(a - bt)^2} = b\,(\mu_{x+t})^2 \tag{3.111}$$

and:

$$\frac{d^2\mu_{x+t}}{dt^2} = \frac{2b^2}{(a - bt)^3} = 2b^2(\mu_{x+t})^3 \tag{3.112}$$

The first derivative never changes sign and the second derivative is always positive.

3.21 Measures to compare the rectangular hyperbolic and Gompertz curves

In order to compare the shape of the rectangular hyperbolic curve with the Gompertz curve and the straight line, we will investigate two features of the curves. Figure 3.1 will illustrate the discussion that now follows.

Firstly we will identify the position of the Gompertz and rectangular hyperbolic curves at age $x+\frac{1}{2}$ and examine their displacements vertically from the straight line i.e. the vertical displacement of the point $(\frac{1}{2},\ \mu_{x+\frac{1}{2}})$ for each curve from the point $(\frac{1}{2},\ \frac{1}{2}\mu_x + \frac{1}{2}\mu_{x+1})$. This vertical displacement will be expressed on a scale in which the displacement $(\mu_{x+1} - \mu_x)$ is one unit and will be denoted by $-\gamma_1$ and $-\gamma_2$ for the Gompertz and rectangular hyperbolic curves respectively. These measures will give an indication of the relative positions and the relative curvatures of the two curves. Let us call the point $(\frac{1}{2},\ \mu_{x+\frac{1}{2}})$ "the sag-point", and let us call the mid-point of the straight line, ie $(\frac{1}{2},\ \frac{1}{2}\mu_x + \frac{1}{2}\mu_{x+1})$, "the mid-marker".

Secondly for each of the Gompertz and rectangular hyperbolic curves we will identify the co-ordinates of the point at which the slope of the curve is parallel to that of the straight line joining the points $\mu = \mu_x$ and $\mu = \mu_{x+1}$. Let us call this point "the parallel-point".

The horizontal and vertical displacements of the parallel-point from the mid-marker, i.e. from the point $(\frac{1}{2},\ \frac{1}{2}\mu_x + \frac{1}{2}\mu_{x+1})$, will be used as further measures of the shape of the Gompertz and rectangular hyperbolic curves. Again the vertical displacement will be expressed on a scale in which the displacement $(\mu_{x+1} - \mu_x)$ is one unit. Using the modified scale for the vertical displacement, let us denote the horizontal and vertical displacements of the parallel-point from the mid-marker by $(-\eta_1,\ \psi_1)$ for the Gompertz curve and by $(-\eta_2,\ \psi_2)$ for the rectangular hyperbolic curve.

The measures $(-\eta,\ \psi)$ will again allow comparison of the positions and curvatures of the curves and the extent of any tendency to skewness.

3.22 Expressions for γ_1 and γ_2

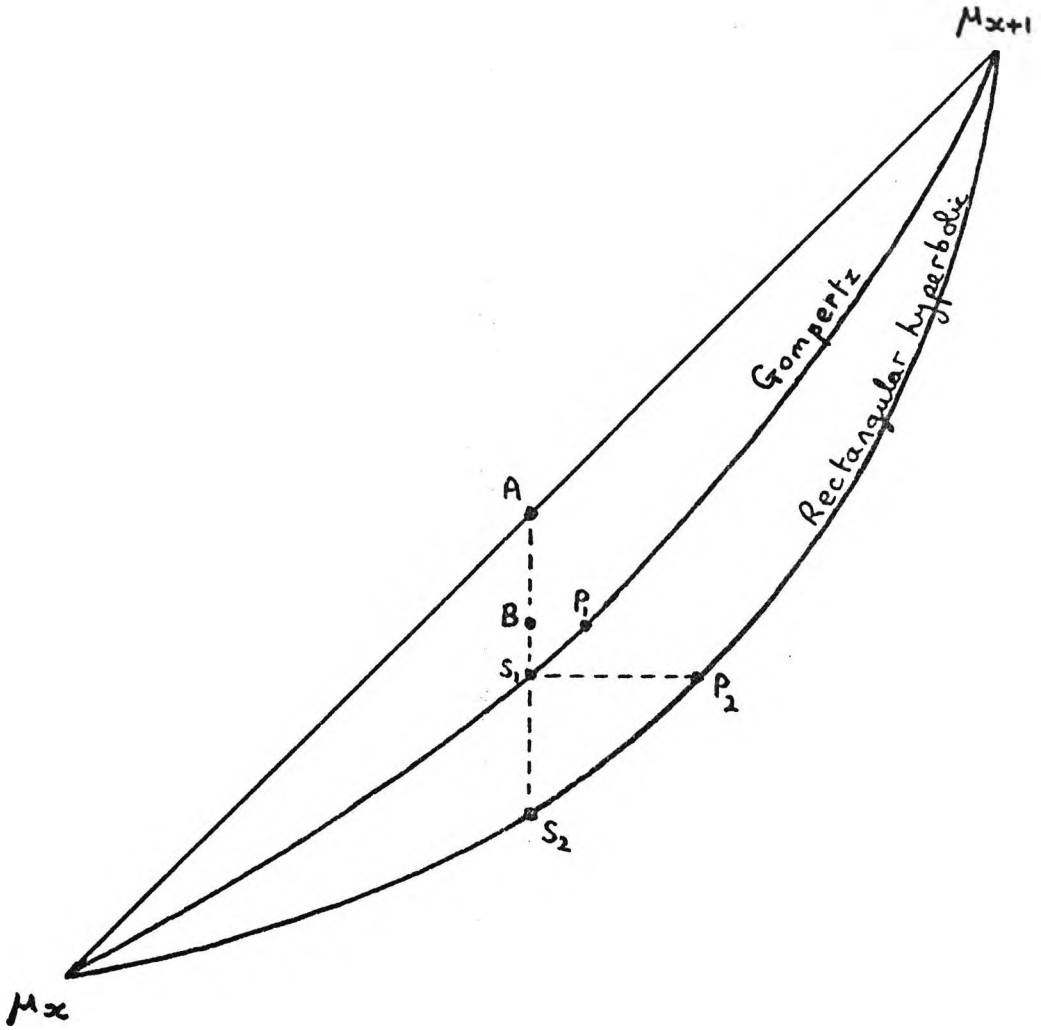
Now, assuming the Gompertz distribution:

$$\gamma_1 = \tfrac{1}{2} - \frac{\mu_{x+\frac{1}{2}} - \mu_x}{\mu_{x+1} - \mu_x}$$

$$= \tfrac{1}{2} - \frac{B'c^{\frac{1}{2}} - B'}{B'c - B'}$$

Figure 3.1 : Comparison of the rectangular hyperbolic and Gompertz curves

The extents of the displacements have been very greatly exaggerated compared to those likely to occur in fitting the curves to mortality data.



Names of points

A	=	mid-marker
S_2	=	Gompertz sag-point
P_1	=	Gompertz parallel-point
S_2	=	rectangular hyperbolic sag-point
P_2	=	rectangular hyperbolic parallel-point

Distances

AS_1	=	$\gamma_1 = \psi_2$
AS_2	=	γ_2
BP_1	=	η_1
AB	=	ψ_1
S_1P_2	=	η_2

$$= \tfrac{1}{2} - \frac{\sqrt{c} - 1}{c - 1}$$

$$= \tfrac{1}{2} - \frac{1}{\sqrt{c} + 1}$$

$$= \tfrac{1}{2} - \frac{1}{\sqrt{\frac{\mu_{x+1}}{\mu_x}} + 1}$$

$$= \tfrac{1}{2} - \frac{\sqrt{\mu_x}}{\sqrt{\mu_x} + \sqrt{\mu_{x+1}}}$$

$$= \frac{\sqrt{\mu_{x+1}}}{\sqrt{\mu_x} + \sqrt{\mu_{x+1}}} - \tfrac{1}{2} \qquad (3.113)$$

And, assuming the rectangular hyperbolic distribution:

$$\gamma_2 = \tfrac{1}{2} - \frac{\mu_{x+\frac{1}{2}} - \mu_x}{\mu_{x+1} - \mu_x}$$

$$= \tfrac{1}{2} - \frac{\frac{1}{a - \frac{1}{2}b} - \frac{1}{a}}{\frac{1}{a - b} - \frac{1}{a}}$$

$$= \tfrac{1}{2} - \frac{a - b}{2a - b}$$

$$= \tfrac{1}{2} - \frac{\frac{1}{\mu_{x+1}}}{\frac{1}{\mu_x} + \frac{1}{\mu_{x+1}}}$$

$$= \tfrac{1}{2} - \frac{\mu_x}{\mu_x + \mu_{x+1}}$$

$$= \frac{\mu_{x+1}}{\mu_x + \mu_{x+1}} - \tfrac{1}{2} \qquad (3.114)$$

There is a remarkable similarity of form between the expressions (3.113) and (3.114) for γ_1 and γ_2 respectively.

Let us consider the ratio of γ_2 to γ_1.

$$\frac{\gamma_2}{\gamma_1} = \frac{\left[\frac{\mu_{x+1}}{\mu_x + \mu_{x+1}} - \frac{1}{2}\right]}{\left[\frac{\sqrt{\mu_{x+1}}}{\sqrt{\mu_x} + \sqrt{\mu_{x+1}}} - \frac{1}{2}\right]}$$

$$= \frac{\left[\frac{\mu_{x+1} - \mu_x}{\mu_{x+1} + \mu_x}\right]}{\left[\frac{\sqrt{\mu_{x+1}} - \sqrt{\mu_x}}{\sqrt{\mu_{x+1}} + \sqrt{\mu_x}}\right]}$$

$$= \frac{\left[\frac{\sqrt{\mu_{x+1}} + \sqrt{\mu_x}}{\mu_{x+1} + \mu_x}\right]}{\left[\frac{1}{\sqrt{\mu_{x+1}} + \sqrt{\mu_x}}\right]}$$

$$= \frac{\mu_{x+1} + \mu_x + 2\sqrt{\mu_x \mu_{x+1}}}{\mu_{x+1} + \mu_x}$$

$$= 1 + \frac{\sqrt{\mu_x \mu_{x+1}}}{(\mu_{x+1} + \mu_x)/2} \qquad (3.115)$$

If μ_x and μ_{x+1} have values of similar size, it can be seen that this ratio will be very slightly less than 2 since $\sqrt{\mu_x \mu_{x+1}}$ is the geometric mean of μ_x and μ_{x+1}, while $(\mu_x + \mu_{x+1})/2$ is the arithmetic mean, and the geometric mean is less than or equal to the arithmetic mean, the values being very close if μ_x and μ_{x+1} are similar in size (and are equal if μ_x and μ_{x+1} are equal).

Thus we can see that, at age $x+\frac{1}{2}$, the rectangular hyperbolic curve will diverge vertically from the straight line virtually twice as far as the Gompertz curve, ie the sag-point will be about twice as far below the mid-marker for the rectangular hyperbolic curve as for the Gompertz curve.

We will now obtain power series expansions for γ_1 and γ_2 in terms of "d", where:

$$d = \frac{\mu_{x+1}}{\mu_x} - 1 \quad , \qquad (3.116)$$

that is, for the Gompertz distribution:

$$d = c - 1 \quad , \qquad (3.117)$$

and for the rectangular hyperbolic distribution:

$$d = \frac{b}{a - b} \quad . \tag{3.118}$$

We have:

$$\begin{aligned}
\gamma_1 &= \tfrac{1}{2} - \frac{\sqrt{c} - 1}{c - 1} \\
&= \tfrac{1}{2} - \frac{1}{d}\{(1+d)^{\frac{1}{2}} - 1\} \\
&= \tfrac{1}{2} - \frac{1}{d}\{(1 + \tfrac{1}{2}d - \tfrac{1}{8}d^2 + \tfrac{1}{16}d^3 - \tfrac{5}{128}d^4 + \ldots) - 1\} \\
&= \tfrac{1}{8}d - \tfrac{1}{16}d^2 + \tfrac{5}{128}d^3 - \ldots
\end{aligned} \tag{3.119}$$

In addition, we have:

$$\begin{aligned}
\gamma_2 &= \tfrac{1}{2} - \frac{\mu_x}{\mu_x + \mu_{x+1}} \\
&= \tfrac{1}{2} - \frac{1}{2 + d} \\
&= \tfrac{1}{2}\left(1 - \frac{1}{1 + \frac{1}{2}d}\right) \\
&= \tfrac{1}{2}\{1 - (1 - \tfrac{1}{2}d + \tfrac{1}{4}d^2 - \tfrac{1}{8}d^3 + \ldots)\} \\
&= \tfrac{1}{4}d - \tfrac{1}{8}d^2 + \tfrac{1}{16}d^3 - \ldots
\end{aligned} \tag{3.120}$$

Now the value of d is typically in the region of 0.1, so that typical values of γ_1 and γ_2 are in the region of:

$$\gamma_1 = 0.012 \quad \text{and} \quad \gamma_2 = 0.024$$

Thus the rectangular hyperbolic curve appears to have a more exaggerated curvature than the Gompertz curve but not, on this evidence, to an implausible extent for the purposes of modelling mortality over a year of age.

It will be noted that the power series expansions of γ_1 and γ_2 are consistent with the result earlier in this section that the ratio γ_2/γ_1 was slightly less than 2:

$$\frac{\gamma_2}{\gamma_1} \simeq \frac{\frac{1}{4}d - \frac{1}{8}d^2 + \frac{1}{16}d^3}{\frac{1}{8}d - \frac{1}{16}d^2 + \frac{5}{128}d^3}$$

$$\simeq \frac{\frac{1}{4}d - \frac{1}{8}d^2 + \frac{10}{128}d^3 - \frac{1}{64}d^3}{\frac{1}{8}d - \frac{1}{16}d^2 + \frac{5}{128}d^3} \tag{3.121}$$

Thus:

$$\frac{\gamma_2}{\gamma_1} \simeq 2 - \frac{1}{8}d^2 \tag{3.122}$$

For a typical value of d = 0.1, this expression gives $\frac{\gamma_2}{\gamma_1} \simeq 1.99875$. (A precise calculation based on equation (3.115) gives $\frac{\gamma_2}{\gamma_1} = 1.9988647....$)

3.23 Expressions for η_1,ψ_1,η_2 and ψ_2

Now firstly for the Gompertz curve, let us derive the value of t at which the parallel-point occurs ie the value of t ($0 \leq t \leq 1$) for which:

$$\frac{d\mu_{x+t}}{dt} = \mu_{x+1} - \mu_x \quad , \tag{3.123}$$

that is, for which:

$$(B' \log c)\, c^t = B'c - B' \tag{3.124}$$

$$\Rightarrow \qquad c^t = \frac{c-1}{\log c} \tag{3.125}$$

$$\Rightarrow \qquad t = \frac{\log\left(\frac{c-1}{\log c}\right)}{\log c} \tag{3.126}$$

Thus we have:

$$\eta_1 = \frac{\log\left(\frac{c-1}{\log c}\right)}{\log c} - \frac{1}{2}$$

$$= \frac{\log\left(\frac{d}{\log(1+d)}\right)}{\log(1+d)} - \frac{1}{2}$$

$$= \frac{\log\left[\frac{d}{d - \frac{1}{2}d^2 + \frac{1}{3}d^3 - \frac{1}{4}d^4 + \frac{1}{5}d^5 - \ldots}\right]}{d - \frac{1}{2}d^2 + \frac{1}{3}d^3 - \frac{1}{4}d^4 + \frac{1}{5}d^5 - \ldots} - \frac{1}{2}$$

$$= \frac{\log\left[\dfrac{1}{1 - \frac{1}{2}d + \frac{1}{3}d^2 - \frac{1}{4}d^3 + \frac{1}{5}d^4 - \ldots}\right]}{d\,(1 - \frac{1}{2}d + \frac{1}{3}d^2 - \frac{1}{4}d^3 + \frac{1}{5}d^4 - \ldots)} - \frac{1}{2}$$

$$= \frac{-\log(1 - K)}{d\,(1 - K)} - \frac{1}{2} \tag{3.127}$$

where:
$$K = \frac{1}{2}d - \frac{1}{3}d^2 + \frac{1}{4}d^3 - \frac{1}{5}d^4 + \ldots \tag{3.128}$$

Thus:

$$\eta_1 = \frac{1}{d}(K + \tfrac{1}{2}K^2 + \tfrac{1}{3}K^3 + \tfrac{1}{4}K^4 + \ldots)(1 + K + K^2 + K^3 + K^4 + \ldots) - \tfrac{1}{2}$$

$$= \frac{1}{d}(K + \tfrac{3}{2}K^2 + \tfrac{11}{6}K^3 + \tfrac{25}{12}K^4 + \ldots) - \tfrac{1}{2}$$

$$= \tfrac{1}{24}d - \tfrac{1}{48}d^2 + \tfrac{13}{960}d^3 - \ldots \tag{3.129}$$

Now let us consider the value of μ_{x+t} corresponding on the Gompertz curve to:

$$t = \frac{\log\left(\frac{c - 1}{\log c}\right)}{\log c} \tag{3.130}$$

This value is:

$$\mu_{x+t} = B'c^{\frac{\log\left(\frac{c-1}{\log c}\right)}{\log c}}$$

$$= B'e^{(\log c)\left(\frac{\log\left(\frac{c-1}{\log c}\right)}{\log c}\right)}$$

$$= B'e^{\log\left(\frac{c-1}{\log c}\right)}$$

$$= B'\left[\frac{c - 1}{\log c}\right] \tag{3.131}$$

From this we have:

$$\psi_1 = \tfrac{1}{2} - \frac{B'\left[\frac{c-1}{\log c}\right] - B'}{B'c - B'}$$

$$= \tfrac{1}{2} - \frac{1}{\log c} + \frac{1}{c-1}$$

$$= \tfrac{1}{2} + \frac{1}{d} - \frac{1}{\log (1+d)}$$

$$= \tfrac{1}{2} + \frac{1}{d} - \frac{1}{d\,(1 - \frac{1}{2}d + \frac{1}{3}d^2 - \frac{1}{4}d^3 + \frac{1}{5}d^4 - \dots)}$$

$$= \tfrac{1}{2} + \frac{1}{d} - \frac{1}{d\,(1-K)} \tag{3.132}$$

where as before: $K = \frac{1}{2}d - \frac{1}{3}d^2 + \frac{1}{4}d^3 - \frac{1}{5}d^4 + \dots$ (3.133)

Thus:

$$\psi_1 = \tfrac{1}{2} + \frac{1}{d} - \frac{1}{d}\,(1 + K + K^2 + K^3 + K^4 + \dots)$$

$$= \tfrac{1}{2} + \frac{1}{d} - \frac{1}{d}\,(1 + \tfrac{1}{2}d - \tfrac{1}{12}d^2 + \tfrac{1}{24}d^3 - \tfrac{19}{720}d^4 + \dots)$$

$$= \tfrac{1}{12}d - \tfrac{1}{24}d^2 + \tfrac{19}{720}d^3 - \dots \tag{3.134}$$

Now secondly for the rectangular hyperbolic curve, let us derive the value of t at which the parallel-point occurs ie the value of t ($0 \leq t \leq 1$) for which:

$$\frac{d\mu_{x+t}}{dt} = \mu_{x+1} - \mu_x \ , \tag{3.135}$$

that is, for which:

$$\frac{b}{(a-bt)^2} = \mu_{x+1} - \mu_x \tag{3.136}$$

$$\Rightarrow \qquad \frac{\frac{1}{\mu_x} - \frac{1}{\mu_{x+1}}}{\left[\frac{1}{\mu_x} - t(\frac{1}{\mu_x} - \frac{1}{\mu_{x+1}})\right]^2} = \mu_{x+1} - \mu_x \tag{3.137}$$

$$\Rightarrow \qquad t = \frac{\mu_{x+1} \pm \sqrt{\mu_x \mu_{x+1}}}{\mu_{x+1} - \mu_x} \tag{3.138}$$

But since $0 \leq t \leq 1$, we adopt the solution:

$$t = \frac{\mu_{x+1} - \sqrt{\mu_x \mu_{x+1}}}{\mu_{x+1} - \mu_x}$$

$$= \frac{\sqrt{\mu_{x+1}}}{\sqrt{\mu_x} + \sqrt{\mu_{x+1}}} \tag{3.139}$$

Thus
$$\eta_2 = \frac{\sqrt{\mu_{x+1}}}{\sqrt{\mu_x} + \sqrt{\mu_{x+1}}} - \tfrac{1}{2} \tag{3.140}$$

$$= \gamma_1 \tag{3.141}$$

Equation (3.141) follows when we recall equation (3.113).

And so, from the power series derived for γ_1 (see equation (3.119), we have:

$$\eta_2 = \tfrac{1}{8}d - \tfrac{1}{16}d^2 + \tfrac{5}{128}d^3 - \ldots \tag{3.142}$$

Now let us consider the value of μ_{x+t} corresponding on the rectangular hyperbolic curve to:

$$t = \frac{\sqrt{\mu_{x+1}}}{\sqrt{\mu_x} + \sqrt{\mu_{x+1}}} \tag{3.143}$$

This value is:

$$\mu_{x+t} = \frac{1}{a - bt}$$

$$= \frac{1}{\frac{1}{\mu_x} - \left[\frac{1}{\mu_x} - \frac{1}{\mu_{x+1}}\right]\left[\frac{\mu_{x+1} - \sqrt{\mu_x \mu_{x+1}}}{\mu_{x+1} - \mu_x}\right]}$$

$$= \sqrt{\mu_x \mu_{x+1}} \tag{3.144}$$

But $\mu_{x+t} = \sqrt{\mu_x \mu_{x+1}}$ is the value of the Gompertz curve when $t = \frac{1}{2}$, and therefore gives the value of the Gompertz curve at its sag-point.

Therefore:
$$\psi_2 = \gamma_1 \tag{3.145}$$

And so, from the power series derived for γ_1 (again see equation (3.119)), we have:

$$\psi_2 = \tfrac{1}{8}d - \tfrac{1}{16}d^2 + \tfrac{5}{128}d^3 - \ldots \tag{3.146}$$

3.24 Discussion of η_1,ψ_1,η_2 and ψ_2

In the last section, we have obtained the following expressions:

$$\eta_1 = \tfrac{1}{24}d - \tfrac{1}{48}d^2 + \tfrac{13}{960}d^3 - \ldots \quad (3.147)$$

$$\psi_1 = \tfrac{1}{12}d - \tfrac{1}{24}d^2 + \tfrac{19}{720}d^3 - \ldots \quad (3.148)$$

$$\eta_2 = \tfrac{1}{8}d - \tfrac{1}{16}d^2 + \tfrac{5}{128}d^3 - \ldots \quad (3.149)$$

$$\psi_2 = \tfrac{1}{8}d - \tfrac{1}{16}d^2 + \tfrac{5}{128}d^3 - \ldots \quad (3.150)$$

It will be seen immediately that, for the rectangular hyperbolic curve, the parallel-point is displaced from the mid-marker by the same distance vertically (ψ_2) as it is horizontally (η_2), whereas, in the case of the Gompertz curve, the parallel-point is displaced about twice as far vertically (ψ_1) from the mid-marker as it is horizontally (η_1), but these distances are respectively about two-thirds and one-third of the corresponding distances for the rectangular hyperbolic curve.

It is quite remarkable that, in making comparisons between the displacements for the Gompertz and rectangular hyperbolic curves, such simple proportions should be almost exactly true, and yet not precisely. A similar phenomenon was seen when we compared the respective displacements of the sag-points from the mid-marker (see equations (3.119) and (3.120) giving γ_1 and γ_2 respectively). It will be noted that as d tends to zero, these approximate proportions appear to become precisely correct.

A further fortuitous relationship between the curves is that the vertical displacement of the parallel-point for the rectangular hyperbolic curve from the mid-marker (ψ_2) is the same as the displacement of the sag-point of the Gompertz curve from the mid-marker (γ_1) i.e. the sag-point of the Gompertz curve is on the same horizontal level as the parallel-point of the rectangular hyperbolic curve (which point of course lies to the right of the Gompertz sag-point, by a distance (η_2) equal to the vertical displacement of the two points from the mid-marker (γ_2)).

If again we consider a typical value for d of 0.1, we obtain

$$\eta_1 = 0.004$$
$$\psi_1 = 0.008$$
$$\eta_2 = 0.012$$
$$\psi_2 = 0.012$$

As before, these figures indicate that the rectangular hyperbolic curve indeed has a more exaggerated curvature than the Gompertz curve, but again the extent to which the shape is more exaggerated does not seem untenable for mortality purposes, in the context of a single year of age. These figures also provide reassurance that skewness does not arise as a problem in using the rectangular hyperbolic curve in this context.

3.25 General comment

The rectangular hyperbolic curve provides a shape for modelling mortality over a year of age which is distinct from the exponential curve of the Gompertz Law, and in which the curvature, and the displacement from a straight line representation, are more pronounced but not to an extent that appears in any way calamitous. In fact the curve seems to provide a useful alternative to the Gompertz curve for experimentation and investigations over a year of age.

It must be borne in mind that our comparison has been based on the premise that the curves are being fitted between given values of μ_x and μ_{x+1}. In fitting a curve for μ_{x+t} to the mortality experience of a year of age, we would not have the constraint of conforming to given values of μ_x and μ_{x+1}, so that a rectangular hyperbolic curve fitted to the mortality experience of a year of age is likely to give values of μ_{x+t} which are very slightly above those of the fitted Gompertz curve, at either end of the year of age, and very slightly below, around the middle of the year of age.

A useful benefit of fitting the rectangular hyperbolic curve to μ_{x+t} over a year of age is the convenient algebraic development which it permits, when other mortality functions are evaluated. The curve is arguably more co-operative in terms of algebraic simplicity than the Gompertz curve.

3.26 Symmetry of the transformed rectangular hyperbolic curve

It is not a coincidence that the vertical and horizontal displacements of the parallel-point from the mid-marker are the same for the rectangular hyperbolic curve. When we changed the vertical scale of measurement so that the distance $(\mu_{x+1} - \mu_x)$ was unity, we were in effect making a transformation which produced a rectangular hyperbolic curve which is symmetrical about the line which passes through the mid-marker at right angles to the line joining the points $\mu = \mu_x$ and $\mu = \mu_{x+1}$. Using the transformed scale, this line (which is the "transverse axis" of the hyperbola) is at 45 degrees to the t and μ axes, so that the point at which the curve intercepts this axis of symmetry is displaced from the mid-marker by

equal amounts on the t-axis and the μ-axis.

These assertions follow from the classical properties of the rectangular hyperbolic curve.

The symmetry can also be confirmed by expressing the formula of the rectangular hyperbolic curve in appropriate transformed Cartesian coordinates and, to demonstrate this, let us start with the formula:

$$\mu_{x+t} = \frac{1}{a - bt} \tag{3.151}$$

Let us adopt the revised variables:

$$y' = \frac{\mu_{x+t} - \mu_x}{\mu_{x+1} - \mu_x} \tag{3.152}$$

and

$$x' = t \tag{3.153}$$

Then $$y' = \frac{(1 - k)x'}{1 - kx'} \quad \text{where } k = \frac{b}{a} \tag{3.154}$$

Let us adopt revised axes, as illustrated in Figure 3.2, such that the new X-axis lies along the straight line joining the original μ_{x+1} and μ_x values on the curve, with the origin lying at the midpoint of that line (i.e. the mid-marker) and with the positive X-axis passing through the original μ_x value. The positive Y-axis is the perpendicular to the X-axis at the new origin which intercepts the rectangular hyperbolic curve.

Then:

$$x' = (\frac{1}{\sqrt{2}} - X)\frac{1}{\sqrt{2}} + \frac{Y}{\sqrt{2}}$$

$$= \tfrac{1}{2} - \frac{X}{\sqrt{2}} + \frac{Y}{\sqrt{2}} \tag{3.155}$$

$$y' = \tfrac{1}{2} - \frac{X}{\sqrt{2}} - \frac{Y}{\sqrt{2}} \tag{3.156}$$

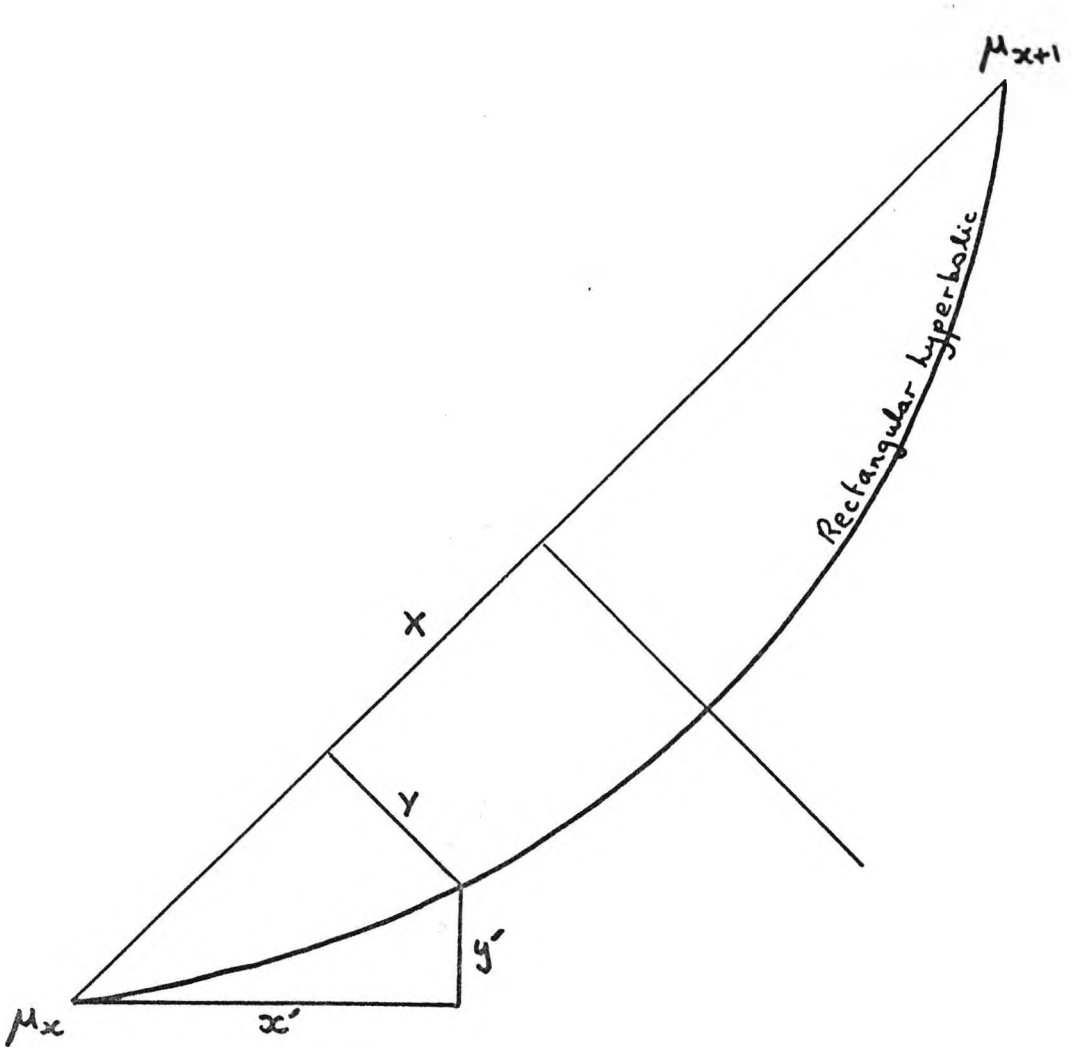
We have:

$$k = \frac{y' - x'}{x'y' - x'} = \frac{\sqrt{2}Y}{(\frac{Y^2}{2} + \frac{Y}{\sqrt{2}} + \frac{1}{4}) - \frac{X^2}{2}} \tag{3.157}$$

$$\Rightarrow \quad X^2 = Y^2 + \sqrt{2}\,(1 - \tfrac{2}{k})\,Y + \tfrac{1}{2} \tag{3.158}$$

Figure 3.2 :

Alternative axes for the rectangular hyperbolic curve



Clearly if (X,Y) satisfies this equation, so does (-X,Y), demonstrating that the curve is symmetrical about the Y-axis.

3.27 Applicability of a fitted mortality curve over a range of years

As is well-known, the Gompertz Law can in theory be applied over a wide age range if the data is appropriate. Obviously the same value of c must apply in each year of age.

Now we will consider whether it is possible for the rectangular hyperbolic curve to apply over a wide age range also, and not just over a single year of age.

For the rectangular hyperbolic curve, we can find:

$$\frac{d\mu_{x+t}}{dt} = \frac{b}{(a - bt)^2} = b\,(\mu_{x+t})^2 \tag{3.159}$$

$$\frac{d^2\mu_{x+t}}{dt^2} = \frac{2b^2}{(a - bt)^3} = 2b^2(\mu_{x+t})^3 \tag{3.160}$$

.....

$$\frac{d^n\mu_{x+t}}{dt^n} = \frac{n!b^n}{(a - bt)^{n+1}} = n!\,b^n(\mu_{x+t})^{n+1} \tag{3.161}$$

It can be seen that the curve can in theory be applied over a wide age range if the same value of b applies in each year of age, since if the curves fitted over each year of age join at the integral ages, all the derivatives of the curve will then be continuous.

However, this curve seems unlikely to be of relevance in studies of human mortality over a wide age range since observed values of b appear to fall quite markedly over the human life span, as illustrated in Table 3.1 in Section 3.2.

The curvature of a rectangular hyperbolic curve increases far more strongly towards the end of the life span than is the case for a Gompertz curve. This can be seen by examining the proportionate rate of growth of μ_{x+t}, namely:

$$\frac{1}{\mu_{x+t}} \frac{d\mu_{x+t}}{dt} .$$

For the Gompertz Law, this is constant and equals log c. For the rectangular hyperbolic law, this gives $b\mu_{x+t}$. It will be recalled that b must be greater than zero for μ_{x+t} to increase with t, as we will need, as the end of the life span approaches. Thus as t and μ_{x+t} increase, $b\mu_{x+t}$ increases, i.e. the proportional rate of growth of μ_{x+t} increases as t increases, unlike the position under the Gompertz Law, where it is constant.

If the rectangular hyperbolic law were fitted to human data over a wide age range, it would involve a large value of a and a small value of b; then there is a small value of μ_x at the lower end of the age range, and values of μ_{x+t} will be generated over a wide age range before values of μ_{x+t} appropriate to the end of the age span are reached.

A feature of the rectangular hyperbolic curve used in this way is that there is a limiting age to the life span beyond which no one can survive. If the curve is given by:

$$\mu_x = \frac{1}{a - bx} \quad , \tag{3.162}$$

this limiting age is $\omega = \frac{a}{b}$.

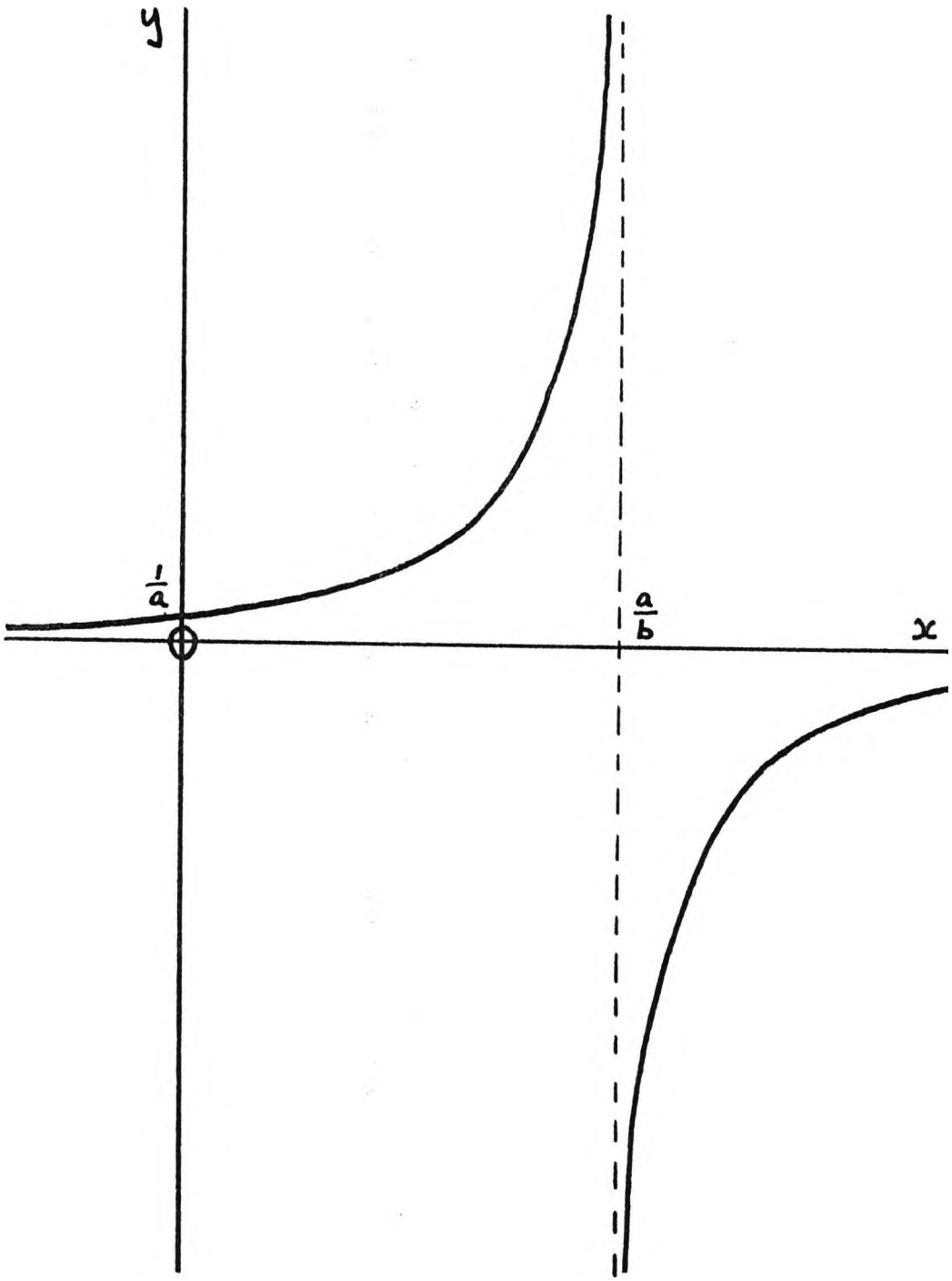
This arises since the line $x = \frac{a}{b}$ on the graph of $y = 1/(a - by)$ is an asymptote of the hyperbola as illustrated in Figure 3.3 .

However as intimated, the shape of the rectangular hyperbolic curve is unlikely to be suitable for use in practice with human mortality data over a wide age range.

It does however provide a useful formula for fitting to μ_{x+t} within a year of age because of the convenient algebraic development which it permits, when other mortality functions are evaluated.

Figure 3.3 : Graph of $y = \frac{1}{a - bx}$ (for $b > 0$)

The range of this curve potentially used for modelling μ_x is that lying between $x = 0$ and $x = \frac{a}{b}$.



CHAPTER IV

A general theory of mortality rate estimators

4.1 The general theory

Let us consider a mortality investigation in which we observe lives for all or part of the year from age x to age x+1. Let the typical life be observed from age $x+s_i$ $(0 \leq s_i \leq 1)$ up to age $x+t_i$ $(0 \leq t_i \leq 1)$.

Let us suppose that the lives are subject to a mortality law which can be expressed as:

$$\mu_{x+t} = f(t,\phi) \tag{4.1}$$

ie the force of mortality at any duration in the year is assumed to be fully determined once a single mortality parameter ϕ is known.

(Later, in Sections 4.7, 4.23 and 4.30, we will also consider situations where μ_{x+t} is a function of a number of mortality parameters ϕ_i).

If there is a single mortality parameter ϕ, the mortality rate q_x will be a function solely of this parameter ϕ, and most plausible mortality laws are likely to be capable of being expressed in a form where q_x itself is actually used as the mortality parameter ϕ. It is also worth remarking that perhaps ϕ could alternatively be m_x, μ_x or $\mu_{x+\frac{1}{2}}$, or a parameter representing the complementary phenomenon of survival, such as p_x.

However for generality, we will denote the mortality parameter by ϕ, and we will proceed to obtain estimators for ϕ.

Consider an element of the year of age from age x+t to age x+t+δt.

Let the number of lives at age x+t be P(t).

Then the number of deaths expected in the time element, considered in isolation, is:

$$P(t)\ \mu_{x+t}\ \delta t \tag{4.2}$$

Let the actual number of deaths in the time element be denoted by $D(t,\delta t)$.

We could regard our element as providing a self-contained sample to estimate ϕ, using the method of moments principle, applied to the deaths, that within the element:

$$\text{Expected deaths} = \text{Actual deaths}$$

This assumes of course that there is sufficient volume of data within the element to give sensible results.

Proceeding in this way gives:

$$P(t)\ \mu_{x+t}\ \delta t = D(t,\delta t) \tag{4.3}$$

Even if we are using only data from a single element of the year of age, we are able in theory to establish ϕ, which applies for the whole of the year of age, because we have assumed a law of mortality which expresses μ_{x+t} at any point in the year of age as a function of t and ϕ.

We can create a bigger sample than that provided by a single element by combining the data of many elements together to give combined values of "expected deaths" and of "actual deaths", and these combined elements should provide a better estimator of ϕ than individual elements, because of the increased sample size.

Since the data of any element on its own can provide an estimate of ϕ, we can give the data from different elements different weightings in the process of combination, in calculating our combined values of "expected deaths" and "actual deaths", and still have a combined sample which gives an estimate of ϕ. (Further discussion of the process of combining the elements is given later, in Section 4.12).

If we proceed in this way, combining the data from all elements in the year of age, our estimate of ϕ is the value which solves the equation:

$$\sum_{t=0}^{t=1^*} P(t)\ \mu_{x+t}\ g(t,\phi)\ \delta t = \sum_{t=0}^{t=1^*} D(t,\delta t)\ g(t,\phi) \tag{4.4}$$

where $g(t,\phi)$ is the weighting inserted at duration t, and the symbol:

$$\sum_{t=0}^{t=1^*}$$

denotes summation over all elements in the year of age. The weights $g(t,\phi)$ will not change

sign for t varying in the range $0 \leq t \leq 1$.

It is important to note that $g(t,\phi)$ will in general be regarded as itself a function of the mortality parameter ϕ. This is allowable since the data from any element can be weighted in any way we like, except that the weighting should not be linked to the actual mortality experience in the element (nor indeed that in other elements). Failure to observe this prohibition could be a serious source of bias in the estimate of the value of ϕ. (For example, if the weighting applied to the experience of an element was proportional to the value of ϕ as calculated solely from the observations of the element, the value of ϕ estimated from the combined experience of all the elements would be positively biased, since those elements indicating higher values for ϕ would be given heavier weighting in the combination).

Now let us express P(t) as:

$$P(t) = \sum_{N} \gamma_i(t) \tag{4.5}$$

where, for the i^{th} life in the investigation:

$$\gamma_i(t) = 0 \quad \text{if } t \leq s_i \text{ or } t > t_i$$

$$\gamma_i(t) = 1 \quad \text{if } s_i < t \leq t_i$$

Then we have:

$$\sum_{t=0}^{t=1^*} \sum_{N} \gamma_i(t)\, \mu_{x+t}\, g(t,\phi)\, \delta t = \sum_{t=0}^{t=1^*} D(t,\delta t)\, g(t,\phi) \tag{4.6}$$

$$\Rightarrow \quad \sum_{N} \sum_{t=s_i}^{t=t_i^*} \mu_{x+t}\, g(t,\phi)\, \delta t = \sum_{t=0}^{t=1^*} D(t,\delta t)\, g(t,\phi) \tag{4.7}$$

where the symbol: $\displaystyle\sum_{t=s_i}^{t=t_i^*}$

denotes summation over all elements between ages $x+s_i$ and $x+t_i$.

Now let $\delta t \rightarrow 0$. Then we have:

$$\sum_{N} \int_{s_i}^{t_i} \mu_{x+t}\, g(t,\phi)\, dt = \sum_{D} g(t_i,\phi) \tag{4.8}$$

where of course the right-hand side is summed over all deaths and t_i denotes the duration at death.

We can alternatively proceed from equation (4.4) without making the substitution given in equation (4.5).

Under this alternative approach, let $\delta t \rightarrow 0$ in equation (4.4), so that:

$$\int_0^1 P(t)\, \mu_{x+t}\, g(t,\phi)\, dt = \sum_D g(t_i,\phi) \qquad (4.9)$$

P(t) is a function that increases or decreases in discrete steps (a step is always an integer since a number of lives is being represented), but the integral in equation (4.9) can nevertheless be evaluated (as confirmed by the alternative form given in equation (4.8)).

4.2 g-estimators

The value of ϕ which solves equation (4.8):

$$\sum_N \int_{s_i}^{t_i} \mu_{x+t}\, g(t,\phi)\, dt = \sum_D g(t_i,\phi)$$

and, equivalently, equation (4.9):

$$\int_0^1 P(t)\, \mu_{x+t}\, g(t,\phi)\, dt = \sum_D g(t_i,\phi)$$

will be called the "g-estimator" of ϕ corresponding to the "g-function" $g(t,\phi)$.

4.3 Category I and Category II

It will quickly become apparent that, once a g-function has been assumed, one or other of equations (4.8) and (4.9) will generally be more convenient for the derivation of the g-estimator, and a g-estimator will be referred to as a "category I" g-estimator or a "category II" g-estimator according to whether equation (4.8) or equation (4.9) gives the more convenient derivation, ie:

Category I equation:
$$\sum_N \int_{s_i}^{t_i} \mu_{x+t}\, g(t,\phi)\, dt = \sum_D g(t_i,\phi)$$

Category II equation:
$$\int_0^1 P(t)\, \mu_{x+t}\, g(t,\phi)\, dt = \sum_D g(t_i,\phi)$$

Obviously all g-estimators will satisfy both equations and the categorisation simply reflects the format of the g-functions.

4.4 Identification of some g-estimators

We will proceed shortly to identify some familiar g-estimators.

It will be seen that most, if not all, known mortality rate estimators which assume a mortality law of the form described in equation 4.1 can apparently be expressed as a g-estimator, ie a g-function can be identified.

In addition to identifying some known estimators, a number of new estimators will also be discovered.

Results for a number of category I g-estimators are presented at this stage, in order to indicate the unexpected power of the theory, before further discussion of the derivation of the g-estimator equations (4.8) and (4.9).

Then, several aspects of the g-estimator theory, including the procedure for combining the experience of elements together, will be given further attention in Sections 4.12–4.19, and in particular, it will be demonstrated that all estimators, assuming a one-parameter mortality law, derived using the theory are asymptotically unbiased (Section 4.13), so long as the estimator assumes the correct mortality law.

Subsequently, some further estimators, mainly from category II, will be discussed in Sections 4.20–4.28, and in Section 4.29, the use of the Dirac delta function in a modified derivation of the general theory is considered.

4.5 Summary of g-estimators

For ease of reference, Table 4.1 summarises the g-estimators of q_x which will be discussed in this chapter.

It should be noted that the g-functions are not unique functions of ϕ. For, if the g-function $g(t,\phi)$ corresponding to a particular g-estimator is multiplied by a function of ϕ, $k(\phi)$ say, the revised g-function $k(\phi)*g(t,\phi)$ will still define the same g-estimator, as can be confirmed by considering equations (4.8) and (4.9). It will be seen that the function $k(\phi)$ can be taken out of the integrals and summations in the equations and cancelled.

Table 4.1 Summary of g-estimators of q_x discussed in Chapter IV

Section	g-function	Category I or II	Name of estimator of q_x, if any
4.6	$\frac{1}{{}_tp_x}$	I	Conventional
4.7	$\frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi}$	I	Maximum likelihood
4.8	constant	I	Log-estimator *
4.9	$\frac{1}{\mu_{x+t}}$	I	Time-count *
4.10	$\frac{{}_sp_x}{{}_tp_x}$	I	Implication-B *
4.11	${}_tp_x$	I	(un-named)
4.11	$(\mu_{x+t})^r \frac{\partial \mu_{x+t}}{\partial t}$	I	(un-named)
4.20	$\frac{1}{P(t)}$	II	Nelson-Aalen
4.21	$\frac{{}_tp_x}{P(t)}$	II	Life-profile *
4.22	$\frac{1}{P(t)\ \mu_{x+t}}$	II	(un-named)
4.23	$\frac{1}{P(t)\ \mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi}$	II	(un-named)
4.24	$\frac{1}{P(t)\ {}_tp_x}$	II	(un-named)
4.25	$\frac{(\mu_{x+t})^r}{P(t)} \frac{\partial \mu_{x+t}}{\partial t}$	II	(un-named)
4.27	$(\mu_{x+t})^n$	I	n-estimator *
4.28	$h(t)\ P(t) \frac{\partial \mu_{x+t}}{\partial \phi}$	depends on h(t)	Weighted least squares

* These names are suggested in this thesis.

Also, it will be noted that the "constant" which forms the g-function for the log-estimator is strictly speaking an arbitrary function of the mortality parameter ϕ; what is important is that the g-function is independent of the duration into the year of age, t.

4.6 Conventional estimator

Firstly let us consider the g-function:

$$g(t,\phi) = \frac{1}{{}_tp_x} \tag{4.10}$$

Then, using the category I equation, the g-estimator for ϕ is given by:

$$\sum_N \int_{s_i}^{t_i} \frac{\mu_{x+t}}{{}_tp_x}\, dt = \sum_D \frac{1}{{}_{t_i}p_x} \tag{4.11}$$

Now μ_{x+t} can be expressed as:

$$\mu_{x+t} = \frac{-1}{{}_tp_x} \frac{\partial {}_tp_x}{\partial t} \tag{4.12}$$

so that we have:

$$\sum_N \int_{s_i}^{t_i} \frac{-1}{({}_tp_x)^2} \frac{\partial {}_tp_x}{\partial t}\, dt = \sum_D \frac{1}{{}_{t_i}p_x}$$

$$\Rightarrow \quad \sum_N \left[\frac{1}{{}_tp_x}\right]_{s_i}^{t_i} = \sum_D \frac{1}{{}_{t_i}p_x}$$

$$\Rightarrow \quad \sum_N \frac{1}{{}_{t_i}p_x} - \sum_N \frac{1}{{}_{s_i}p_x} = \sum_D \frac{1}{{}_{t_i}p_x}$$

$$\Rightarrow \quad \sum_N \frac{1}{{}_{s_i}p_x} = \sum_{WS} \frac{1}{{}_{t_i}p_x} \tag{4.13}$$

But this is the equation that gives the conventional estimator.

Thus the g-estimator for ϕ is the conventional estimator when the g-function is:

$$g(t,\phi) = \frac{1}{{}_tp_x}$$

It is of interest to note that introduction of this particular g-function into the integral on the left-hand side of the category I equation is equivalent to writing the integral in the form:

$$\int f'(t)\, e^{f(t)}\, dt$$

where $f'(t) = \mu_{x+t}$ and $e^{f(t)} = \frac{1}{{}_tP_x} = g(t,\phi)$

It is perhaps worth emphasing that the conventional estimator determined using the "constant μ" mortality assumption is *not* the familiar estimator for μ based on the central exposed-to-risk. The equation determining the conventional estimator for this mortality assumption was quoted in equation (1.28) and will generally require an iterative solution. Equation (1.28) can be readily derived by applying the "constant μ" assumption in equation (4.11).

It will be recalled, from Section 2.22, that the familiar estimator for μ involving the central exposed-to-risk arises from the use of the *maximum likelihood* criterion when the "constant μ" mortality law applies.

4.7 Maximum likelihood estimator

For our consideration of the maximum likelihood estimator, we will consider the more general situation where the mortality law involves a number of mortality parameters ϕ_i:

$$\mu_{x+t} = f(t,\phi_1,\phi_2,.....\phi_n) \tag{4.14}$$

We will assume that the values of n – 1 of these parameters are being held constant and we wish to establish the value of the remaining parameter, denoted by ϕ.

(The situation where we work with just one parameter could in fact be a representation of this situation with the other parameters being assigned values by virtue of mortality assumptions like "level deaths").

Let us consider the g-function:

$$g(t,\phi) = \frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi} \tag{4.15}$$

Then, using the category I equation, the g-estimator for ϕ is given by:

$$\sum_{N} \int_{s_i}^{t_i} \frac{\partial \mu_{x+t}}{\partial \phi} \, dt = \sum_{D} \left[\frac{1}{\mu_{x+t_i}} \frac{\partial \mu_{x+t_i}}{\partial \phi} \right] \tag{4.16}$$

Let us consider the left-hand side of this equation.

$$\sum_{N} \int_{s_i}^{t_i} \frac{\partial \mu_{x+t}}{\partial \phi} \, dt = \sum_{N} \int_{s_i}^{t_i} \frac{\partial}{\partial \phi} \left[\frac{-1}{{}_tp_x} \frac{\partial {}_tp_x}{\partial t} \right] dt$$

$$= \sum_{N} \int_{s_i}^{t_i} \left[\frac{1}{({}_tp_x)^2} \frac{\partial {}_tp_x}{\partial \phi} \frac{\partial {}_tp_x}{\partial t} - \frac{1}{{}_tp_x} \frac{\partial^2 {}_tp_x}{\partial \phi \partial t} \right] dt$$

$$= \sum_{N} \int_{s_i}^{t_i} \frac{\partial}{\partial t} \left[\frac{-1}{{}_tp_x} \frac{\partial {}_tp_x}{\partial \phi} \right] dt$$

$$= \sum_{N} \left[\frac{-1}{{}_tp_x} \frac{\partial {}_tp_x}{\partial \phi} \right]_{s_i}^{t_i}$$

Thus:

$$\sum_{N} \frac{\frac{\partial {}_{s_i}p_x}{\partial \phi}}{{}_{s_i}p_x} - \sum_{N} \frac{\frac{\partial {}_{t_i}p_x}{\partial \phi}}{{}_{t_i}p_x} = \sum_{D} \frac{\frac{\partial \mu_{x+t_i}}{\partial \phi}}{\mu_{x+t_i}} \tag{4.17}$$

But this is equation (2.89), one form of the equation giving the maximum likelihood estimator of ϕ when the likelihood is maximised with respect to the mortality parameter ϕ.

Thus the g-estimator for ϕ when the g-function is:

$$g(t,\phi) = \frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi}$$

is the maximum likelihood estimator of ϕ when the likelihood is maximised with respect to the mortality parameter ϕ.

To summarise, if we have a set of parameters ϕ_i (i = 1, 2, ... n) of which n – 1 are being held constant, we can obtain an equation to evaluate the remaining parameter.

This is the same equation as obtained from the traditional approach using partial differential coefficients of the likelihood.

As with the traditional approach, an equation for each of the ϕ_i can be obtained assuming

the other n – 1 parameters are held constant. We will then have n equations each expressing one of the ϕ_i in terms of the other n – 1 parameters. These equations can then be solved for each of the ϕ_i.

It is interesting to note the form of the g-function given by:

$$g(t,\phi) = \frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi}$$

for some specific mortality laws.

When the Gompertz Law, $\mu_{x+t} = B'c^t$, applies:

if $\phi = B'$, $$g(t,\phi) = \frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial B'} = \frac{c^t}{B'c^t} = \frac{1}{B'} \tag{4.18}$$

if $\phi = c$, $$g(t,\phi) = \frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial c} = \frac{B'tc^{t-1}}{B'c^t} = \frac{t}{c} \tag{4.19}$$

Both of these g-functions are interesting. The first is constant over the year of age, while the second varies drastically over the year of age starting from nil at age x.

When the rectangular hyperbolic mortality law applies:

if $\phi = a$,

$$\begin{aligned} g(t,\phi) &= \frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial a} \\ &= \frac{-1}{(a - bt)^2} \Big/ \frac{1}{(a - bt)} \\ &= \frac{-1}{(a - bt)} \\ &= -\mu_{x+t} \end{aligned} \tag{4.20}$$

if $\phi = b$,

$$\begin{aligned} g(t,\phi) &= \frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial b} \\ &= \frac{t}{(a - bt)^2} \Big/ \frac{1}{(a - bt)} \\ &= \frac{t}{(a - bt)} \\ &= t\mu_{x+t} \end{aligned} \tag{4.21}$$

The first of these g-functions will usually vary only gradually over the year of age whereas the second will show drastic variation over the year of age.

It will be recalled (Sections 1.9, 2.23, 3.12) that the conventional estimator and the maximum likelihood estimator for q_x are identical for the "level deaths" assumption. This can be confirmed by examining the relevant g-functions.

For the conventional estimator, the g-function is $1/{}_tp_x$ while, for the maximum likelihood estimator with b held constant, the g-function has just been identified as $-\mu_{x+t}$.

If the two estimators are the same, we must have:

$$\frac{1}{{}_tp_x} = K*(-\mu_{x+t}) \tag{4.22}$$

where K is a constant independent of t (since such a factor will not alter the effect of the weights). The value of K will be determined by the population value of the mortality parameter ϕ.

Thus, if these two estimators are the same, we have:

$${}_tp_x\ \mu_{x+t} = \text{constant independent of t,} \tag{4.23}$$

and of course this is indeed a property of the "level deaths" mortality assumption, confirming the identity of these two estimators.

Again, it will also be recalled that, when the "constant μ" mortality law applies, the maximum likelihood estimator for μ is the familiar estimator using the central exposed-to-risk (as shown in Section 2.22). In this case, the g-function is seen to be a constant, since (remembering $\phi = \mu$ and $\mu_{x+t} = \mu$) we have:

$$g(t,\phi) = \frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi} = \frac{1}{\mu}$$

and it will be seen in the next section that this estimator is therefore identical with the newly identified "log-estimator" when the "constant μ" mortality law applies.

Further comments on the use of the general theory when the mortality law involves more than one mortality parameter are given in Section 4.30 .

4.8 Log-estimator

Let us consider the g-function:

$$g(t,\phi) = \text{constant} \tag{4.24}$$

Then, using the category I equation, the g-estimator for ϕ is given by:

$$\sum_N \int_{s_i}^{t_i} \mu_{x+t}\, dt = \sum_D 1 \tag{4.25}$$

$$\Rightarrow \quad \sum_N (\log {}_{s_i}p_x - \log {}_{t_i}p_x) = D \tag{4.26}$$

remembering that:

$${}_tp_x = \exp\left(- \int_0^t \mu_{x+t}\, dt\right) . \tag{4.27}$$

This clearly defines an estimator which is a general version, for any mortality distribution, of the estimator which was stumbled across in Section 3.16 when we considered the application of the method of maximum likelihood to the rectangular hyperbolic distribution to evaluate both parameters. This estimator was referred to as the "log-estimator".

Thus the g-estimator for ϕ is the log-estimator when the g-function is:

$$g(t,\phi) = \text{constant}$$

As discussed previously (Section 3.16), the equation which defines the log-estimator can be expressed in a number of alternative forms:

$$\sum_N (\log {}_{s_i}p_x - \log {}_{t_i}p_x) = D \tag{4.28}$$

$$\Rightarrow \quad \sum_N \log \frac{1}{{}_{t_i-s_i}p_{x+s_i}} = D \tag{4.29}$$

$$\Rightarrow \quad \prod_N {}_{t_i-s_i}p_{x+s_i} = e^{-D} \tag{4.30}$$

The derivation of this equation did not here exclude the use of the "constant μ" mortality law; the "constant μ" law implies:

$$_{t-s}p_{x+s} = e^{-\mu(t-s)} \tag{4.31}$$

so that when this law applies, equation (4.29) implies that:

$$\mu \sum_{N} (t_i - s_i) = D \tag{4.32}$$

$$\Rightarrow \qquad \mu = \frac{D}{\sum_{N} (t_i - s_i)} \tag{4.33}$$

which is the familiar estimator for μ normally obtained by the method of maximum likelihood when the "constant μ" law applies (see Section 2.22).

This is clearly a situation where the log-estimator coincides with the maximum likelihood estimator.

When the Gompertz law applies, the equation solved by the log-estimator can be expressed as:

$$\sum_{N} (\log h^{(c^{s_i}-1)} - \log h^{(c^{t_i}-1)}) = D \tag{4.34}$$

$$\Rightarrow \qquad \log h \sum_{N} (c^{s_i} - c^{t_i}) = D \tag{4.35}$$

But $$h = \exp\left(-\frac{B'}{\log c}\right) \tag{4.36}$$

$$\Rightarrow \qquad B' = \frac{D}{\frac{1}{\log c} \sum_{N} (c^{t_i} - c^{s_i})} \tag{4.37}$$

This is of course the maximum likelihood estimator for B' when c is fixed and it should be no surprise that this coincidence occurs as we have already seen that, when we consider the g-function for the maximum likelihood estimator for B', we obtain $g(t,\phi) = 1/B'$, ie $g(t,\phi) =$ constant, showing that this estimator coincides with the log-estimator.

The log-estimator was included in the simulation studies and appears to have performed very satisfactorily.

4.9 Time-count estimator

Let us consider the g-function:

$$g(t,\phi) = \frac{1}{\mu_{x+t}} \tag{4.38}$$

Then, using the category I equation, the g-estimator for ϕ is given by:

$$\sum_N \int_{s_i}^{t_i} dt = \sum_D \frac{1}{\mu_{x+t_i}} \tag{4.39}$$

$$\Rightarrow \qquad \sum_N (t_i - s_i) = \sum_D \frac{1}{\mu_{x+t_i}} \tag{4.40}$$

Thus when the g-function is:

$$g(t,\phi) = \frac{1}{\mu_{x+t}} \quad ,$$

we obtain a quite simple equation which is solved by the g-estimator for ϕ in which the left-hand side is simply the total amount of time that lives were present in the investigation.

We will call this estimator the "time-count estimator".

This is a very interesting estimator because it always involves the actual exposure of the lives during the investigation. Whether it will lead to an expression for ϕ which is easily evaluated will depend on the expression which the mortality law produces for the right-hand side.

When the rectangular hyperbolic distribution applies, we have the g-function:

$$g(t,\phi) = 1/\frac{1}{a - bt} = a - bt \tag{4.41}$$

Then the time-count estimator is given by:

$$\sum_N (t_i - s_i) = \sum_D (a - bt_i) \tag{4.42}$$

$$= Da - b \sum_D t_i \tag{4.43}$$

Thus if b is chosen, ie a mortality assumption specified, we have a very simple equation

giving a, namely:

$$\frac{1}{a} = \mu_x = \frac{D}{\sum_N (t_i - s_i) + b \sum_D t_i} \tag{4.44}$$

q_x can then be obtained by applying the result:

$$q_x = 1 - (1 - \frac{b}{a})^{\frac{1}{b}} \tag{4.45}$$

When the "level deaths" assumption applies, we have b = 1, giving the following time-count estimator:

$$q_x = 1 - (1 - \frac{D}{\sum_N (t_i - s_i) + \sum_D t_i})$$

$$= \frac{D}{\sum_N (t_i - s_i) + \sum_D t_i} \tag{4.46}$$

Thus we have an exposed-to-risk style expression leading to q_x in which all lives are exposed for the time they are actually present in the investigation and deaths are given additional exposure for the period from the beginning of the year of age up to the point of death.

These exposures are of course those given by version (b) of the "exposures per life" for the "level deaths" assumption discussed in Sections 2.3 and 2.4. This set of exposures per life had been presented in Greville (1978), where it is reported that this set of exposures per life arose from a method of derivation suggested by D. Schuette.

It is fascinating to see that "version (b)" fits into the well-defined structure of estimators.

When the Balducci assumption applies, ie b = -1, we have:

$$q_x = 1 - (1 + \frac{1}{a})^{-1} = \frac{1}{1 + a} \tag{4.47}$$

where from equation (4.44):

$$a = \frac{1}{D} (\sum_N (t_i - s_i) - \sum_D t_i) \tag{4.48}$$

$$\Rightarrow \quad q_x = \frac{D}{\sum_N (t_i - s_i) - \sum_D t_i + D}$$

$$= \frac{D}{\sum_{N}(t_i - s_i) + \sum_{D}(1 - t_i)} \tag{4.49}$$

This is obviously the very familiar conventional estimator under which lives are exposed for the time that they are present in the investigation, except for deaths which are exposed to the end of the year of death.

The g-function for the conventional estimator is $1/{}_tp_x$ and the g-function for the time-count estimator is $1/\mu_{x+t}$. If the two estimators are identical, we have:

$$\frac{1}{{}_tp_x} = K\left(\frac{1}{\mu_{x+t}}\right) \tag{4.50}$$

for some constant K independent of t, since such a factor will not alter the effect of the weights. The value of K will be determined by the population value of the mortality parameter ϕ.

This relationship can be re-expressed as:

$$l_{x+t} = \mu_{x+t} * \text{constant} \tag{4.51}$$

and, as we have seen in Section 3.2, this relationship is true when the Balducci assumption applies, thus confirming that the conventional estimator and the time-count estimator are identical when this mortality assumption applies.

It is ironic that, for so long, much exposed-to-risk theory relied so heavily on the unrealistic Balducci assumption when, for example, a method could have been employed involving equally simple calculations using the "level deaths" assumption which, although not ideal, is clearly preferable to the Balducci assumption. And indeed many alternative mortality assumptions could have been considered, including the whole rectangular hyperbolic family, ie for any value of b.

When the "constant μ" assumption applies, ie b = 0, we obtain:

$$\sum_{N}(t_i - s_i) = Da \tag{4.52}$$

$$\Rightarrow \qquad \mu = \frac{D}{\sum_{N}(t_i - s_i)} \tag{4.53}$$

thus giving once more the familiar result generally associated with the method of maximum likelihood.

We also obtained this result for the log-estimator. The g-functions are respectively $1/\mu_{x+t}$ (time-count estimator) and a constant (log-estimator) so that, if they give the same estimator, we have:

$$\mu_{x+t} = \text{constant.} \tag{4.54}$$

This confirms that the estimators are identical if (and only if) the mortality law is "constant μ".

For the Gompertz law with fixed c, the time-count estimator for B' is given by the equation:

$$\sum_{N} (t_i - s_i) = \frac{1}{B'} \sum_{D} \frac{1}{c^{t_i}} \tag{4.55}$$

$$\Rightarrow \qquad B' = \frac{\sum_{D} \frac{1}{c^{t_i}}}{\sum_{N} (t_i - s_i)} \tag{4.56}$$

This is a relatively easy estimator to evaluate, based on actual exposure time, and just requiring in addition the calculation of the factor $1/c^{t_i}$ for each death, which is certainly trivial if a computer is involved, and is even very practicable in a paper and pencil study if a calculator with a key giving powers of numbers is available.

Moreover it is easy to study the results of assuming several different values of c. When $c = 1$, we obviously again get the "constant μ" assumption.

This estimator appeals very strongly to the author, by virtue of the realistic mortality law, the ease of its application and the flexibility in allowing several values of c to be considered.

The time-count estimator was included in the simulation studies and appears to have performed very satisfactorily.

4.10 Implication-B estimator

It is also possible to bring the implication-B estimator into the g-estimator framework, but

this requires our analysis to commence with an elemental equation relating to deaths occurring in the element from age x+t to age x+t+δt in respect of lives who were age x+s at entry.

Then, if a factor of:

$$g(t,s,\phi) = \frac{{}_{s}p_{x}}{{}_{t}p_{x}} = \frac{1}{{}_{t-s}p_{x+s}} \tag{4.57}$$

is applied to each such elemental equation and summation is made over all values of t and s, this can be seen to produce an equation for a g-estimator which is in fact the implication-B estimator.

This will now be demonstrated. As already indicated, our analysis commences with an elemental equation relating to deaths occurring in the element from age x+t to age x+t+δt for lives aged x+s at entry. Our criterion for estimating ϕ from the experience of this element and these lives is:

$$P(t,s)\ \mu_{x+t}\ \delta t = D(t,\delta t,s) \tag{4.58}$$

where P(t,s) is the number of lives present at age x+t who entered at age x+s, and D(t,δt,s) is the actual number of deaths occurring in the element to lives who entered at age x+s.

We then introduce the factor g(t,s,ϕ) so that we have:

$$P(t,s)\ \mu_{x+t}\ g(t,s,\phi)\ \delta t = D(t,\delta t,s)\ g(t,s,\phi) \tag{4.59}$$

Proceeding as before, but also summing over all values of s, we have:

$$\sum_{i=1}^{N} \sum_{t=0}^{t=1^{*}} P(t,s_i)\ \mu_{x+t}\ g(t,s_i,\phi)\ \delta t = \sum_{D} g(t_i,s_i,\phi) \tag{4.60}$$

where, as before, the symbol:

$$\sum_{t=0}^{t=1^{*}}$$

denotes summation over all elements in the year of age.

Further development similar to that used previously will give:

$$\sum_{N} \int_{s_i}^{t_i} \mu_{x+t}\, g(t,s_i,\phi)\, dt = \sum_{D} g(t_i,s_i,\phi) \tag{4.61}$$

If we then adopt the function:

$$g(t,s,\phi) = \frac{{}_sp_x}{{}_tp_x} = \frac{1}{{}_{t-s}p_{x+s}} \tag{4.62}$$

we have:

$$\sum_{N} {}_{s_i}p_x \int_{s_i}^{t_i} \frac{\mu_{x+t}}{{}_tp_x}\, dt = \sum_{D} \frac{{}_{s_i}p_x}{{}_{t_i}p_x} \tag{4.63}$$

Taking note of the development we saw when the g-function is $1/{}_tp_x$, we have:

$$\sum_{N} {}_{s_i}p_x \left(\frac{1}{{}_{t_i}p_x} - \frac{1}{{}_{s_i}p_x}\right) = \sum_{D} \frac{{}_{s_i}p_x}{{}_{t_i}p_x} \tag{4.64}$$

$$\Rightarrow \quad \sum_{N} \left(\frac{{}_{s_i}p_x}{{}_{t_i}p_x} - 1\right) = \sum_{D} \frac{{}_{s_i}p_x}{{}_{t_i}p_x} \tag{4.65}$$

$$\Rightarrow \quad \sum_{WS} \frac{{}_{s_i}p_x}{{}_{t_i}p_x} = N \tag{4.66}$$

And this equation is solved by the value of ϕ which is the implication-B estimator.

Thus the g-estimator corresponding to the g-function:

$$g(t,s,\phi) = \frac{{}_sp_x}{{}_tp_x} = \frac{1}{{}_{t-s}p_{x+s}}$$

is the implication-B estimator.

4.11 Some other category I estimators

It is possible to identify a number of further g-functions $g(t,\phi)$ which allow the analytical development of the category I g-estimator equation.

Briefly we will consider the following possibilities:

(a) $g(t,\phi) = {}_tp_x$

(b) $g(t,\phi) = (\mu_{x+t})^r \frac{\partial \mu_{x+t}}{\partial t}$ for any r.

(a) Using: $$g(t,\phi) = {}_tp_x, \tag{4.67}$$

we obtain: $$\sum_N \int_{s_i}^{t_i} {}_tp_x \, \mu_{x+t} \, dt = \sum_D {}_{t_i}p_x \tag{4.68}$$

$$\Rightarrow \quad \sum_N ({}_{t_i}q_x - {}_{s_i}q_x) = \sum_D {}_{t_i}p_x \tag{4.69}$$

or $$\sum_N ({}_{s_i}p_x - {}_{t_i}p_x) = \sum_D {}_{t_i}p_x \tag{4.70}$$

or $$\sum_N {}_{s_i}p_x \, {}_{t_i-s_i}q_{x+s_i} = \sum_D {}_{t_i}p_x \tag{4.71}$$

or $$\sum_N {}_{t_i}q_x + \sum_D {}_{t_i}q_x - \sum_N {}_{s_i}q_x = D \tag{4.72}$$

This estimator is identical with the time-count estimator when the "level deaths" assumption applies and is identical with the maximum likelihood estimator for the Balducci assumption.

(b) Using: $$g(t,\phi) = (\mu_{x+t})^r \frac{\partial \mu_{x+t}}{\partial t} \quad \text{for any r,} \tag{4.73}$$

we obtain:

$$\sum_N \int_{s_i}^{t_i} (\mu_{x+t})^{r+1} \frac{\partial \mu_{x+t}}{\partial t} \, dt = \sum_D (\mu_{x+t_i})^r \left[\frac{\partial \mu_{x+t}}{\partial t}\right]_{t=t_i} \tag{4.74}$$

If $r \neq -2$, this gives:

$$\frac{1}{r+2} \sum_N ((\mu_{x+t_i})^{r+2} - (\mu_{x+s_i})^{r+2}) = \sum_D (\mu_{x+t_i})^r \left[\frac{\partial \mu_{x+t}}{\partial t}\right]_{t=t_i} \tag{4.75}$$

If $r = -2$, equation (4.74) gives:

$$\sum_{N} (\log \mu_{x+t_i} - \log \mu_{x+s_i}) = \sum_{D} \frac{1}{(\mu_{x+t_i})^2} \left[\frac{\partial \mu_{x+t}}{\partial t}\right]_{t=t_i} \tag{4.76}$$

or

$$\sum_{N} \log \frac{\mu_{x+t_i}}{\mu_{x+s_i}} = \sum_{D} \frac{1}{(\mu_{x+t_i})^2} \left[\frac{\partial \mu_{x+t}}{\partial t}\right]_{t=t_i} \tag{4.77}$$

If the rectangular hyperbolic distribution applies with any assumed value of b except 0, this estimator is identical with the time-count estimator when r = -3, with the log-estimator when r = -2 and with the maximum likelihood estimator of a when r = -1.

If the Gompertz Law applies with any assumed value of c except 1, this estimator is identical with the time-count estimator when r = -2 and with the log-estimator when r = -1, and also with the maximum likelihood estimator of B' when r = -1.

4.12 Review of the process of combining the experience of elements of the year of age

It is of interest to review the effect of the process by which the experience of the individual elements of the year of age are combined.

As before, let us consider an element of the year of age of width δt from which we estimate the value of ϕ by means of the relationship:

$$P(t)\ \mu_{x+t}\ \delta t = D(t,\delta t) \tag{4.78}$$

and the one-parameter mortality law:

$$\mu_{x+t} = f(t,\phi) \tag{4.79}$$

Let this element be the j^{th} element located at time t_j, and let us now use ϕ_j to denote the estimate of ϕ it gives. We assume that all elements are of equal width δt.

Let us rewrite equation (4.78) as:

$$P(t_j)\ f(t_j,\phi_j)\ \delta t = D(t_j,\delta t) \tag{4.80}$$

where we will describe ϕ_j as the observed value of ϕ for the j^{th} element, and $f(t_j,\phi_j)$ as the observed force of mortality for the j^{th} element.

Now in combining the experience of the individual elements, we multiply equation (4.80) for each element by the appropriate weighting factors, sum the left-hand and right-hand sides of the equations, and then create a revised equation by replacing all the individual values of ϕ_j by the new unknown ϕ.

Thus we create the equation:

$$\sum_j^* g(t_j,\phi)\ P(t_j)\ f(t_j,\phi)\ \delta t = \sum_j^* g(t_j,\phi)\ D(t_j,\delta t) \tag{4.81}$$

where the symbol: $\sum_j^*$

denotes summation over all elements in the year of age.

We will describe the value of ϕ solving equation (4.81) as the estimated value of ϕ and the value of $f(t_j,\phi)$ corresponding to the estimated value of ϕ as the estimated force of mortality for the j^{th} element.

Substituting in equation (4.81) for $D(t_j,\delta t)$ using equation (4.80) and cancelling δt, we obtain:

$$\sum_j^* g(t_j,\phi)\ P(t_j)\ (f(t_j,\phi) - f(t_j,\phi_j)) = 0 \tag{4.82}$$

Now we will assume that $f(t_j,\phi)$, the force of mortality in the j^{th} element corresponding to the value of ϕ, is a strictly monotonic function of ϕ, which is obviously the only admissible situation if ϕ is a parameter representing mortality (eg q_x, m_x, μ_x or $\mu_{x+\frac{1}{2}}$) or the complementary phenomenon of survival (eg p_x).

We will note also that $g(t_j,\phi)$ does not change sign for t varying in the range $0 \leq t \leq 1$.

Firstly, we will consider the assumption that $f(t_j,\phi)$ is a strictly increasing function of ϕ (eg ϕ equals q_x, m_x, μ_x or $\mu_{x+\frac{1}{2}}$).

Then: $$f(t_j,\phi) > f(t_j,\phi_j) \quad \Rightarrow \quad \phi > \phi_j$$

and: $$f(t_j,\phi) < f(t_j,\phi_j) \quad \Rightarrow \quad \phi < \phi_j$$

So, obviously, the estimated value of ϕ is greater than all those ϕ_j (observed values of ϕ) for which $f(t_j,\phi) > f(t_j,\phi_j)$, ie for which the estimated force of mortality in the j^{th} element is

greater than the observed force of mortality in that element, and similarly the estimated value of ϕ is less than all those ϕ_j for which $f(t_j,\phi) < f(t_j,\phi_j)$.

And, secondly, we will consider the assumption that $f(t_j,\phi)$ is a strictly decreasing function of ϕ (eg ϕ equals p_x).

Then: $$f(t_j,\phi) > f(t_j,\phi_j) \quad \Rightarrow \quad \phi < \phi_j$$

and: $$f(t_j,\phi) < f(t_j,\phi_j) \quad \Rightarrow \quad \phi > \phi_j$$

Now here we can see that the estimated value of ϕ is greater than all those ϕ_j for which $f(t_j,\phi) < f(t_j,\phi_j)$, and similarly the estimated value of ϕ is less than all those ϕ_j for which $f(t_j,\phi) > f(t_j,\phi_j)$.

Whether we assume that $f(t_j,\phi)$ is a strictly increasing or decreasing function of ϕ, equation (4.82) implies that some of the $(f(t_j,\phi) - f(t_j,\phi_j))$ will be positive and the rest will be negative (or zero). The effect of the expression (4.82) is to equate the weighted sum of the positive values of $(f(t_j,\phi) - f(t_j,\phi_j))$ to the absolute value of the weighted sum of the negative values of $(f(t_j,\phi) - f(t_j,\phi_j))$, and the estimated value of ϕ will obviously be the value of ϕ for which this equality occurs. Clearly, the estimated value of ϕ, the value at which the equality occurs, will depend on the choice of the $g(t,\phi)$ function.

This balance is generally struck for a different value of ϕ for each estimator though, as we have seen, the same value of ϕ can be reached for different estimators in special circumstances.

The analysis in this section demonstrates that the estimated value of ϕ will lie somewhere in the range between the smallest and the largest values of the $\{\phi_j\}$, the precise position in the range depending on the choice of the $g(t,\phi)$ function.

4.13 Every g-estimator which assumes a one-parameter mortality law is asymptotically unbiased, so long as the g-estimator assumes the correct mortality law

Let us continue to assume that the one-parameter equation:

$$\mu_{x+t} = f(t,\phi) \tag{4.83}$$

correctly represents the mortality law (where $f(t,\phi)$ is a strictly monotonic function of ϕ).

Let us denote the population value of ϕ by the symbol ϕ^*, and let us use the symbol ϕ_{all} to denote a g-estimator of ϕ^*, ie the estimate of ϕ^* based on the combined experience of all the elements, using the weighting function corresponding to the g-estimator concerned.

Consider the j^{th} element of the year of age.

In the j^{th} element, we have $P(t_j)$ Bernoulli trials each of which can yield a death with probability $f(t_j,\phi^*)\ \delta t$. From the properties of Bernoulli trials (see for example Larson 1982), we know that $f(t_j,\phi_j)\ \delta t$, the observed proportion of deaths to the population starting the j^{th} element, will be an unbiased estimator of $f(t_j,\phi^*)\ \delta t$ and that:

$$f(t_j,\phi_j)\ \delta t \rightarrow f(t_j,\phi^*)\ \delta t \qquad \text{as } P(t_j)\rightarrow\infty$$

$$\Rightarrow \qquad f(t_j,\phi_j) \rightarrow f(t_j,\phi^*) \qquad \text{as } P(t_j)\rightarrow\infty$$

Then, since $f(t,\phi)$ is a strictly monotonic function of ϕ, it follows that:

$$\phi_j \rightarrow \phi^* \qquad \text{as } P(t_j)\rightarrow\infty$$

Now we have seen (Section 4.12) that, in combining the experience of all the elements to obtain an estimate of ϕ, we obtain a value which lies in the range between the smallest and largest values of the $\{\phi_j\}$.

So if we let $P(t_j)\rightarrow\infty$ for all j, then $\phi_j\rightarrow\phi^*$ for all j with the consequence that the estimate of ϕ based on the combined experience of all the elements, ϕ_{all}, is such that $\phi_{all}\rightarrow\phi^*$, ie it tends to the population value ϕ^* as $P(t_j)\rightarrow\infty$ for all elements.

Thus every g-estimator which assumes a one-parameter mortality law is asymptotically unbiased so long as the g-estimator assumes the correct mortality law. It should be noted that this discussion has not considered the position for g-estimators which assume a mortality law involving more than one parameter.

An alternative, and intuitively simple, argument can be put forward if we are prepared to make the very mild assumption that the value of the g-estimator, ϕ_{all}, does actually tend to a limit as the sample size approaches infinity.

This is based on the argument that, as the sample size approaches infinity, the experience in the sample will come to resemble the probability distribution in the population.

When the experience in the sample does resemble the probability distribution in the

population, ϕ_j will equal ϕ^* so long as the g-estimator assumes the correct mortality law.

This follows if we remember that, in the j^{th} element, we have $P(t_j)$ Bernoulli trials each of which can yield a death with probability $f(t_j,\phi^*)\ \delta t$, and that $f(t_j,\phi_j)\ \delta t$ will be an unbiased estimator of $f(t_j,\phi^*)\ \delta t$. Since we are arguing that the experience in the sample from the j^{th} element resembles the corresponding population distribution, and since $f(t_j,\phi_j)\ \delta t$ is an unbiased estimator of $f(t_j,\phi^*)\ \delta t$, we know therefore that:

$$f(t_j,\phi_j) = f(t_j,\phi^*) \tag{4.84}$$

Then, remembering that $f(t,\phi)$ is a strictly monotonic function of ϕ, it follows that:

$$\phi_j = \phi^* \tag{4.85}$$

Now we have seen (Section 4.12) that, in combining the experience of all the elements to obtain an estimate of ϕ, we obtain a value which lies in the range between the smallest and largest values of the $\{\phi_j\}$.

Thus, in the situation where ϕ_j equals ϕ^* for every j, we know that the estimate of ϕ based on the combined experience of all the elements, ϕ_{all}, equals ϕ^*.

Thus, when the experience in the sample resembles the probability distribution in the population, the estimated value ϕ_{all} equals ϕ^*, ie the g-estimator is unbiased and, as we have noted, the experience in the sample will come to resemble the probability distribution in the population, as the sample size approaches infinity.

Therefore, if in this alternative approach we make the very mild assumption that the value of the g-estimator, ϕ_{all}, does tend to a limit as the sample size approaches infinity, we know that the g-estimator will be asymptotically unbiased (so long as the g-estimator assumes the correct one-parameter mortality law).

The first approach we considered also indicated that the value of the g-estimator does indeed tend to a limit as the sample size approaches infinity.

The result proved in this section is very notable since it states an important asymptotic property of *all* g-estimators, when the correct one-parameter mortality law has been assumed; moreover, this general result is shown using very simple arguments.

An even more powerful result, were its proof to be possible, would be that such estimators are also *consistent* under these circumstances. The property of consistency, which refers not

only to the asymptotic behaviour of an estimator but also to the manner in which the fluctuation of values of the estimator behaves as the sample size approaches infinity, was introduced in Section 1.13 .

Preliminary investigations suggest that, if it is true that a g-estimator is consistent when a correct one-parameter mortality law has been assumed, a proof of this would be analytically more demanding than the comparatively simple proof of asymptotic unbiasedness presented in this section. It is intended that further research will be undertaken to obtain such a proof, if the property of consistency does indeed apply, as appears intuitively plausible.

4.14 If a g-estimator assumes an incorrect one-parameter mortality law, it is not generally asymptotically unbiased

If the wrong one-parameter mortality law is assumed, the wrong set of $\{\phi_j\}$ values is obtained, and as $P(t_j)\rightarrow\infty$ for all j, each ϕ_j will in general tend to a different limit, ϕ_j^* say. This is fairly obvious since, if the correct law produces the value ϕ^* in the limit in the j^{th} element, the incorrect law will produce the incorrect value ϕ_j^* in the j^{th} element in the limit, and there is no reason to expect that the incorrect value ϕ_j^* will be the same for all j.

And there is certainly no reason to expect that the estimate of the population value produced in the limit by combining the experience of the individual elements as $P(t_j)\rightarrow\infty$ will be ϕ^*, which would have to be the result if the estimator is to be asymptotically unbiased.

That this cannot be expected to be the case is conveniently demonstrated by an example.

Suppose that the correct mortality law is:

$$\mu_{x+t} = f(t,\phi) \tag{4.86}$$

and that the incorrect mortality law which is assumed is:

$$\mu_{x+t} = f(t, \phi+k_1+k_2t) \tag{4.87}$$

$$\text{where} \quad k_1 > 0 \quad \text{and} \quad k_2 > 0$$

Then use of this incorrect law will produce values of ϕ_j^* which are related to ϕ^* by the relationship:

$$\phi_j^* = \phi^* - k_1 - k_2 t_j \tag{4.88}$$

The incorrect function $f(t, \phi+k_1+k_2t)$ still obeys the requirement of being a strictly monotonic function of ϕ (because the correct function $f(t,\phi)$ did so), so that in the limit, as the $P(t_j) \rightarrow \infty$ for all j, the estimated value of ϕ based on the combined experience of all the elements will tend to a value which lies somewhere between the values:

$$\phi^* - k_1 \quad \text{and} \quad \phi^* - k_1 - k_2$$

This estimated value will be clearly different from ϕ^* so that, in this example, the assumption of the incorrect mortality law means that the estimator is not asymptotically unbiased.

4.15 Concerning the possible presence of bias in g-estimators when applied to a finite number of lives

When we are considering an investigation in which a finite number of lives are observed, there is not in general any immediately apparent demonstration that a given g-estimator, even if based on the correct mortality law, will provide an unbiased estimate of the mortality parameter and, in the absence of any such demonstration, the presence of bias must be accepted by default as a likely possibility.

It has already been commented in Section 1.15 that the analysis by Roberts (1987), which would appear to show unbiasedness of certain g-estimators when the correct mortality assumption is made, involves approximations, and similarly for an apparent demonstration of unbiasedness in Forfar et al (1988), repeating one of Roberts' results.

Slawski (1991) points out some simplified situations in which there would be no bias, for example if there are no "withdrawals" or "enders" in a population subject to the Balducci mortality law, but then goes on to argue that bias must exist in all other situations. However this author has difficulty with the safety of the latter inference, as it appears to be based on the argument that certain conditions that provide unbiasedness are the only conditions that can provide unbiasedness (ie that an "if" condition is also an "only if" condition), and this author could not see that this had been proved.

Clearly on the face of it, there appears no reason to assume that the procedure described in Section 4.1, for estimating ϕ in each element of the year of age and then amalgamating the estimates to provide an estimate of ϕ for the whole year of age, will necessarily provide a bias-free estimate when finite numbers of lives are observed.

Of course, as discussed in Section 1.12, one estimator which is known to be virtually unbiased for all but the very smallest number of lives is the product limit estimator and, in the simulations, the values given by this estimator provide something of a bench-mark against which the values given by other estimators can be compared.

As will be discussed in Chapter 5, there is some evidence in the simulations to suggest the presence of bias in one or two of the estimators studied but, for g-estimators where the correct mortality law is assumed, the degree of any possible bias appears encouragingly small and, in particular, too small to be distinguished in the simulation results from the random fluctuations (as summarisd in Section 5.28).

4.16 Some comments on the general theory

In principle, $g(t,\phi)$ can be any function of t. However in general it seems sensible to use g-functions that give approximately balanced weights over the age range, so that the data from one point of the year of age does not have undue influence, which would thereby reduce the effect of the sample in balancing the random fluctuations of the individual observations.

The following weights can be seen to approximately achieve this or seem to be likely to do so:

$$\frac{1}{{}_tp_x}, \quad \frac{1}{\mu_{x+t}}, \quad \text{constant}, \quad {}_tp_x, \quad \frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi}$$

There might be an intuitive argument in favour of the g-function $1/{}_tp_x$ (conventional estimator), since this weighting seems to compensate for the natural reduction in the volume of data over the year of age due to mortality, though random fluctuations could be slightly accentuated.

The research has however revealed that some accepted estimation techniques do throw up some g-functions which vary drastically over the year of age: namely when the method of maximum likelihood is applied to the Gompertz distribution to estimate c, the g-function is t/c and when the same method is applied to the rectangular hyperbolic distribution to estimate b, the g-function is ${}_t\mu_{x+t}$. (See Section 4.7 for derivation of these g-functions).

Clearly data at the beginning of the year of age is being given very little weighting in the equation defining the estimators of c and b, and very heavy weighting at ages approaching x+1.

If however B' or a is also derived from the method of maximum likelihood, the relevant equations for those parameters have much more balanced g-functions, respectively $1/B'$ (i.e. constant) or $-\mu_{x+t}$. (Again, see Section 4.7 for derivation of these g-functions). If we regard the two equations used to evaluate B' and c, or to evaluate a and b, as a system of two simultaneous equations, it can be argued that the apparent imbalance in the use of the data is ameliorated, the two equations providing a contrast, which is greatest when the second equation appears to make least use of the data, and it is impossible to say that data at either end of the year of age is being neglected or over-emphasised.

It is difficult to conceive of a practical situation where we would assume B' or a, and then seek to establish c or b.

The simulation studies appear to indicate that the use of the maximum likelihood estimators for (B',c) or (a,b) tends to produce values of B' and a which are fairly stable as data fluctuates, but values of c and b which appear to fluctuate much more considerably. The values of c and b appear to require significantly more data in order to obtain reliable values, than is the case with B' and a; c and b depend on the *variation* of μ_{x+t} over the year of age whereas B' and c depend on the *level* of μ_{x+t} during the year of age, and random fluctuations will tend to obscure the former while averaging out in the latter.

If the estimator is based on a mortality law which is not quite correct, distortions are likely to become significant since the contribution of each element towards estimating ϕ, drawn from the effect of μ_{x+t} in the element, will not be correctly determined since the relationship:

$$\mu_{x+t} = f(t,\phi) \tag{4.89}$$

will not be quite correct.

In other words the estimator will tend to give a distorted estimate of ϕ. This is perhaps an argument in support of the obvious, especially in the light of the discussion about asymptotic unbiasedness, and it has been borne out in the simulation studies, as will be discussed in Section 5.27 .

4.17 Identification of estimators

It can be seen that for a given mortality law, g-functions provide a simple and immediate specification of an estimator and we do not necessarily have to refer to the estimation method, but can instead simply refer to the g-function.

The g-function also has the attraction of having a simple and readily understandable role in the estimation procedures, defining the weights given to the elements of the year of age.

As has been apparent, the g-function also provides a powerful tool for identifying those cases where different methods of estimation give the identical estimator for a particular mortality law.

4.18 Why is the general theory possible?

It is very intriguing that a theory, which permits most forms of mortality rate estimator to be derived from a common starting point, can be developed in the context of a mortality investigation. This is not a situation which is familiar in other contexts.

It appears to this author that the general theory is possible in the context of a mortality investigation because we are applying our analysis to an experimental situation that lasts a finite time. An individual time element of the investigation presents us with a very simple scenario but it is the manner in which we combine the experience of the individual time elements to obtain an estimator embracing the experience of the entire investigation that determines the character of the estimator concerned.

Again the author would express the opinion that the particular feature of a mortality investigation in being of finite length is one whose significance has probably not been properly recognised in the past.

4.19 Category II g-estimators

We will shortly consider some category II g-estimators. It will be seen that the g-function for all the category II g-estimators which will be considered includes the factor $\frac{1}{P(t)}$. This eliminates the factor P(t) in the category II equation:

$$\int_0^1 P(t)\, \mu_{x+t}\, g(t,\phi)\, dt = \sum_D g(t_i,\phi) \tag{4.90}$$

and this generally opens the door to a convenient mathematical development.

Indeed it will be seen that in general, that if $g(t,\phi)$ is a g-function which allows a convenient mathematical development of a category I g-estimator, then it is very likely that a g-function in the form:

$$\frac{g(t,\phi)}{P(t)}$$

will allow the convenient mathematical development of a category II g-estimator.

The inclusion of the factor $\frac{1}{P(t)}$ in the g-function needs to approached with a little caution for fear of the factor being a possible source of bias.

Strictly speaking, P(t) is a function of the mortality experience in the elements of the year of age preceding time t and, if for example the preceding mortality experience has been predominantly heavy, then P(t) will be slightly reduced as a result and the factor $\frac{1}{P(t)}$ somewhat increased.

Thus if the experience in the elements up to time t has been predominantly heavy, this will have the effect of giving greater weight to the experience of the element at time t which implies that the elements in which the heavy mortality occurred will be given a relatively reduced weighting, so that, assuming that ϕ is a parameter representing mortality (eg q_x, m_x, μ_x or $\mu_{x+\frac{1}{2}}$) and not the complementary phenomenon of survival (eg p_x), the estimated value of ϕ may tend to be subject to negative bias from this source. (Of course, there may also be bias present from the sources discussed in Section 4.15).

If the experience in the preceding elements has been predominantly light, the weighting given to the element at time t will tend to be reduced with the result that the earlier elements will be given relatively increased weighting, so that again the estimated value of ϕ, if once more assumed to represent mortality and not survival, may tend to be subject to negative bias from this source.

It seems almost unavoidable that this source of negative bias will operate, whatever the actual observations of deaths might be, because the population mortality will correspond to an idealised situation in which the life table population changes continuously as age advances and not in discrete jumps, so that any set of actual observations which necessarily consists of deaths occurring in discrete units of one will represent a fluctuation from the population mortality, thus causing the negative bias from this source to be manifested. The only apparent circumstance in which an exception could occur would seem to be if the population mortality could be assumed to that actually observed, including the deaths occurring in units of one, and the product limit estimator seems to be the only estimator which could offer this possibility. In Section 4.21, an adaption of a category II estimator which leads to the product limit estimator will be discussed.

However, it may be possible that this biasing effect could be feared to be more important

than it really is, bearing in mind that the effect of mortality on P(t) within a year of age is likely to be relatively very small, so that the biasing effect may also be very small.

Unfortunately, the author only realised the potential of using g-functions which included the factor $\frac{1}{P(t)}$ at a very late stage in the research, and such estimators have not been included in the simulation studies. The author hopes in due course to conduct further research using simulation studies to investigate the performance of such estimators and, in particular, to investigate the extent to which the apparent potential for bias due to the $\frac{1}{P(t)}$ factor is of any practical importance.

Of course the factor $\frac{1}{P(t)}$ does have a perverse effect in exaggerating the importance of elements where there is little data and suppressing the importance of elements where there is a large amount of data, and as a general principle this perverse treatment of the weight of data is unattractive because of the enlarging effect it will have on the variance of the estimated value of ϕ given by the estimator.

Bearing in mind the adverse effect on the variance of such g-estimators of having P(t) that fluctuates greatly through the year of age, it appears good policy to avoid using g-estimators which have a g-function that includes the factor $\frac{1}{P(t)}$, in those situations where P(t) is not reasonably steady over the year of age. This does not appear a very restrictive stipulation as generally it seems unlikely that P(t) would fluctuate greatly over a single year of age.

We will now consider some category II g-estimators, in which the g-functions include the factor $\frac{1}{P(t)}$.

4.20 Nelson-Aalen estimator

Let us consider the g-function:

$$g(t,\phi) = \frac{1}{P(t)} \tag{4.91}$$

Then, using the category II equation, the g-estimator for ϕ is given by:

$$\int_0^1 \mu_{x+t}\, dt = \sum_D \frac{1}{P(t_i)} \tag{4.92}$$

But life contingencies tells us that:

$$p_x = \exp\left[- \int_0^1 \mu_{x+t}\, dt \right] \tag{4.93}$$

$$\Rightarrow \qquad p_x = \exp\left[- \sum_D \frac{1}{P(t_i)} \right] \tag{4.94}$$

$$\Rightarrow \qquad q_x = 1 - \exp\left[- \sum_D \frac{1}{P(t_i)} \right] \tag{4.95}$$

This estimator is noteworthy in not requiring the assumption of a mortality law, a characteristic which it shares with the product limit estimator. It is also to be noted that the estimator does not require an iterative evaluation.

In fact the estimator has been described in the literature by Nelson (1972). Accounts are also given in Elandt-Johnson and Johnson (1980) where it is referred to as "Nelson's Method for Ungrouped Data" and in London (1988) where it is referred to as the "Nelson-Aalen Estimator".

In London (1988), the estimator is obtained by approximating the cumulative hazard function of the product limit estimator, and the derivation in Elandt-Johnson and Johnson (1980) also involves the approximation of a cumulative hazard function. In Nelson (1972), the estimation method is developed by assuming initially an exponential distribution (constant μ).

In Section 4.19 it was argued that where a g-estimator of q_x is obtained using a g-function including the factor $\frac{1}{P(t)}$, the presence of the factor will tend to introduce a negative bias. This estimator, for which the g-function is just $\frac{1}{P(t)}$, appears to be strongly consistent with the argument, although it has to be recognised that there may also be other sources contributing to the net bias observed; as London (1988) reports, where the Nelson-Aalen estimator gives a non-zero value of q_x, this value will be less than that given by the product limit estimator. And, of course, the product limit estimator is known to be virtually unbiased for all but the very smallest experiences.

This relationship between the Nelson-Aalen estimator and the product limit estimator is easily demonstrated, as shown below.

The product limit estimator of q_x can be written in the form:

$$^{PL}q_x = 1 - {}^{PL}p_x \tag{4.96}$$

with

$$^{PL}p_x = \prod_{r=1}^{m} \left[\frac{P_r - d_r}{P_r} \right] \tag{4.97}$$

where:

(a) P_r is the population present immediately after the r^{th} movement in or out of the population present during the year of age (embracing both deaths and non-death movements), and P_1 in particular is the population present immediately after the start of the year of age.

(b) d_r is the number of lives dying at the next movement in or out of the population, following the r^{th} movement. It will be noted that d_r can be 0 if the next movement does not include a death, 1 if the next movement consists of (or includes) one death, or more than 1 if several deaths coincide at the next movement.

(c) m+1 is the total number of movements (deaths or non-deaths) and includes the movement on of all the lives starting the year of age, and excludes the movement off of the lives reaching the end of the year of age.

Now:

$$-\log {}^{PL}p_x = -\log \prod_{r=1}^{m} \left[\frac{P_r - d_r}{P_r}\right]$$

$$= \sum_{r=1}^{m} \left[-\log\left(1 - \frac{d_r}{P_r}\right)\right]$$

$$= \sum_{r=1}^{m} \left[\frac{d_r}{P_r} + \tfrac{1}{2}\left(\frac{d_r}{P_r}\right)^2 + \tfrac{1}{3}\left(\frac{d_r}{P_r}\right)^3 + \ldots \right]$$

$$> \sum_{r=1}^{m} \frac{d_r}{P_r}$$

(assuming the right-hand side is non-zero).

ie
$$-\log {}^{PL}p_x > \sum_{r=1}^{m} \frac{d_r}{P_r} \tag{4.98}$$

where the summation on the right hand side is taken over the individual deaths. and $P(t_i)$ is the population present when the i^{th} life dies.

$\Rightarrow$
$${}^{PL}p_x < \exp\left[-\sum_{D} \frac{1}{P(t_i)}\right] \tag{4.99}$$

where $P(t_i)$ is the population present when the i^{th} life dies.

$$\Rightarrow \qquad {}^{PL}q_x > 1 - \exp\left[- \sum_D \frac{1}{P(t_i)} \right] \tag{4.100}$$

ie the product limit estimator of q_x is always greater than the Nelson-Aalen estimator of q_x, so long as the values are non-zero.

Another feature of this estimator is that it only appears to use data relating to the points at which deaths occur. Of course the $P(t_i)$ items will reflect influences affecting the size of the population before time t_i, but P(t) could behave in a variety of contrasting manners during non-death periods without this affecting the calculation of q_x; the estimator does not appear to consider exposure, nor any similar measure, during the non-death periods, relying instead on the fact that no deaths occur and what that implies.

If the factor $\frac{1}{P(t)}$ is removed from the g-function for this estimator, we are left with a constant, which would be the g-function for the log-estimator. Thus if the population P(t) is reasonably steady over the year-of-age, which appears a desirable situation for the use of category II g-estimators such as the Nelson-Aalen estimator, the results given by the Nelson-Aalen estimator may possibly be similar to those of the log-estimator, without requiring a mortality assumption or iterative evaluation, as in the case of the log-estimator.

4.21 Life-profile estimator

Let us consider the g-function:

$$g(t,\phi) = \frac{{}_tp_x}{P(t)} \tag{4.101}$$

Then, using the category II equation, the g-estimator for ϕ is given by:

$$\int_0^1 {}_tp_x \, \mu_{x+t} \, dt = \sum_D \frac{{}_{t_i}p_x}{P(t_i)} \tag{4.102}$$

$$\Rightarrow \qquad q_x = \sum_D \frac{{}_{t_i}p_x}{P(t_i)} \tag{4.103}$$

The g-estimator given by the g-function $\frac{{}_tp_x}{P(t)}$ has been named the "life-profile" estimator since in combining the experience of each element, the weight of the number of lives actually present in each element, P(t), has been scaled to ${}_tp_x$, the weighting in the life table obeyed by the population.

We obviously need to assume a mortality law to express ${}_{t_i}p_x$ in terms of the mortality parameter (generally denoted by ϕ, but probably taken as q_x). Generally this will lead to an iterative derivation of q_x, but for certain mortality assumptions this is avoided.

Suppose we make the "level deaths" assumption.

Then
$$q_x = \sum_D \frac{1 - t_i * q_x}{P(t_i)} \tag{4.104}$$

$\Rightarrow$
$$q_x = \frac{\sum_D \frac{1}{P(t_i)}}{1 + \sum_D \frac{t_i}{P(t_i)}} \tag{4.105}$$

Thus, here, an iterative derivation is not required.

If in expression (4.103), we calculate ${}_{t_i}p_x$ using the same principle as in the product limit estimator, ie reflecting the proportions surviving between movements in the actual experience, the expression we obtain for q_x is the product limit estimator.

This is readily demonstrated. If ${}_{t_i}p_x$ is determined in this way, the expression (4.103) can be expressed in the form:

$$q_x = \sum_{r=1}^{m} \frac{d_r}{P_r} \prod_{u=1}^{r-1} \frac{P_u - d_u}{P_u} \tag{4.106}$$

where P_r, d_r and m are defined as in the previous section, and where:

$$\prod_{u=1}^{r-1} \frac{P_u - d_u}{P_u}$$

equals unity when $r = 1$.

Then:
$$q_x = \sum_{r=1}^{m} \frac{P_r - (P_r - d_r)}{P_r} \prod_{u=1}^{r-1} \frac{P_u - d_u}{P_u}$$

$$= \sum_{r=1}^{m} \left(\prod_{u=1}^{r-1} \frac{P_u - d_u}{P_u} - \prod_{u=1}^{r} \frac{P_u - d_u}{P_u} \right)$$

$$= 1 - \prod_{u=1}^{m} \frac{P_u - d_u}{P_u} \qquad (4.107)$$

and the latter expression on the right-hand side defines the product limit estimator.

It is very interesting that defining the factor ${}_tp_x$ in the g-function, $\frac{{}_tp_x}{P(t)}$, in this way leads to the virtually unbiased product limit estimator. In reaching this result, we have also implicitly based the formula in equation (4.1):

$$\mu_{x+t} = f(t,\phi)$$

on this definition of ${}_tp_x$.

When the life table is based on ${}_tp_x$ items which are determined using the product limit principle, it is interesting that the product limit estimator is obtained, which is virtually an unbiased estimator for all but the smallest experiences.

As has been discussed in Section 1.12, such bias as is present in the product limit estimator is due to the generally remote possibility of the sample mortality experience not being available throughout the entire year of age, so that an expected value of the product limit estimator based on all possible sample outcomes cannot be determined. As demonstrated in Section 1.12, this can be a source of either positive or negative bias.

Since this particular life-profile estimator is virtually unbiased for all but the very smallest experiences, and the source of any such bias is known to be due to the generally remote possiblity of the product limit estimator being undefined, we can deduce that the normally ubiquitous biasing effect of the factor $\frac{1}{P(t)}$ contained in the g-estimator is absent.

This might probably be rationalised by noting that the mortality experience observed is exactly the same as that expected on the basis of the mortality assumed to apply in the population. Hence the factor $\frac{1}{P(t)}$, which generally tends to introduce negative bias due to fluctuations in the experience before duration t, will not have this effect here because the mortality assumption means that there are no fluctuations.

This argument appears to provide an independent collaboration of the conventional demonstration, discussed in Section 1.12, that the product limit estimator is virtually unbiased.

4.22 The g-estimator with $g(t,\phi) = \frac{1}{P(t)\ \mu_{x+t}}$

Let us consider the g-function:

$$g(t,\phi) = \frac{1}{P(t)\ \mu_{x+t}} \tag{4.108}$$

Then, using the category II equation, the g-estimator for ϕ is given by:

$$\int_0^1 dt = \sum_D \frac{1}{P(t_i)\ \mu_{x+t_i}} \tag{4.109}$$

$$\Rightarrow \qquad 1 = \sum_D \frac{1}{P(t_i)\ \mu_{x+t_i}} \tag{4.110}$$

Again we need to assume a mortality law.

Firstly let us assume the Gompertz Law, $\mu_{x+t} = B'c^t$, with an assumed value of c.

$$\Rightarrow \qquad 1 = \frac{1}{B'} \sum_D \frac{1}{P(t_i)\ c^{t_i}} \tag{4.111}$$

$$\Rightarrow \qquad B' = \sum_D \frac{1}{P(t_i)\ c^{t_i}} \tag{4.112}$$

This gives a relatively easy non-iterative calculation.

Secondly let us use the rectangular hyperbolic mortality law with an assumed value of b, that is:

$$\mu_{x+t} = \frac{1}{a - bt} \tag{4.113}$$

Then:
$$1 = \sum_D \frac{(a - bt_i)}{P(t_i)} \tag{4.114}$$

$$= a \sum_D \frac{1}{P(t_i)} - b \sum_D \frac{t_i}{P(t_i)} \tag{4.115}$$

$$\Rightarrow \qquad \mu_x = \frac{1}{\mathring{a}} = \frac{\sum_D \frac{1}{P(t_i)}}{1 + b \sum_D \frac{t_i}{P(t_i)}} \tag{4.116}$$

Then: $$q_x = 1 - (1 - \frac{b}{\mathring{a}})^{\frac{1}{b}} \qquad \text{for } b \neq 0 \tag{4.117}$$

or: $$q_x = 1 - e^{-\mu_x} \qquad \text{for } b = 0 \tag{4.118}$$

Again this gives a non-iterative calculation.

It will be noted that, when $b = 1$, this estimator is identical with the life-profile estimator for the "level deaths" assumption, which is confirmed by equating the g-functions:

$$\frac{{}_tp_x}{P(t)} = \frac{K}{P(t)\ \mu_{x+t}} \tag{4.119}$$

$$\Rightarrow \qquad {}_tp_x\ \mu_{x+t} = K \tag{4.120}$$

which is a relationship that is true if (and only if) the "level deaths" assumption applies.

When the "constant μ" mortality assumption applies, ie when $b = 0$, this estimator coincides with the Nelson-Aalen estimator, as is confirmed by considering the g-functions. When the "constant μ" assumption applies, the g-function for this estimator becomes

$$\frac{\text{Constant}}{P(t)}$$

which defines the Nelson-Aalen estimator.

4.23 The g-estimator with $g(t,\phi) = \frac{1}{P(t)\ \mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi}$

Let us consider the g-function:

$$g(t,\phi) = \frac{1}{P(t)\ \mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi} \tag{4.121}$$

Then, using the category II equation, the g-estimator for ϕ is given by:

$$\int_0^1 \frac{\partial \mu_{x+t}}{\partial \phi}\, dt = \sum_D \left[\frac{1}{P(t_i)\ \mu_{x+t_i}} \frac{\partial \mu_{x+t_i}}{\partial \phi} \right] \tag{4.122}$$

From the mathematical development in Section 4.7, we see that:

$$\int_0^1 \frac{\partial \mu_{x+t}}{\partial \phi}\, dt = \left[\frac{-1}{{}_tp_x}\,\frac{\partial\, {}_tp_x}{\partial \phi}\right]_0^1$$

$$= -\frac{1}{p_x}\,\frac{\partial p_x}{\partial \phi} \tag{4.123}$$

Thus the value of q_x given by this estimator is the value of q_x that satisfies the equation:

$$-\frac{1}{p_x}\,\frac{\partial p_x}{\partial \phi} = \sum_D \left[\frac{1}{P(t_i)\,\mu_{x+t_i}}\,\frac{\partial \mu_{x+t_i}}{\partial \phi}\right] \tag{4.124}$$

or:

$$-\frac{\partial(\log p_x)}{\partial \phi} = \sum_D \left[\frac{1}{P(t_i)}\,\frac{\partial(\log \mu_{x+t_i})}{\partial \phi}\right] \tag{4.125}$$

Let us suppose that the Gompertz Law applies, that is:

$$\mu_{x+t} = B'c^t \tag{4.126}$$

By using equation (4.125), we can successively take $\phi = B'$ and $\phi = c$. Alternatively it appears that we can assume a fixed value for one of the parameters and use the appropriate equation to determine the other parameter, ie the equation in which ϕ is the parameter to be estimated.

This procedure can be seen as analogous to the derivation of maximum likelihood estimators, and of course the g-function involved is the g-function for the maximum likelihood estimator multiplied by the further factor of $\frac{1}{P(t)}$.

Taking $\phi = B'$, the g-function becomes:

$$\frac{1}{B'\,P(t)} \tag{4.127}$$

But B' is constant with respect to t and so this g-function is the same as that applicable for the Nelson-Aalen estimator. This means that equation (4.125) with $\phi = B'$ can be manipulated to provide a value for q_x, and this value will be the Nelson-Aalen estimate.

We can verify this by considering equation (4.125) with $\phi = B'$.

Firstly we will note that the Gompertz Law gives:

$$p_x = h^{c-1} = \exp\left(-B'(c-1)/\log c\right) \tag{4.128}$$

ie
$$\log p_x = -B'(c-1)/\log c \tag{4.129}$$

and also:
$$\log \mu_{x+t} = \log B' + t \log c \tag{4.130}$$

Thus equation (4.125) with $\phi = B'$ gives:

$$\frac{(c-1)}{\log c} = \sum_D \frac{1}{P(t_i)\, B'} \tag{4.131}$$

$$\Rightarrow \quad -\frac{B'(c-1)}{\log c} = -\sum_D \frac{1}{P(t_i)} \tag{4.132}$$

$$\Rightarrow \quad \log p_x = -\sum_D \frac{1}{P(t_i)} \tag{4.133}$$

$$\Rightarrow \quad q_x = 1 - \exp\left[-\sum_D \frac{1}{P(t_i)}\right] \tag{4.134}$$

which is the Nelson-Aalen estimator.

Thus to establish q_x, we do not need to assume a value of c (nor indeed a value of B'). However if we need to estimate the value of either B' or c, we can use the second equation with $\phi = c$ for this purpose.

Now equation (4.125) with $\phi = c$ gives:

$$\frac{B'}{\log c} - \frac{B'(c-1)}{c(\log c)^2} = \sum_D \left[\frac{1}{P(t_i)} \frac{t_i}{c}\right] \tag{4.135}$$

$$\Rightarrow \quad \frac{B'c}{\log c} - \frac{B'(c-1)}{(\log c)^2} = \sum_D \frac{t_i}{P(t_i)} \tag{4.136}$$

$$\Rightarrow \quad \log p_x \left[\frac{1}{\log c} - \frac{c}{c-1}\right] = \sum_D \frac{t_i}{P(t_i)} \tag{4.137}$$

The estimate of q_x can be used to evaluate $\log p_x$ yielding an equation for c.

It will also be noted that, since c is typically in the range 1.05 to 1.10, there may be scope for expanding the functions of c as power series in d, where d = c – 1, and obtaining an easily solved approximate equation for d, and hence c, by ignoring higher powers of d.

If the rectangular hyperbolic mortality distribution is assumed to apply, it is found that the values of a and b, which solve the simultaneous equations formed by taking $\phi = a$ and $\phi = b$ successively in equation (4.125), will combine together to give an estimate of q_x which is again the Nelson-Aalen estimate. It should be noted that, in this case, it is necessary for both equations to be solved to obtain this value of q_x, whereas when we considered the Gompertz Law, only one of the two equations was involved in obtaining the estimate of q_x.

For the rectangular hyperbolic law, we have:

$$\mu_{x+t} = \frac{1}{(a - bt)} \quad \text{and} \quad p_x = (1 - \tfrac{b}{a})^{\frac{1}{b}}$$

or:

$$\log \mu_{x+t} = - \log (a - bt) \tag{4.138}$$

$$\log p_x = \tfrac{1}{b} (\log (a - b) - \log a) \tag{4.139}$$

Now applying equation (4.125) with $\phi = a$ gives:

$$- \tfrac{1}{b} \left[\frac{1}{a - b} - \tfrac{1}{a}\right] = \sum_D \frac{1}{P(t_i)} \frac{- 1}{(a - bt_i)} \tag{4.140}$$

$$\Rightarrow \quad \frac{1}{a (a - b)} = \sum_D \frac{1}{P(t_i)} \frac{1}{(a - bt_i)} \tag{4.141}$$

If a fixed value of b were assumed, the equation could of course be used alone to estimate a.

It is curious to note that this equation is equivalent to:

$$\mu_x * \mu_{x+1} = \sum_D \frac{\mu_{x+t_i}}{P(t_i)} \tag{4.142}$$

Now if we take $\phi = b$ in equation (4.125), we obtain:

$$\frac{1}{b^2} (\log (a - b) - \log a) - \tfrac{1}{b} \left(\frac{- 1}{a - b}\right) = \sum_D \frac{1}{P(t_i)} \frac{t_i}{(a - bt_i)} \tag{4.143}$$

$$\frac{1}{b}(\log(a-b) - \log a) + \frac{1}{a-b} = \sum_D \frac{1}{P(t_i)} \frac{bt_i}{(a-bt_i)} \tag{4.144}$$

Thus equations (4.141) and (4.144) constitute a pair of simultaneous equations that can be solved for a and b. In fact these values of a and b, when used together to calculate q_x, will give the Nelson-Aalen estimate of q_x.

This can be seen by writing equation (4.144) in the form:

$$\log p_x + \frac{a}{a(a-b)} = \sum_D \frac{1}{P(t_i)} \frac{bt_i}{(a-bt_i)} \tag{4.145}$$

and substituting for:

$$\frac{1}{a(a-b)}$$

from equation (4.141) to give:

$$\log p_x + \sum_D \frac{1}{P(t_i)} \frac{a}{(a-bt_i)} = \sum_D \frac{1}{P(t_i)} \frac{bt_i}{(a-bt_i)} \tag{4.146}$$

Equation (4.146) simplifies to:

$$\log p_x = -\sum_D \frac{1}{P(t_i)} \tag{4.147}$$

$$\Rightarrow \qquad q_x = 1 - \exp\left[-\sum_D \frac{1}{P(t_i)}\right] \tag{4.148}$$

which is the Nelson-Aalen estimator.

4.24 The g-estimator with $g(t,\phi) = \frac{1}{P(t)\ {}_tp_x}$

Let us consider the g-function:

$$g(t,\phi) = \frac{1}{P(t)\ {}_tp_x} \tag{4.149}$$

Then, using the category II equation, the g-estimator for ϕ is given by:

$$\int_0^1 \frac{\mu_{x+t}}{{}_tp_x}\,dt = \sum_D \frac{1}{P(t_i)\ {}_{t_i}p_x} \tag{4.150}$$

From the mathematical development in Section 4.6, we can see that:

$$\int_0^1 \frac{\mu_{x+t}}{{}_tp_x}\,dt = \left[\ \frac{1}{{}_tp_x}\ \right]_0^1 = \frac{1}{p_x} - 1 \tag{4.151}$$

Thus the value of q_x given by this estimator is the value of q_x that satisfies the equation:

$$\frac{1}{p_x} - 1 = \sum_D \frac{1}{P(t_i)\ {}_{t_i}p_x} \tag{4.152}$$

$$\Rightarrow \qquad q_x = \frac{\sum_D \frac{1}{P(t_i)\ {}_{t_i}p_x}}{1 + \sum_D \frac{t_i}{P(t_i)\ {}_{t_i}p_x}} \tag{4.153}$$

This expression is deceptive in appearing to give a neat formula for q_x, because it is necessary to assume a mortality law and express the ${}_{t_i}p_x$ items on the right-hand side in terms of q_x.

A development which is algebraically simple occurs if we make the rather unattractive Balducci assumption. When this assumption applies, we have the following relationships:

$${}_tp_x = \frac{1}{1 + t*\mu_x} \quad \text{and} \quad \mu_x = \frac{q_x}{1 - q_x} = \frac{1}{p_x} - 1 \tag{4.154}$$

Therefore when we make the Balducci assumption, equation (4.152) can the be written as:

$$\mu_x = \sum_D \frac{1 + t_i*\mu_x}{P(t_i)} \tag{4.155}$$

$$\Rightarrow \qquad \mu_x = \frac{\sum_D \frac{1}{P(t_i)}}{1 - \sum_D \frac{t_i}{P(t_i)}} \tag{4.156}$$

$$\Rightarrow \qquad q_x = \frac{\sum_D \frac{1}{P(t_i)}}{1 + \sum_D \frac{(1 - t_i)}{P(t_i)}} \tag{4.157}$$

because when the Balducci assumption applies, we have:

$$q_x = \frac{\mu_x}{1 + \mu_x} \tag{4.158}$$

Thus if the Balducci assumption is adopted, a relatively simple expression for q_x, not involving an iterative evaluation, is obtained.

It can also be seen that, when the Balducci assumption applies, this estimator is identical with the estimator for which the g-function is:

$$g(t,\phi) = \frac{1}{P(t)\ \mu_{x+t}} \tag{4.159}$$

4.25 The g-estimator with $g(t,\phi) = \frac{(\mu_{x+t})^r}{P(t)} \frac{\partial \mu_{x+t}}{\partial t}$

Let us consider the g-function:

$$g(t,\phi) = \frac{(\mu_{x+t})^r}{P(t)} \frac{\partial \mu_{x+t}}{\partial t} \tag{4.160}$$

Then, using the category II equation, the g-estimator for ϕ is given by:

$$\int_0^1 (\mu_{x+t})^{r+1} \frac{\partial \mu_{x+t}}{\partial t}\, dt = \sum_D \frac{(\mu_{x+t_i})^r}{P(t_i)} \left[\frac{\partial \mu_{x+t}}{\partial t}\right]_{t=t_i} \tag{4.161}$$

If $r \neq -2$, this gives:

$$\frac{1}{r+2} \left((\mu_{x+1})^{r+2} - (\mu_x)^{r+2}\right) = \sum_D \frac{(\mu_{x+t_i})^r}{P(t_i)} \left[\frac{\partial \mu_{x+t}}{\partial t}\right]_{t=t_i} \tag{4.162}$$

If $r = -2$, equation (4.161) gives:

$$(\log \mu_{x+1} - \log \mu_x) = \sum_D \frac{1}{P(t_i)\ (\mu_{x+t_i})^2} \left[\frac{\partial \mu_{x+t}}{\partial t}\right]_{t=t_i} \tag{4.163}$$

or:

$$\log \frac{\mu_{x+1}}{\mu_x} = \sum_D \frac{1}{P(t_i)\ (\mu_{x+t_i})^2} \left[\frac{\partial \mu_{x+t}}{\partial t}\right]_{t=t_i} \tag{4.164}$$

A number of circumstances can be identified in which this g-estimator is identical with other g-estimators. For example, the estimator is identical with the Nelson-Aalen estimator if r = -1 when the Gompertz Law applies with any assumed value of c except 1, or if r = -2 when the rectangular hyperbolic distribution applies with any assumed value of b except 0.

4.26 Some further estimators and other topics

We will continue this chapter with a discussion of "n-estimators" which were developed by the author as an embryonic form of the g-estimator and a discussion of a weighted least squares estimator which the author developed very much as an intellectual exercise, having noted the very wide range of estimators that were possible.

Then Section 4.29 will consider the use of the Dirac delta function in a modified derivation of the general theory, and Section 4.30 will briefly discuss the application of the general theory when a multiple-parameter mortality law is assumed to apply.

Finally, Section 4.31 examines an approach which is presented by Slawski (1991) as "equivalent to the conventional approach".

4.27 n-estimators

The simulation programs were developed before the general theory had been evolved into its full form.

Included in the simulations were an embryonic form of the g-estimators in which the g-functions were limited to functions of the form:

$$(\mu_{x+t})^n \qquad \text{for any value of n.}$$

These estimators were named n-estimators in reference to the arbitrary power n.

The n-estimators were given especial attention because it had been noted that, when the rectangular hyperbolic mortality distribution with an assumed value of b applies, a number of important estimators are obtained for particular values of n. It was subsequently realised that the g-function could be generalised so that virtually any estimator assuming a parametric mortality law could be produced.

The following n-estimators are of particular interest:

$\underline{n = -1}$

For any one-parameter mortality law, the n-estimator with $n = -1$ is the time-count estimator.

$\underline{n = 0}$

For any one-parameter mortality law, the n-estimator with $n = 0$ is the log-estimator, and for the Gompertz Law, it is also the maximum likelihood estimator of B'.

$\underline{n = 1}$

For the rectangular hyperbolic distribution, the n-estimator with $n = 1$ is the maximum likelihood estimator of a.

$\underline{n = \frac{1}{b}}$

When the rectangular hyperbolic distribution with a given value of b applies, the n-estimator with $n = 1/b$ is the conventional estimator.

All of these estimators were calculated in the simulations and, in addition, n-estimators for the rectangular hyperbolic distribution (incorporating a given value of b) with $n = -2$, $n = 2$ and $n = 3$ were also calculated.

It will be noted that, when the "constant μ" law applies, the n-estimators for all finite values of n are identical and give the familiar maximum likelihood estimator based on the central exposed-to-risk.

It will also be noted however that the n-estimator corresponding to the conventional estimator, when the rectangular hyperbolic law applies, has $n = 1/b$ for $b \neq 0$. As the mortality law approaches the "constant μ" position, $n \to \infty$ and the conventional estimator approaches a value which is different from that taken by the n-estimator for finite n when the "constant μ" law applies.

The fact that all n-estimators for finite n coincide, if "constant μ" mortality is assumed, implies that, if μ_{x+t} is assumed to vary only very slightly over the range $(0 \leq t \leq 1)$, n-estimators with $n = -1$, 0 or 1 are likely to give very similar results, regardless of how the data fluctuates, because we are close to the "constant μ" situation. As we have seen,

these values of n include the time-count estimators, the log-estimators and the maximum likelihood estimators for a in the rectangular hyperbolic distribution and B' in the Gompertz distribution. It does not necessarily include the conventional estimator nor its close relatives the implication-B estimator and the ethereal method of moments estimator.

4.28 A weighted least squares estimator

The author was encouraged that estimators based on so many different criteria could be identified and fitted into the g-estimator framework of the general theory and become intrigued by the possibility of an estimator based on the least squares principle, a principle not previously employed in the context of the year of age mortality scenario under investigation.

A weighted least squares estimator applicable in this scenario was developed and this will now be described.

Let us consider the observations over a year of age from age x to age x+1, where P(t) is the number of lives observed as alive at exact age x+t during the investigation. Let us consider the year of age as split into a series of time elements each of length δt. Let $D(t,\delta t)$ denote the number of deaths observed to occur in the element δt at age x+t.

Let us consider the weighted sum of squares:

$$Q = \sum_{t=0}^{t=1^*} \left(\frac{h(t)}{\delta t}\right) \left(D(t,\delta t) - P(t)\, \mu_{x+t}\, \delta t\right)^2 \qquad (4.165)$$

where:

$$\left(D(t,\delta t) - P(t)\, \mu_{x+t}\, \delta t\right)^2$$

is the square of the difference between the observed deaths and the expected deaths in the element δt at age x+t, considered in isolation, and:

$$\frac{h(t)}{\delta t}$$

is the weighting applied to the squared difference for the element δt at age x+t, where h(t) can be a function of t but is not a function of ϕ,

and where the symbol:

$$\sum_{t=0}^{t=1^*}$$

denotes summation over all elements in the year of age.

Thus, multiplying out the squared item, we have:

$$Q = \sum_{t=0}^{t=1}{}^{*} \left(\frac{h(t)}{\delta t}\right) (D(t,\delta t))^2 - 2 \sum_{t=0}^{t=1}{}^{*} h(t)\, D(t,\delta t)\, P(t)\, \mu_{x+t} + \sum_{t=0}^{t=1}{}^{*} h(t)\, (P(t))^2\, (\mu_{x+t})^2\, \delta t \tag{4.166}$$

Now, we can make δt as small as we like, and as δt decreases, the first term in Q becomes increasingly large, the second term is unaffected and the third term approaches an integral.

We are interested in minimising Q with respect to the mortality parameter ϕ. If we differentiate Q with respect to ϕ, we see that, however small δt is and however large the first term in Q is, the differential coefficient of the first term is zero, since the term is not a function of ϕ, while the second and third terms give:

$$\frac{\partial Q}{\partial \phi} = -2 \sum_{t=0}^{t=1}{}^{*} h(t)\, D(t,\delta t)\, P(t)\, \frac{\partial \mu_{x+t}}{\partial \phi} + 2 \sum_{t=0}^{t=1}{}^{*} h(t)\, (P(t))^2\, \mu_{x+t}\, \frac{\partial \mu_{x+t}}{\partial \phi}\, \delta t \tag{4.167}$$

It seems legitimate to regard the limit as $\delta t \to 0$, of the differential coefficient of the first term in Q, also as zero, since this differential coefficient took the value zero for all $\delta t > 0$, however small.

If then, in the expression for $\frac{\partial Q}{\partial \phi}$, we let $\delta t \to 0$, we obtain:

$$\frac{\partial Q}{\partial \phi} = -2 \sum_{D} h(t_i)\, P(t_i)\, \frac{\partial \mu_{x+t_i}}{\partial \phi} + 2 \int_0^1 h(t)\, (P(t))^2\, \mu_{x+t}\, \frac{\partial \mu_{x+t}}{\partial \phi}\, dt \tag{4.168}$$

where, in the first of the terms in $\frac{\partial Q}{\partial \phi}$ shown above, the summation is taken over the individual deaths and t_i denotes the duration at death.

It will be noted that as $\delta t \to 0$, the weighting $h(t)/\delta t$, applied to the squared quantity for an element, approaches infinity.

This is not viewed as any difficulty, since it is the result that we achieve in the limit for $\frac{\partial Q}{\partial \phi}$ that is of relevance.

Equating $\frac{\partial Q}{\partial \phi}$ to zero gives:

$$\int_0^1 h(t)\,(P(t))^2\,\mu_{x+t}\,\frac{\partial \mu_{x+t}}{\partial \phi}\,dt = \sum_D h(t_i)\,P(t_i)\,\frac{\partial \mu_{x+t_i}}{\partial \phi} \tag{4.169}$$

This relationship can also be expressed as

$$\sum_N \int_{s_i}^{t_i} h(t)\,P(t)\,\mu_{x+t}\,\frac{\partial \mu_{x+t}}{\partial \phi}\,dt = \sum_D h(t_i)\,P(t_i)\,\frac{\partial \mu_{x+t_i}}{\partial \phi} \tag{4.170}$$

By introducing a mortality law of the form:

$$\mu_{x+t} = f(t,\phi) \tag{4.171}$$

either relationship can in principle be used to obtain an equation which may be solved to give a weighted least squares estimator of ϕ. A practical difficulty may arise in choosing a function h(t) which represents a sensible weighting function whilst allowing a convenient algebraic development.

It is interesting to compare equation (4.169) with the equation for a category II g-estimator obtained from the general theory, namely:

$$\int_0^1 P(t)\,\mu_{x+t}\,g(t,\phi)\,dt = \sum_D g(t_i,\phi) \tag{4.172}$$

It will be seen that the equations for the g-estimator and the least squares estimator are the same when:

$$g(t,\phi) = h(t)\,P(t)\,\frac{\partial \mu_{x+t}}{\partial \phi} \tag{4.173}$$

where it will be remembered that h(t) is part of the weighting function in the weighted squares expression and can be a function of t, but not of ϕ. The g-function $g(t,\phi)$ may be function of both t and ϕ.

Thus the weighted least squares estimator fits into the g-estimator framework of the general theory, and is obtained when the g-function is:

$$g(t,\phi) = h(t)\,P(t)\,\frac{\partial \mu_{x+t}}{\partial \phi}$$

The estimator was developed at a late stage in the research and consequently it was not included in any form in the simulations.

4.29 Use of the Dirac delta function

In developing the equation which defines the general g-estimator, and also in developing the equation which defines the weighted least squares estimator, it was necessary to reconcile expressions involving expected deaths, based on the density of a continuous variable, with expressions involving actual deaths based on discrete observations of observed deaths. In the event, it was possible to achieve this even in the limit as the length of the time elements approaches zero, and no special methodology was explicitly introduced.

It is interesting to note however that the Dirac delta function, originally developed by PAM Dirac in the context of quantum mechanics, and also used in engineering applications, can also be employed in an alternative presentation of the derivation of these equations.

The properties of the Dirac delta function are well discussed in many textbooks, and the author has found a number of textbooks helpful, notably the classic text by Dirac (1930) and texts by Miller (1956) and Dicke and Wittke (1960).

It is sufficient for our purpose to note that the Dirac delta function $\delta(t)$ is defined by the relationships

$$\int_{-\infty}^{\infty} \delta(t)\, dt = 1 \tag{4.174}$$

and

$$\delta(t) = 0 \qquad \text{if } t \neq 0 \tag{4.175}$$

We will also note the following results:

$$\int_{-\infty}^{\infty} f(t)\, \delta(t)\, dt = f(0) \tag{4.176}$$

$$\int_{-\infty}^{\infty} \delta(t - t')\, dt = 1 \tag{4.177}$$

$$\delta(t - t') = 0 \qquad \text{if } t \neq t' \tag{4.178}$$

$$\int_{-\infty}^{\infty} f(t)\, \delta(t - t')\, dt = f(t') \tag{4.179}$$

Now when we refer to the deaths observed in an element δt at age x+t, let us write them, not as previously:

$$D(t,\delta t) \tag{4.180}$$

but now instead as:

$$P(t)\ \mu'_{x+t}\ \delta t \tag{4.181}$$

where μ'_{x+t} is the observed mortality density defined by:

$$P(t)\ \mu'_{x+t} = \sum_{D} \delta(t - t_i) \tag{4.182}$$

where $x+t_i$ is the age at death of the i^{th} life.

Then the total number of observed deaths over the year of age is given by:

$$\int_0^1 P(t)\ \mu'_{x+t}\ dt = \sum_{D} \int_0^1 \delta(t - t_i)\ dt \tag{4.183}$$

Now since $\delta(t - t_i) = 0$ for all $t \neq t_i$ and $0 < t_i \leq 1$, we have:

$$\int_0^1 \delta(t - t_i)\ dt = \int_{-\infty}^{\infty} \delta(t - t_i)\ dt = 1 \tag{4.184}$$

The total number of observed deaths is:

$$\int_0^1 P(t)\ \mu'_{x+t}\ dt = \sum_{D} 1 = D \tag{4.185}$$

which is correct.

In our development of the category I and category II equations defining the g-estimator, we previously had (in equation (4.4)) the term:

$$\sum_{t=0}^{t=1^*} D(t,\delta t)\ g(t,\phi) \tag{4.186}$$

representing the weighted sum of actual deaths over the elements of the year of age.

In the alternative presentation, this would be written as:

$$\sum_{t=0}^{t=1^*} P(t)\ \mu'_{x+t}\ g(t,\phi)\ \delta t = \sum_{t=0}^{t=1^*} g(t,\phi) \sum_{D} \delta(t - t_i)\ \delta t$$

$$= \sum_{D} \sum_{t=0}^{t=1^*} g(t,\phi)\ \delta(t - t_i)\ \delta t \qquad (4.187)$$

As $\delta t \rightarrow 0$, this becomes:

$$\sum_{D} \int_0^1 g(t,\phi)\ \delta(t - t_i)\ dt \qquad (4.188)$$

which, remembering that $\delta(t - t_i) = 0$ for all $t \neq t_i$ (with here $0 < t_i \leq 1$) and applying the well-established property of the Dirac delta function expressed by equation (4.179), gives:

$$\sum_{D} g(t_i,\phi) \qquad (4.189)$$

thus leading to the same result as before (as in equations (4.8) and (4.9)).

Similarly in the derivation of the weighted least squares estimator, the following item in the expression for $\frac{\partial Q}{\partial \phi}$ when $\delta t > 0$ (equation (4.167)):

$$-\ 2 \sum_{t=0}^{t=1^*} h(t)\ D(t,\delta t)\ P(t)\ \frac{\partial \mu_{x+t}}{\partial \phi} \qquad (4.190)$$

would alternatively be written as:

$$-\ 2 \sum_{t=0}^{t=1^*} h(t)\ P(t)\ \frac{\partial \mu_{x+t}}{\partial \phi}\ (P(t)\ \mu'_{x+t}\ \delta t)$$

$$= -\ 2 \sum_{t=0}^{t=1^*} h(t)\ P(t)\ \frac{\partial \mu_{x+t}}{\partial \phi} \sum_{D} \delta(t - t_i)\ \delta t$$

$$= -\ 2 \sum_{D} \sum_{t=0}^{t=1^*} h(t)\ P(t)\ \frac{\partial \mu_{x+t}}{\partial \phi}\ \delta(t - t_i)\ \delta t \qquad (4.191)$$

As $\delta t \rightarrow 0$, this becomes:

$$-2 \sum_{D} \int_{0}^{1} h(t)\, P(t)\, \frac{\partial \mu_{x+t}}{\partial \phi}\, \delta(t - t_i)\, dt \tag{4.192}$$

which again, remembering that $\delta(t - t_i) = 0$ for all $t \neq t_i$ (with here $0 < t_i \leq 1$) and applying the well-established property of the Dirac delta function expressed by equation (4.179), gives:

$$-2 \sum_{D} h(t_i)\, P(t_i)\, \frac{\partial \mu_{x+t_i}}{\partial \phi} \tag{4.193}$$

thus leading to the same result as before (as in equation (4.168)).

4.30 Application of the general theory when a multiple-parameter mortality law is assumed to apply

In developing and discussing the general theory, attention has been given predominantly to its application where a mortality law applies which involves one mortality parameter, ie a law of the form:

$$\mu_{x+t} = f(t,\phi) \tag{4.194}$$

However, in discussing the maximum likelihood estimator (Section 4.7), we did consider mortality laws which involved n mortality parameters ($n > 1$), ie laws of the form:

$$\mu_{x+t} = f(t,\phi_1,\phi_2,.....\phi_n) \tag{4.195}$$

and obtained the familiar simultaneous equations for the parameters, normally obtained by equating the partial differential coefficients of the likelihood to zero, by the use of g-functions. Each g-function gives arise to one of the equations. The equation conventionally given by considering the partial differential coefficient of the likelihood with respect to the mortality parameter ϕ' is obtained using the g-function given by:

$$g(t,\phi') = \frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi'} \tag{4.196}$$

This application of the general theory in the context of a multiple-parameter mortality law, when maximum likelihood estimators are used, illustrates how the general theory may be applied in the context of a multiple-parameter law using g-functions chosen more generally.

So, for example, if we have a mortality law which involves two parameters ϕ_1 and ϕ_2, we can adopt two g-functions $g_1(t,\phi_1,\phi_2)$ and $g_2(t,\phi_1,\phi_2)$ and form the simultaneous equations (if using Category I equations):

$$\sum_{N} \int_{s_i}^{t_i} \mu_{x+t}\, g_1(t,\phi_1,\phi_2)\, dt = \sum_{D} g_1(t_i,\phi_1,\phi_2) \tag{4.197}$$

$$\sum_{N} \int_{s_i}^{t_i} \mu_{x+t}\, g_2(t,\phi_1,\phi_2)\, dt = \sum_{D} g_2(t_i,\phi_1,\phi_2) \tag{4.198}$$

Thus for the maximum likelihood approach, we saw that:

$$g_1(t,\phi_1,\phi_2) = \frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi_1} \tag{4.199}$$

and

$$g_2(t,\phi_1,\phi_2) = \frac{1}{\mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi_2} \tag{4.200}$$

More generally we could choose other g-functions than those adopted in the maximum likelihood approach and obtain other simultaneous equations for the mortality parameters.

Obviously we might obtain two simultaneous equations that are very similar, so that the solution for the two unknowns is very unstable in that a minor fluctuation in the observations might cause a big fluctuation in the values of ϕ_1 and ϕ_2 obtained. However it might possibly be the case that the value of q_x calculated from the solutions for ϕ_1 and ϕ_2 might be more stable.

A phenomenon of this type appeared possibly to occur in the simulations involving the two-parameter maximum likelihood estimators, where values of q_x, calculated during single runs of simulation studies, seemed more stable than the related pairs of values (B', c) or (a, b).

It is also interesting to recall that, in Section 4.23, we considered the Category II g-function:

$$g(t,\phi) = \frac{1}{P(t)\, \mu_{x+t}} \frac{\partial \mu_{x+t}}{\partial \phi} \tag{4.201}$$

which has obvious structural similarities to the maximum likelihood Category I g-function given by equation (4.196), and its application when the two-parameter Gompertz and rectangular hyperbolic mortality distributions apply. Among other things, we solved the simultaneous equations (4.141) and (4.144) corresponding to $\phi = a$ and $\phi = b$ to obtain an expression for q_x when the rectangular hyperbolic mortality distribution was assumed.

It should be emphasized that, apart from the use of the maximum likelihood criterion to estimate the parameters of the Gompertz law and the rectangular hyperbolic law, and the discussion of the g-function given by equation (4.201) in Section 4.23, no further attention has been given to the use of the general theory when multiple-parameter mortality laws apply.

Clearly this is a possible area for further research.

4.31 Comments on the alternative "conventional" approach of Slawski (1991)

When research work for this thesis was nearly complete, the author received a copy of a Master of Business Science dissertation by Slawski (1991) in which several issues addressed in this thesis had also been considered, for example, as we have seen, the comments by Hoem (1984) concerning the conventional estimator and his approximated "operational moment relations" (Sections 1.9 and 1.10) and the question of bias in estimators of q_x (Section 4.15).

Also, an approach to estimating q_x is given in Slawski (1991) which is interpreted as an alternative version of the conventional estimation of q_x, but which in fact leads, not to the conventional estimator, but to the log-estimator. This arises because Slawski gives two equivalent expressions for the expected number of deaths, both involving expectations, which if equated to actual deaths will define the method of moments estimator, namely:

$$E[\theta_x] = \sum_N {}_{1-s_i}q_{x+s_i} - E\left[\sum_W {}_{1-t_i}q_{x+t_i}\right] \tag{4.202}$$

$$E[\theta_x] = E\left[\sum_N \int_{s_i}^{t_i} \mu_{x+t}\, dt\right] \tag{4.203}$$

and then makes approximations by substituting suitable expressions to eliminate the expectations on the right-hand sides, giving in the case of equation (4.202) the estimator that is described in this thesis as the conventional estimator and in the case of equation (4.203) the estimator that is described in this thesis as the log-estimator. In the case of the conventional estimator, Slawski's derivation from equation (4.202) is the same in general principle as the derivation of the Balducci conventional estimator given by Broffitt and Klugman (1983).

The modifications introduced by Slawski have produced two estimators operating according to different statistical criteria, but Slawski appears to regard them as simply two versions of

one approach, which she describes as the "conventional approach".

Thus Slawski claims that the "conventional estimator of μ" is the same as the maximum likelihood estimator of μ when the "constant μ" assumption applies. In fact she is referring to her derivation that yields the log-estimator and not the conventional estimator, and this result is in fact the same as one reported in Section 4.8 of this thesis. The conventional estimator, as defined in this thesis and as determined in Slawski's first approach using equation (4.202), is different to the maximum likelihood estimator when the "constant μ" mortality assumption is made.

As has been observed in Section 1.13, Slawski also obtains two simultaneous equations for the maximum likelihood estimators of the parameters B and c, when the Gompertz law $\mu_x = Bc^x$ applies, by differentiating the log-likelihood.

The equation obtained by differentiating the log-likelihood with respect to B is of course the equation that gives the maximum likelihood estimator of B when c is fixed.

In fact the maximum likelihood estimator for B when c is fixed is the same as the log-estimator for B. This is noted in Section 4.8 of this thesis in respect of B', where $B = B' * c^x$, and the result in respect of B' applies also to B, given that c is held constant and x is fixed, being the age at the beginning of the year of age, so that $B = B' *$ constant.

Given that the maximum likelihood estimator for B coincides with the log-estimator for B, it is not surprising that Slawski interprets the equation obtained by differentiating the log-likelihood with respect to B as representing a version of the conventional estimation of B when the value of c is assumed, and goes on to say therefore that "the maximum likelihood estimators [of B and c] are one possible pair of solutions from the set of solutions satisfying the conventional approach". Obviously this is not true if the "conventional approach" is as defined in this thesis and as derived by Slawski from equation (4.202).

CHAPTER V

The Simulations

5.1 Introduction

As the author developed the ideas discussed in this thesis, he naturally became concerned whether the ideas were soundly based. Therefore a computer program was developed which would generate simulated bodies of mortality data from known mortality laws, subject to known mortality parameters, so that the various mortality estimators could be calculated and their values compared with each other and with the known population values underlying the simulated mortality experience.

A particular early motivation was increasing disagreement with the position argued for by Hoem (1984), that the conventional estimator was flawed, and the apparent suggestion that the approximated "operational moment relations" estimator developed in Hoem (1984) represented an improvement on the conventional estimator.

The original simulation program written by the author was relatively unsophisticated in structure and was written in BBC Basic to run on a BBC Master computer. However, the speed of computation when iterative calculations were involved proved simply too slow to allow simulations of adequate size and number to be contemplated. Nevertheless the results that were obtained appeared supportive of the theoretical developments reported in this thesis and encouraged the author to invest considerable time and effort to develop a more sophisticated program on more capable equipment.

The author in fact developed four new programs, each a variant of the same underlying model. The programs were written in Fortran to run on a Personal Computer employing a 80286 processor, and with the benefit of a mathematics co-processor. The speed of computation was spectacularly increased although, with the subsequent availability of machines employing 80386 and 80486 processors, the simulations reported in this thesis employ a more modest number of repetitions than would be possible with the equipment now readily available.

Obviously, the simulation programs provided a very useful test-bed for comparing the results given by different mortality estimators and became particularly valuable as new estimators such as the "time-count" estimator were developed, and as other estimators were

extended, in particular the maximum likelihood estimator when two parameters are estimated from the data.

5.2 The general model underlying the simulation programs

The model deals with a single year of age. A tranche of n_1 lives is regarded as starting at duration $t = 0$ in the year of age, and a further tranche of n_2 lives is regarded as entering at the beginning of a chosen month of the year of age, when duration equals r months, where all months are regarded as being one-twelfth of a year in length. Withdrawals are regarded as taking place at the end of every month of the year of age.

Lives can die of course at any time and the model allows the assumption of either the rectangular hyperbolic mortality law or the Gompertz mortality law as the mortality law governing the population. The parameters of either law can be assigned any values that the experimenter wishes to consider. Thus for example the "level deaths" and Balducci assumptions can be used, as particular cases of the rectangular hyperbolic law, and the "constant μ" assumption can be used as a particular case of either the Gompertz or rectangular hyperbolic law. Deaths are generated at random using a pseudo-random number generator, whilst ensuring that their probability of occurrence conforms to the chosen mortality law.

The programs allow the distribution of withdrawals to be specified in several ways. The primary option is to specify the annual withdrawal rate w_x and to allow the program to calculate and apply the equivalent monthly withdrawal rate on the assumption that the underlying population rate of withdrawal applicable at the end of each month is constant. However the option is also provided for the experimenter to specify individually the equivalent annual underlying population rates of withdrawal applicable at the end of each month of the year of age (eleven such values, as the withdrawals occurring at the end of the last month are irrelevant for the purpose of calculating the mortality rate). Withdrawals are generated at random using a pseudo-random number generator, whilst ensuring that their probability of occurrence conforms to the chosen withdrawal distribution.

Further options for specifying withdrawals are also available in two variants of the model, to be discussed shortly.

5.3 Comments on the general model underlying the simulation programs

The model provides for withdrawals occurring at the end of each month, rather than

occurring continuously. This design was adopted for the practical purpose of simplifying the programming. The main purpose of the programs is to compare different estimators and it was felt that this design was more than adequate to test how the different estimators performed in the presence of withdrawals.

With regard to new entrants, the model allows for one tranche of new entrants to enter "en bloc" at the beginning of a month. This is of course a rather restricted new entrant model, but it is believed to be more than sufficient to allow the performance of different estimators to be compared in the presence of new entrants. Again a simplified model was adopted in order to simplify the programming.

The benefits of adopting these simple models in respect of the withdrawals and new entrants arises at two stages in the programs: firstly when the simulated data is generated, and secondly when the values of the mortality estimators are calculated. As well as the benefits at the programming stage, the speed of operation of the program may also be assisted.

Another benefit of the relatively straight-forward model was that further structure was able to be incorporated fairly easily into the model. Also the relatively simple structure of the models assisted in the testing of the programs and the tracing of programming errors, which was undertaken very assiduously.

However, even with these simple models, the programming to produce the simulated data and to calculate estimators was not without its complexities; the full development of the programs took many weeks, and was only possible because the author had been granted sabbatical leave.

The four variants of the simulation program are denoted by the names ASP, ASPSIM, ASPMOM and ASPMMSIM. These will now be briefly introduced.

5.4 Program ASP

The first variant of the Fortran program, denoted by the name "ASP", produces a single set of simulated data as described above and calculates the values of a variety of mortality estimators based on the simulated data.

5.5 Program ASPSIM

The second variant of the Fortran program, denoted by the name "ASPSIM", essentially

allows the programming of ASP to be run a specified number of times and the average value of each estimator based on all the runs in a simulation study to be calculated, together with an estimate of the standard deviation of a single observed value of each estimator, and lower and upper confidence limits for the population value of the mortality rate q_x, based on each estimator.

The confidence limits are set at distances of two standard deviations of the average observed value of the estimator concerned, above and below the observed average value of the estimator. Therefore, given the large number of runs used in each simulation study, namely 500, and bearing in mind the Central Limit Theorem (as discussed for example in Larson 1982), the distribution of the average observed value of an estimator can be taken as virtually normal, and the lower and upper confidence limits produced by the program can be taken as defining 95% confidence intervals for the population value of q_x.

The standard deviation of a single observed value, q'_x say, of an estimator is determined as the square root of the variance of q'_x estimated using the following formula:

$$\text{variance of } q'_x = \frac{1}{m-1}\left[\frac{1}{m}\sum_{r=1}^{r=m} ({}^{r}q'_x)^2 - \left(\frac{1}{m}\sum_{r=1}^{r=m} {}^{r}q'_x \right)^2 \right] \qquad (5.1)$$

where m is the number of runs made in a simulation study and ${}^{r}q'_x$ is the value of the estimator observed in the r^{th} run of the simulation. It will be noted that the estimate of the population value of the estimator obtained from the data is used in estimating the variance and not the true value, which is known from the parameters of the simulation. It was felt appropriate to use the estimated figure, so that, if the estimator were biased, we would be estimating the standard deviation of the biased estimate.

5.6 Program ASPMOM

The third variant of the Fortran program, denoted by the name "ASPMOM", produces a single set of simulated data similarly to the program ASP, but from a modified simulation model.

The program **ASPMOM** operates by firstly obtaining values of m(t) and mr(t), the number of lives entering respectively at durations 0 and r months, who will withdraw at duration t months (t = 1, 2, 3, ... 11) if they do not die first, and the values of m(12) and mr(12) representing all the lives who will reach the end of the year of age if they do not die first.

The primary option for creating the values of m(t) and mr(t) is to specify an annual withdrawal rate, together with the values of n_1 and n_2, and then to randomly generate the values of m(t) and mr(t) for each month as withdrawals occurring at the end of each month in the presence of a zero force of mortality, assuming that the underlying population rate of withdrawal per month is constant, with m(12) and mr(12) being the numbers of lives reaching the end of the year of age.

Alternatively, the values of all the m(t) and mr(t) may be directly specified by the experimenter, in which case the values of n_1 and n_2 are automatically determined as the sums of the m(t) and mr(t) respectively.

These are the further options for specifying withdrawals briefly alluded to previously.

Having established the values of m(t) and mr(t), the program ASPMOM follows each set of m(t) and mr(t) lives through to duration t, ie the date on which they are predestined to exit if they do not die first, and generates deaths randomly from them according to the chosen mortality law.

The purpose of ASPMOM is to generate mortality data in which each individual life is predestined to exit at a known date if he does not die first. The purpose of creating such data was to allow the method of moments estimator to be calculated, since the expected number of deaths, as "expected" in the statistical sense, can be calculated if the date on which lives are predestined to exit, if they do not die first, is known. Such information can be made available for simulated lives, despite being seldom available for real lives. As the program was intended to facilitate calculation of the "method of moments" estimator, it was denoted by the name ASPMOM.

The program ASPMOM enables the performance of all the estimators discussed in Hoem (1984) to be compared, and in particular allows a comparison to be made between the "method of moments" estimator and the conventional estimator which, in Hoem (1984), appeared to be viewed as a poor replacement for the "method of moments" estimator, the latter being impossible to calculate in practice with normal data.

As has already been intimated, the simulations appear to show that there is a very close similarity between the values given by the conventional estimator and the "method of moments" estimator, both estimators appearing to give sound estimates of the population mortality rate; the simulations also appear to confirm this author's suspicions that values of q_x given by the approximated "operational moment relations" estimator will have a negative bias.

5.7 Program ASPMMSIM

The fourth variant of the Fortran program, denoted by the name "ASPMMSIM", essentially allows the programming of ASPMOM to be run a specified number of times and the average value of each estimator based on all the runs in a simulation study to be calculated, together with an estimate of the standard deviation of a single calculation of each estimator, and lower and upper confidence limits defining 95% confidence intervals for the population value of the mortality rate q_x, based on each estimator.

5.8 Determination of the simulated deaths and withdrawals

It may be of interest to briefly describe the procedure by which the simulated deaths and withdrawals are determined. This brief description is made with reference to program **ASP**, but the same principles are used for the other programs.

Let us consider the lives entering at duration 0. For these we construct a double decrement table showing, for a radix of 999999.99 lives, the number of lives surviving mortality in month 1, then the number of lives surviving after the withdrawals at the end of month 1, then the number of lives surviving mortality in month 2, then the number of lives surviving after the withdrawals at the end of month 2 and so on through the year of age, culminating with the number of lives surviving at the end of the year of age after all deaths and withdrawals. The double decrement table is obviously constructed using the chosen mortality law and withdrawal distribution.

Then, in turn for each simulated life in the tranche, a pseudo-random number, taken from a uniform distribution between 0 and 1, is generated and multiplied by 999999.99. The resulting "life identity number" is then compared with the numbers of lives calculated in the double decrement table as surviving at each stage and is used to identity the life's position in the sequence of exits from the population, and hence to identify the monthly group of deaths or withdrawals, if any, to which the life belongs. If the life identity number is less than the number of lives surviving the year in the double decrement table, the life is regarded as completing the year.

In order to evaluate some of the estimators, it is also necessary to know the durations at which deaths occur, and therefore, for the simulated lives identified as exiting by death, the "life identity number" is used in conjunction with the chosen mortality law and the double decrement table to calculate the precise duration within the month at which the life dies, and hence the duration from the beginning of the year of age at which death occurs, which is the information needed for the estimators concerned.

This procedure is also used, after appropriate modification, to determine the simulated deaths and withdrawals in respect of the tranche of new entrants entering at duration r months.

The pseudo-random numbers are obtained using the routines G05CCF and G05CAF from the NAG Fortran Workstation Library.

To assist the testing of the programs during development, all the programs include the option of using a set of uniformly distributed numbers in place of the pseudo-random numbers. This provides a representative and repeatable sample of deaths and withdrawals.

5.9 Years of age with only partial exposure

It will be noted that, by taking n_1 as equal to zero, it is possible to study the derivation of mortality rates from a year of age in which mortality experience is only available after a specifed duration, r months, up to the end of the year of age.

Further, by also using the option available in programs **ASPMOM** and **ASPMMSIM** of specifying the durations at which surviving lives definitely withdraw, it is possible to study the derivation of mortality rates from a year of age in which mortality experience is only available between two specifed durations within that year of age.

Such studies have not yet been undertaken.

5.10 The estimators calculated in Programs ASP and ASPSIM

In the programs **ASP** and **ASPSIM**, the values of 41 different estimators are given in the output, although only 34 separate calculations are required, because of duplications.

For those estimators which require a mortality assumption to be made, five different assumptions are generally used, namely:

(a) the rectangular hyperbolic distribution with b = 2

(b) the rectangular hyperbolic distribution with b = 1 (ie the "level deaths" assumption)

(c) the rectangular hyperbolic distribution with b = 0 (ie the "constant μ" assumption)

(d) the rectangular hyperbolic distribution with b = -1 (ie the Balducci assumption)

(e) the Gompertz distribution with c = 1.1

Thus values of the conventional, implication-B, time-count and maximum likelihood estimators are calculated for all five of these assumptions. Four n-estimators, for values of n equal to -2, 0 (the log-estimator), 2 and 3, are calculated for the first four of these assumptions, ie excluding the Gompertz assumption.

The programs also calculate the approximated "operational moment relations" estimators for the "level deaths" and "Balducci" assumptions using the formulae given by Hoem (1984), and quoted in Section 1.9 of this thesis (equations (1.40) and (1.41)).

Finally, the programs calculate the product limit estimator (so long as the simulations cover the entire year of age) and two maximum likelihood estimators of q_x, assuming respectively the rectangular hyperbolic and Gompertz mortality distributions, but with the values of b or c also being estimated from the data by the method of maximum likelihood.

Thus, in the latter two cases, the data largely "chooses" the mortality assumption used in the calculation of the estimator. Along with the average for all the runs of the estimated values of q_x, the output also presents the averages of the estimated values of the mortality parameters b and c, and ASPSIM also gives estimates of the standard deviations of single calculations of b and c, and of 95% confidence limits for the population values of b and c.

In addition to the values presented in ASPSIM of the average observed q_x (Table I of the output), the estimated standard deviations (Table II of the output) and the estimated lower and upper confidence limits (Tables III and IV of the output), ASPSIM also gives, in Table V, the difference of the average observed value of each estimator from the average observed value of the two-parameter maximum likelihood estimator for the general mortality law, ie rectangular hyperbolic or Gompertz, assumed for the population in generating the simulated data.

The purpose of this was to give a strong visual impression of the degree to which the two-parameter maximum likelihood estimator concerned had agreed in its average value with the estimators in which the correct mortality distribution parameter had been assumed.

The program ASP also contains the facility, after the standard results have been produced, to request the calculation of further estimators using the same body of simulated mortality and withdrawal data but with different mortality assumptions being made in estimators, ie different values of b and c assumed, and in the case of n-estimators, with different values of n. In addition, ASP gives the facility to display the numbers of deaths and withdrawals in each month in the simulated data.

5.11 The estimators calculated in Programs ASPMOM and ASPMMSIM

In the programs **ASPMOM** and **ASPMMSIM**, the values of 25 different estimators are given in the output, although only 22 separate calculations are required, because of duplications.

For those estimators which require a mortality assumption to be made, four different assumptions are generally used, namely:

(a) the rectangular hyperbolic distribution with b = 1 (ie the "level deaths" assumption)
(b) the rectangular hyperbolic distribution with b = 0 (ie the "constant μ" assumption)
(c) the rectangular hyperbolic distribution with b = -1 (ie the Balducci assumption)
(d) the Gompertz distribution with c = 1.1

Thus values of the method of moments, conventional, implication-B, time-count and maximum likelihood estimators are calculated for all four of these assumptions.

The "method of moments" estimator is calculated using the formulae given by Hoem (1984), when the "level deaths" and Balducci assumptions apply (equations (1.36) and (1.37) in this thesis) and by the following corresponding equation for the "constant μ" assumption:

$$\sum_{N} (1 - (1 - q_x)^{\tau_i - s_i}) = D \qquad (5.2)$$

Again the programs also calculate the approximated "operational moment relations" estimators for the "level deaths" and Balducci assumptions using the formulae given by Hoem (1984) (equations (1.40) and (1.41) in this thesis), the product limit estimator (if calculable) and the two maximum likelihood estimators of q_x involving the estimation of the distribution parameter b or c from the data.

For each estimator, the output of **ASPMOM** gives the same details as **ASP**, and similarly **ASPMMSIM** gives the same details as **ASPSIM**. Also **ASPMOM** gives the same options for further information as **ASP**.

5.12 Iterative derivations of estimator values

The values of many of the estimators are of necessity obtained from the defining equations using an iterative approach. The iterative solution of equations is achieved by the use of routine C05ADF from the NAG Fortran Workstation Library. This routine locates a zero

of a continuous function in a given interval by a combination of the methods of linear interpolation, extrapolation and bisection.

Iterative calculations were continued until successive iterations gave values of the estimator which differed by less than .0000001 . The values of the estimators are shown in the printouts to seven decimal places and therefore any calculation error due to the iterative method is of the same order as the rounding applied in displaying the estimator values.

The estimators for which iterative methods of solution are employed are:

(1) All conventional estimators, except when the Balducci assumption is made.

(2) All implication-B estimators.

(3) All maximum likelihood estimators, except when the Gompertz Law is assumed with a given value of c which includes the "constant μ" assumption.

(4) All method of moments estimators.

(5) The approximated "operational moment relations" estimators (calculated for the "level deaths" and "Balducci" assumptions only).

(6) The n-estimators for n = -2, 0 (the log-estimator), 2 and 3, except when the "constant μ" assumption is made and in the case of the log-estimator when the Gompertz Law is assumed.

In fact the only estimators for which an iterative solution is not used are the product limit estimator, the entire family of time-count estimators (which includes the conventional estimator for the Balducci assumption, the maximum likelihood estimator for the "constant μ" assumption and indeed all n-estimators for the "constant μ" assumption) and maximum likelihood estimators for the Gompertz Law if a given value of c is assumed (which also includes the "constant μ" assumption and embraces the log-estimator which is identical with the maximum likelihood estimator for the Gompertz Law if a given value of c is assumed).

5.13 A technical complication in determining the two-parameter maximum likelihood estimators

The two-parameter maximum likelihood estimators are calculated by solving two

simultaneous equations in the two parameters. A complication arises when b equals 0 or when c equals 1 in that one of the two equations is not then properly defined. Depending on how the equations have been expressed, one of them will then either contain items which cannot be evaluated, such as zero divided by zero, or will become identical with the other equation, so that solution for the two unknowns becomes impossible. This creates general difficulties as the simultaneous equations have to be solved iteratively and, even if the eventual solution is not in the region of $b = 0$ or $c = 1$, the anomalous value can still arise as a trial value during the iterations.

Although in theory, the anomaly only occurs at one point, in practice severe complications arise in a band of values around the anomalous point as the computer experiences difficulty in calculating the necessary values close to the anomalous point, where the situation becomes increasingly extreme. If the program is not designed to cope with this in some way, there is the high probability that it will malfunction at some stage of its use and will terminate or, more insidiously, continue to run but produce spurious values.

Such a malfunction will be disastrous if the program is being used to produce a large number of simulations, the results of which are to be averaged.

In the programs **ASP**, **ASPSIM**, **ASPMOM** and **ASPMMSIM**, this problem is overcome by the provision that when a value of $k = b/a$ in the range -0.05 to 0.05, or a value of c in the range 0.98 to 1.02, is to be used as a trial value in the iterations, the values $k = -0.05$ and $k = 0.05$, or $c = 0.98$ and $c = 1.02$, are used and first difference interpolation employed to obtain values corresponding to the actual values of k or c involved.

Even when the values of the two parameters which solve the simultaneous equations have been successfully obtained, problems can still remain, in that the value of q_X, corresponding to the parameter values, has to calculated and, in the region of $b = 0$ or $c = 1$, a similar anomaly has to be coped with.

At precisely $b = 0$ or $c = 1$, the "constant μ" assumption applies and the formula for calculating q_X is different from the formula when $b \neq 0$ or $c \neq 1$, this latter formula being undefined at the anomalous point, and indeed impossible for the computer to calculate in the immediate region of the anomalous point.

In the programs **ASP**, **ASPSIM**, **ASPMOM** and **ASPMMSIM**, this problem is overcome by a provision that when, for example, a value of q_X is to be calculated for $k = b/a$ in the range 0.0 to 0.1, values at $k = 0$ and $k = 0.1$ are calculated by the appropriate formulae and the value of q_X for the required value of k obtained by first difference interpolation; similar methods are used when a value of q_X is required for $k = b/a$ in the range -0.1 to 0.0, c in

the range 0.995 to 1.000 or c in the range 1.000 to 1.005.

5.14 Population and sample parameters assumed for the simulation runs

All the simulation runs were made for a standard set of population and sample parameters. These were:

$q_x = 0.2$	$w_x = 0.4$	$r = 3$
$n_1 = 10000$	$n_2 = 10000$	no. of runs = 500

For both programs **ASPSIM** and **ASPMMSIM**, simulations have been made assuming population mortality in which b = 2, 1, 0, -1 and c = 1.1, 1.05. Obviously, the runs with b = 0 are equivalent to runs with c = 1.

The values assumed in the population for the mortality rate, of 0.2, and for the withdrawal rate, of 0.4, are very high, but have been deliberately chosen so, in order to test the different estimators under fairly extreme circumstances, so that any differences might be emphasised.

The monthly withdrawal rate in the population is assumed to be constant.

The tranche of new entrants are assumed to enter at duration three months, which is regarded as providing a suitable test of the different estimators in the presence of new entrants.

The number of lives assumed to enter at duration zero in the year of age, and subsequently at duration 3 months, namely 10000 in each case, was regarded as providing a suitably substantial number of lives to give stable calculations of the estimators. The main purpose of these investigations was to compare the general performance of the different estimators, and comparison of their performance for smaller numbers of lives is a possible area for future work.

The speed of computation provided by the 80286 processor then dictated that a practical number of individual runs in a simulation study would be 500. For the program **ASPSIM**, 500 runs take about 28 hours, while for the program **ASPMMSIM**, 500 runs take about 35 hours.

It will be noted that the results of 500 such runs are thus based on the experience of ten million simulated lives.

5.15 Comments on the population and sample parameters common to all the simulation runs

The estimators have been studied in the simulations using one set of values for the parameters q_x, w_x, n_1, n_2 and r, and this needs to be borne in mind in interpreting the behaviour of individual estimators.

The benefits of the simulations are considered to lie in checking that proposed new methods of estimating q_x do indeed work satisfactorily, and in the comparisons that are facilitated between different estimators; it is felt that the comparisons made using the common parameter values assumed in these simulations will provide conclusions about the relative behaviour of the estimators that can be expected to be broadly valid over a wide range of values of these parameters. However it remains a possibility that an apparent effect, observed when two estimators are compared, could be modified significantly if alternative values of the parameters were adopted. This obviously provides an area where further research could be undertaken.

It should be noted that the simulations using $b = 2$ provide a test of the estimators which is more extreme and demanding with $q_x = 0.2$ than any situation likely to be met in practice. The roughly equivalent value of c in a Gompertz distribution is shown in the simulations, by the maximum likelihood estimator of c, to be of the order of 1.57 . Moreover the shape of the rectangular hyperbolic curve for μ_{x+t} will be significantly more skewed to the right than the Gompertz curve.

To a somewhat lesser degree, the same comment applies to the "level deaths" assumption ($b = 1$) where, with $q_x = 0.2$, the roughly equivalent value of c appears to be about 1.25 .

It is felt that if estimators can perform satisfactorily under such demanding situations, they are likely to perform no less adequately under more moderate circumstances such as where the roughly equivalent value of c is 1.1 or less.

5.16 The tabulations of the simulation outputs

Printouts showing the outputs from the simulations are presented in Appendix II. The twelve simulations have been labelled 1A, 1B, 2A etc as indicated in the Table 5.1.

Appendix II also provides a key to the layout of the simulation outputs.

Table 5.1 Labelling of the simulations

Simulation label	Distribution parameter	Simulation program
1A	b = 2	ASPSIM
1B	b = 2	ASPMMSIM
2A	b = 1	ASPSIM
2B	b = 1	ASPMMSIM
3A	b = 0 & c = 1	ASPSIM
3B	b = 0 & c = 1	ASPMMSIM
4A	b = -1	ASPSIM
4B	b = -1	ASPMMSIM
5A	c = 1.1	ASPSIM
5B	c = 1.1	ASPMMSIM
6A	c = 1.05	ASPSIM
6B	c = 1.05	ASPMMSIM

5.17 Software quality

It is perhaps appropriate at this point to consider the possibility that, while the programs appear to have run without apparent malfunctions, the results could be unreliable due to errors in the programming.

As the programs have been developed, they have been tested most assiduously and any apparently inconsistent aspects of the outputs have been investigated very carefully for possible programming error.

If results were contaminated by software errors, there would seem to be three main areas in which this could occur:

(1) The simulation of deaths and withdrawals in the population according to the assumed distributions.
(2) The calculation of the values of individual estimators.
(3) Failure of the pseudo-random number generator to provide random numbers.

The results of the virtually unbiased product limit estimator and the two-parameter maximum likelihood estimators appear to suggest strongly that the assumed population mortality distributions have been simulated correctly. Although the evidence available

concerning withdrawals is less exacting, the withdrawal distributions also appear to have been simulated satisfactorily. The programs ASP and ASPMOM, which produce single runs, allow the numbers of deaths and withdrawals occurring in each month to be printed out, and this evidence is satisfactory.

With regard to the calculation of the individual estimators, all the values obtained appear reasonable, especially in the light of the 95% confidence intervals. In each case in the results, where a 95% confidence interval does not contain the population value of $q_x = 0.2$, an obvious explanation can be found in terms of an inappropriate mortality assumption being used in the calculation of the estimator value or of a methodological shortcoming, for example as argued in the case of Hoem's approximated "operational moment relations" estimator.

Given that the distributions appear to have been satisfactorily simulated, it is also believed that the pseudo-random number generator has performed satisfactorily.

Perhaps the biggest residual risk is of the survival of a programming error that produces a very minor effect in the calculation of an individual estimator, which is not of a sufficient size to be apparent as an obvious aberration. It is strongly felt that the stringent checking of results in the development stages of the programs means that the possibility of this is very small. However the most reliable check would appear to be for another researcher to develop programs independently which duplicate the specifications of the existing programs and for the characteristics of the outputs from the duplicate and original programs to be compared. This would appear to be an exercise which would be virtually prohibited by the amount of work involved.

Although the printouts shown in Appendix II do not show any details of individual runs, but only averages and other statistics based on all 500 runs, the fuller printouts generated by the programs also include summarised details for each individual run, namely the values of a selection of estimators, in order that any unexpected malfunction of the program leading to obviously spurious values in an individual run can be detected by a visual check of the full printouts.

Obviously it is very important to avoid the possibility that a simulation study of 500 runs would be accepted despite being tainted by a run in which the program had "crashed". No such spurious results indicating a "crash" have been detected in any of the runs performed for use in this thesis, using the fully tested versions of the programs.

Also, if for any reason the iterative method of solution by which the routine C05ADF locates a zero of a continuous function in a given interval were unsuccessful, an error

message would be printed out, although the program would not be not terminated. Therefore the full printouts have also been carefully inspected for such error messages, but not a single one has occurred.

5.18 The product limit estimator

Table 5.2 summarises the 95% confidence limits for the value of the population q_x, based on the observed values of the product limit estimator in each of the 12 simulations. In view of the large number of lives involved in each individual repetition within a simulation program, the product limit estimator is effectively unbiased here and so its simulated values can provide an indication of whether the programs are correctly simulating the adopted population mortality distribution and correctly calculating the product limit estimator.

Table 5.2 The product limit estimator: 95% confidence intervals for population q_x

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.1999008	.2004999	.1995682	.2001447
b = 1	.1996938	.2003005	.1998742	.2004546
b = 0	.1996041	.2001961	.1998425	.2004628
b = -1	.1995400	.2001436	.1998066	.2004278
c = 1.1	.1997424	.2003433	.1995761	.2001371
c = 1.05	.1999333	.2005470	.1997168	.2003300

It can be seen that the population value of $q_x = 0.2$ falls very satisfactorily within each confidence interval, which is an encouraging indication that the programs are performing correctly in the areas mentioned.

5.19 The conventional estimator

Table 5.3 summarises the 95% confidence limits for the value of the population q_x, based on the observed values of the conventional estimator, calculated using the same mortality assumption as that adopted in the population from which the simulated observations were derived, for the 9 simulations where this estimator was calculated in this way.

Table 5.3 The conventional estimator: 95% confidence intervals for population q_x

(Estimator uses the same mortality assumption as in the population).

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.1999414	.2005103		
b = 1	.1996035	.2001968	.1999105	.2004679
b = 0	.1995766	.2001567	.1998453	.2004434
b = -1	.1995819	.2001706	.1997758	.2003848
c = 1.1	.1997738	.2003723	.1995396	.2001036

It will be seen that the population value of $q_x = 0.2$ falls satisfactorily within each confidence interval. This result appears to support the contention of this thesis that the principle of the conventional estimator is not flawed, despite the views put forward by Hoem (1984).

If the conventional estimator is subject to bias in the circumstances simulated here, such bias does not appear to be of a sufficient magnitude to be apparent compared with the effect of the random fluctuations.

5.20 Hoem's approximated "operational moment relations" estimator

Table 5.4 summarises the 95% confidence limits for the value of the population q_x, based on the observed values of Hoem's approximated "operational moment relations" estimator, calculated using the same mortality assumption as that adopted in the population from which the simulated observations were derived, for the 4 simulations where this estimator was calculated in this way.

It will be seen that in every case the upper limit of the confidence interval for the population value of q_x falls well below the true value of $q_x = 0.2$, the distance of the population value of q_x from the centre of the confidence interval being an average of about 18 times the standard deviation of the average observed value of the estimator, ie this distance is about $4\frac{1}{2}$ times as big as the width of the confidence interval.

This appears to provide very strong evidence to support the contention in Section 1.9 that the approximation used in constructing this estimator introduces a negative bias, and that therefore the estimator is not satisfactory.

Table 5.4 Hoem's approximated "operational moment relations" estimator: 95% confidence intervals for population q_x

(Estimator uses the same mortality assumption as in the population).

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 1	.1969729	.1975527	.1972732	.1978160
b = -1	.1969815	.1975543	.1971685	.1977624

5.21 The method of moments estimator

Table 5.5 compares the average observed values of the method of moments and conventional estimators, calculated using the same mortality assumption as that adopted in the population from which the simulated observations were derived, for the 4 simulations where the method of moments estimator was calculated in this way.

Table 5.5 Comparison of the average observed values of the method of moments and conventional estimators of q_x

(Estimator uses the same mortality assumption as in the population).

Pop. distn.	ASPMMSIM	ASPMMSIM
Parameter	Method of moments	Conventional
b = 1	.2001887	.2001892
b = 0	.2001428	.2001443
b = -1	.2000702	.2000803
c = 1.1	.1998304	.1998216

It will be seen in each case that the values of the two estimators are very close.

These simulation results appear to give strong evidence to support the contention in Section 2.10 of this thesis that the values of the conventional estimator and the method of moments estimator are likely to be very similar when the correct mortality assumption is made, and to support the more general contention that the conventional estimator is not flawed.

The argument against the conventional estimator in Hoem (1984) appears to be that the principle underlying the conventional estimator differs from that of the method of moments estimator, which is regarded in Hoem (1984) as a satisfactory estimator, in a way which renders the conventional estimator unsatisfactory. However if the two estimators give similar values, the argument that the difference in the principle renders the conventional estimator unsatisfactory would not appear to be sustainable.

Some further discussion of the relationship between the conventional estimator and the method of moments estimator is given in Section 5.27 .

5.22 The implication-B, maximum likelihood, log and time-count estimators

Table 5.6 summarises the 95% confidence limits for the value of the population q_x, based on the observed values of the implication-B estimator, calculated using the same mortality assumption as that adopted in the population from which the simulated observations were derived, for the 9 simulations where this estimator was calculated in this way.

Table 5.6 The implication-B estimator: 95% confidence intervals for population q_x

(Estimator uses the same mortality assumption as in the population).

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.1999445	.2005161		
b = 1	.1996015	.2001966	.1999067	.2004653
b = 0	.1995744	.2001540	.1998383	.2004366
b = -1	.1995797	.2001685	.1997727	.2003822
c = 1.1	.1997796	.2003783	.1995432	.2001063

Table 5.7 summarises the 95% confidence limits for the value of the population q_x, based on the observed values of the maximum likelihood estimator, calculated using the same mortality assumption as that adopted in the population from which the simulated observations were derived, for the 9 simulations where this estimator was calculated in this way.

Table 5.7 The maximum likelihood estimator with mortality assumption: 95% confidence intervals for population q_x

(Estimator uses the same mortality assumption as in the population).

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.1999355	.2005059		
b = 1	.1996035	.2001968	.1999105	.2004679
b = 0	.1995708	.2001485	.1998515	.2004510
b = -1	.1995723	.2001598	.1997770	.2003781
c = 1.1	.1997689	.2003647	.1995545	.2001146

Table 5.8 summarises the 95% confidence limits for the value of the population q_x, based on the observed values of the log-estimator, calculated using the same mortality assumption as that adopted in the population from which the simulated observations were derived, for the 6 simulations where this estimator was calculated in this way. It will be remembered from Section 4.8, that when the Gompertz mortality distribution is assumed in the estimator, the log-estimator is identical with the one-parameter maximum likelihood estimator.

Table 5.8 The log-estimator: 95% confidence intervals for population q_x

(Estimator uses the same mortality assumption as in the population).

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.1999445	.2005161	ASPMMSIM does not	
b = 1	.1996064	.2002022	calculate the log-estimator	
b = 0	.1995708	.2001485	for the rect. hyper. dist.	
b = -1	.1995781	.2001645		
c = 1.1	.1997689	.2003647	.1995545	.2001146

Table 5.9 summarises the 95% confidence limits for the value of the population q_x, based on the observed values of the time-count estimator, calculated using the same mortality assumption as that adopted in the population from which the simulated observations were derived, for the 9 simulations where this estimator was calculated in this way.

Table 5.9 The time-count estimator: 95% confidence intervals for population q_x

(Estimator uses the same mortality assumption as in the population).

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.1999443	.2005310		
b = 1	.1996106	.2002099	.1999279	.2004906
b = 0	.1995708	.2001485	.1998515	.2004510
b = -1	.1995819	.2001706	.1997758	.2003848
c = 1.1	.1997669	.2003612	.1995608	.2001197

It will be seen that, in every case, the population value of $q_x = 0.2$ falls satisfactorily within each confidence interval. Again if any of these estimators are subject to bias in the circumstances simulated here, such bias does not appear to be of a sufficient magnitude to be apparent compared with the effect of the random fluctuations.

5.23 Comparison of mortality rate estimators which generally require assumption of the population one-parameter mortality distribution

When Tables 5.6, 5.7, 5.8 and 5.9 are studied, one gains the impression that the values taken by the various estimators concerned are very similar, when the estimators adopt the same one-parameter mortality assumption as that applicable in the population. This impression is confirmed in Tables 5.10 and 5.11 which compare the average values of the estimators, and also the product limit estimator which does not require a mortality assumption. The estimators shown are the product limit estimator ("ple"), the conventional estimator ("Conv"), the implication-B estimator ("ImpB"), the maximum likelihood estimator ("mle"), the log-estimator ("log"), the time-count estimator ("Time") and the method of moments estimator ("Mom").

It is seen that all the estimators which require an explicit mortality assumption generally have very similar average observed values and in fact this also tends to be the case for observed values in single runs from the 500 constituting a simulation study.

It is especially interesting to note the close similarity between the values of the conventional estimator and the maximum likelihood estimator, in view of the comments in Hoem (1984) which are critical of the conventional approach but favourable to the maximum likelihood approach.

Table 5.10 ASPSIM : Comparison of the averaged observed values of estimators

(If needed, the mortality assumption is same as in the population).

Para	ple	Conv	ImpB	mle	log	Time
b = 2	.2002003	.2002258	.2002303	.2002207	.2002303	.2002376
b = 1	.1999971	.1999002	.1998990	.1999002	.1999043	.1999102
b = 0	.1999001	.1998666	.1998642	.1998596	.1998596	.1998596
b = -1	.1998418	.1998762	.1998741	.1998660	.1998713	.1998762
c = 1.1	.2000429	.2000730	.2000789	.2000668	.2000668	.2000641

Table 5.11 ASPMMSIM : Comparison of the averaged observed values of estimators

(If needed, the mortality assumption is same as in the population).

Para	ple	Mom	Conv	ImpB	mle	Time
b = 1	.2001644	.2001887	.2001892	.2001860	.2001892	.2002093
b = 0	.2001527	.2001428	.2001443	.2001374	.2001512	.2001512
b = -1	.2001172	.2000702	.2000803	.2000775	.2000776	.2000803
c = 1.1	.1998566	.1998304	.1998216	.1998247	.1998346	.1998403

The greatest differences between estimators appears to arise between the product limit estimator on the one hand and all the other estimators on the other. Of course it has to be born in mind that, due to random fluctuations, the observed data may not be perfectly representative of the mortality distribution underlying the population so that the estimators which use the mortality assumption may estimate values of the population rate of q_x which are marginally biased for this reason.

The most compelling conclusion arising from these figures appears to be that, if one is confident of making a reasonably accurate mortality assumption, there seems little to choose between any of the estimators requiring a mortality assumption, which are considered in Tables 5.10 and 5.11.

Tables 5.12 and 5.13 show the estimated standard deviations of single observed values of the estimators considered in Tables 5.10 and 5.11 . The feature which appears most striking is that the estimated standard deviation of the product limit estimator is greater than the estimated standard deviation of each of the other estimators in 42 out of 45 possible comparisons.

Table 5.12 ASPSIM: Estimated standard deviations of single observed values of estimators

(If needed, the mortality assumption is same as in the population).

Para	ple	Conv	ImpB	mle	log	Time
b = 2	.0033495	.0031801	.0031951	.0031891	.0031958	.0032798
b = 1	.0033918	.0033168	.0033267	.0033168	.0033305	.0033498
b = 0	.0033094	.0032429	.0032401	.0032295	.0032295	.0032295
b = -1	.0033741	.0032909	.0032915	.0032840	.0032781	.0032909
c = 1.1	.0033591	.0033454	.0033470	.0033309	.0033309	.0033220

Table 5.13 ASPMMSIM: Estimated standard deviations of single observed values of estimators

(If needed, the mortality assumption is same as in the population).

Para	ple	Mom	Conv	ImpB	mle	Time
b = 1	.0032442	.0031250	.0031164	.0031230	.0031164	.0031459
b = 0	.0034677	.0033561	.0033437	.0033444	.0033516	.0033516
b = -1	.0034726	.0034018	.0034041	.0034070	.0033604	.0034041
c = 1.1	.0031362	.0031390	.0031525	.0031480	.0031309	.0031244

The estimated standard deviations of the other estimators are generally quite similar to each other and usually the estimated standard deviation of the product limit estimator can be seen to be greater by an unambiguous margin, although the distinction is least pronounced among the estimators that assume the Gompertz law with $c = 1.1$, most notably in the results of the simulation using **ASPMMSIM** with $c = 1.1$, where the estimated standard deviations of the method of moments, conventional and implication-B estimators are slightly higher than that of the product limit estimator. In the corresponding simulation from **ASPSIM**, the estimated standard deviation of the product limit estimator is the largest of those considered, but by a relatively modest margin.

Intuitively one might expect the product limit estimator to have a larger standard deviation than those estimators which assume a mortality law, because the latter use additional information. Of course the additional information will only benefit the estimators which are rivals to the product limit estimator so long as the information is correct. If the assumed mortality law were not correct, bias would be likely to be introduced into those estimators making the incorrect assumption.

A consequence of the results, when the Gompertz law with c = 1.1 applies, may be that the product limit estimator should be regarded as the best estimator to use out of the selection considered in Tables 5.10–5.13, assuming its computational requirements can be met, since if the assumed law does indeed apply, giving its rivals additional information, the product limit estimator still appears to perform similarly to its rivals and if the assumed law does not apply, the product limit estimator will continue to give virtually unbiased results, whereas its rivals will be likely to produce values which are biased.

Of course this conclusion is drawn from observations based on a single set of population and sample parameters, and it would be necessary for the effects, if any, on these conclusions of varying the population and sample parameters to be investigated.

The possible biasing effect of making wrong mortality assumptions in estimators is discussed in Section 5.27, and also the asymptotic effect of wrong mortality assumptions was considered in Section 4.14 .

5.24 The maximum likelihood estimator, where the mortality distribution parameter is not assumed

As has been explained, the method of maximum likelihood was also applied to estimate both parameters, a and b, where the rectangular hyperbolic mortality distribution was assumed to apply, and both parameters, B' and c, where the Gompertz mortality distribution was assumed to apply.

In Table 5.14 the average estimated value of the population q_x obtained in this way assuming the rectangular hyperbolic distribution, "ML H", and the corresponding value assuming the Gompertz mortality distribution, "ML G", are compared with the value of the product limit estimator for each of the 12 simulations.

The comparison is interesting as the three estimators make either no mortality assumption (product limit estimator) or a minimal assumption as to the general shape of the mortality distribution (ML H and ML G).

Table 5.14 shows that the average observed values of the three estimators are similar. However it is quickly apparent that the average observed value of the ML H estimator is greater than the average observed value of the ML G estimator for all the simulations.

Further the difference between these values can be seen to follow a pattern in which the difference between the two appears to fall to a minimum (for the distribution parameters

tabulated) when b = 0, ie when the force of mortality is constant and the two mortality distributions take the same shape. There is a reassuring similarity in the "differences" between ML H and ML G produced by the ASPSIM and ASPMMSIM programs.

Table 5.14 Comparison of the two-parameter maximum likelihood estimators and the product limit estimator

Program	Distn para	product limit est	mle ML H	mle ML G	difference: H minus G
ASPSIM	b = 2	.2002003	.2002398	.2000295	.0002102
ASPMMSIM	b = 2	.1998565	.1999311	.1997198	.0002113
ASPSIM	b = 1	.1999971	.1999161	.1998588	.0000573
ASPMMSIM	b = 1	.2001644	.2002110	.2001542	.0000568
ASPSIM	b = 0	.1999001	.1998702	.1998620	.0000082
ASPMMSIM	b = 0	.2001527	.2001689	.2001608	.0000081
ASPSIM	b = -1	.1998418	.1998782	.1998187	.0000595
ASPMMSIM	b = -1	.2001172	.2000893	.2000280	.0000613
ASPSIM	c = 1.1	.2000429	.2000870	.2000705	.0000165
ASPMMSIM	c = 1.1	.1998566	.1998616	.1998463	.0000153
ASPSIM	c = 1.05	.2002401	.2002021	.2001921	.0000100
ASPMMSIM	c = 1.05	.2000234	.2000854	.2000749	.0000105
		---	---	---	
Average		.2000328	.2000451	.1999846	

It is tempting to hypothesise that the value of the ML H estimator is always greater than the ML G estimator. However a small number of individual runs when b = 0 appear to show the value of ML H as less than that of ML G. This is an area where further research could be undertaken to confirm that this is a genuine effect.

However it does appear that it can be stated with some confidence that the ML G estimator of q_x is more negatively biased or less positively biased than the ML G estimator of q_x.

The averages of values of the three tabulated estimators over the 12 simulations provides a very crude comparison which shows an average for the product limit estimator which lies between the average values of the ML H and ML G estimators; from these figures, the value of the product limit estimator appears to lie much closer to the ML H value than to the ML G value, the averaged product limit estimator value splitting the distance between

the average ML H value and the average ML G value in the ratio 1:4.

Given that the product limit estimator is effectively unbiased here, it may be the case that the ML G provides a negatively biased estimator of q_x. Certainly if the ML G estimator is negatively biased relative to the ML H estimator, then obviously one or both of these estimators must be biased in some way. However it is true that in three of the simulations the average observed value of the ML G estimator was greater than that of the product limit estimator.

It is to be noted that the three simulations, for which the average observed value of ML G is greater than the average observed value of the product limit estimator, all assume a Gompertz population distribution (including c = 1.0, ie when b = 0) and represent more moderate shapes of the μ_{x+t} curve (more moderate than for b = -1, 1, 2).

If we consider the average values of the three tabulated estimators over the six simulations for which c = 1.0, 1.05 and 1.1 in the population, we obtain the following averages:

Table 5.15 Observed averages of product limit estimator, ML H and ML G for c = 1.0, 1.05 and 1.1

Average ple	= .2000360
Average ML H	= .2000459
Average ML G	= .2000344

Here it can be seen that the average ML G value is very close to the average product limit estimator value, whereas the average ML H value is relatively higher. In fact the average product limit estimator value splits the distance between the average ML H value and the average ML G value in the ratio 6:1.

A different situation is found if we consider the average values of the three tabulated estimators over the six simulations for which b = -1, 1 and 2 in the population; we obtain the averages shown in Table 5.16.

It is seen that the average product limit estimator and ML H values are of a similar order as previously but the average ML G value is markedly lower than the average ML G value calculated for the six simulations using c = 1.0, 1.05 and 1.1 .

In fact the averaged product limit estimator value now splits the distance between the average ML H value and the average ML G value approximately in the ratio 1:6 .

Table 5.16 Observed averages of product limit estimator, ML H and ML G for b = -1, 1 and 2

Average ple	= .2000296
Average ML H	= .2000443
Average ML G	= .1999348

The hypothesis that is now suggested by these results is that:

(a) The ML H estimator might have a slight positive bias, although the apparent effect is of such modest proportions that it could simply be a random effect in the data and further research would be advisable to establish whether the effect is genuine. If positive bias is genuinely present, the simulations suggest that it may not be greatly affected by the distribution shape parameter applicable in the population, at least within the range considered in the simulations.

(b) The ML G estimator may have negligible bias when used in populations with c of the order 1.0, 1.05 and 1.1 , but a distinctly negative bias when used in rectangular hyperbolic populations with b of the order -1, 1 and 2. What is not clear is whether the distinction may be ascribed to the fact that, in the first group of populations, the population mortality distribution is Gompertz and, in the second group of populations, the population mortality distribution is rectangular hyperbolic, or to the fact that the population mortality distribution is simply more extreme in the second group of populations than in the first.

Obviously further research could help resolve these speculations.

Tables 5.17 and 5.18 give the 95% confidence limits for the values of q_x given by the ML H and ML G estimators in the 12 simulations. Despite the probable existence of some bias, the population value of $q_x = 0.2$ falls within all these confidence intervals although, in the **ASPMMSIM** simulation with b = 2, it is a very close run thing for ML G as the upper limit is .2000008! This again indicates that further evidence is necessary in order to resolve the earlier speculations about possible bias in these estimators of q_x.

Table 5.17 The two-parameter maximum likelihood estimator, assuming the rectangular hyperbolic mortality distribution (ML H): 95% confidence intervals for population q_x

Pop. distn. parameter	ASPSIM		ASPMMSIM	
	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.1999537	.2005260	.1996486	.2002136
b = 1	.1996178	.2002143	.1999312	.2004908
b = 0	.1995801	.2001604	.1998691	.2004686
b = -1	.1995859	.2001705	.1997887	.2003899
c = 1.1	.1997896	.2003845	.1995817	.2001415
c = 1.05	.1999026	.2005015	.1997912	.2003797

Table 5.18 The two-parameter maximum likelihood estimator, assuming the Gompertz mortality distribution (ML G): 95% confidence intervals for population q_x

Pop. distn. parameter	ASPSIM		ASPMMSIM	
	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.1997447	.2003143	.1994388	.2000008
b = 1	.1995600	.2001576	.1998740	.2004343
b = 0	.1995718	.2001522	.1998611	.2004606
b = -1	.1995256	.2001119	.1997272	.2003288
c = 1.1	.1997733	.2003678	.1995667	.2001258
c = 1.05	.1998925	.2004917	.1997813	.2003686

An interesting feature becomes apparent if we compare the values of q_x given by the one-parameter maximum likelihood estimator and the two-parameter maximum likelihood estimator, where the mortality distribution assumed (rectangular hyperbolic or Gompertz) is that applicable in the population, for the nine simulations where both the one-parameter and two parameter maximum likelihood estimators have been determined. These values are given in Table 5.19, together also with values of the product limit estimator for comparative purposes.

Table 5.19 Comparison of the two-parameter and one-parameter maximum likelihood estimators where the assumed mortality law corresponds to that applying in the population (also showing values of the product limit estimator)

Program	Distn para	product limit est	mle (α) ML H or ML G	mle (β) one-para	difference: α minus β
ASPSIM	b = 2	.2002003	.2002398 (ML H)	.2002207	.0000191
ASPSIM	b = 1	.1999971	.1999161 (ML H)	.1999002	.0000159
ASPMMSIM	b = 1	.2001644	.2002110 (ML H)	.2001892	.0000218
ASPSIM	b = 0	.1999001	.1998702 (ML H)	.1998596	.0000106
ASPMMSIM	b = 0	.2001527	.2001689 (ML H)	.2001512	.0000177
ASPSIM	b = -1	.1998418	.1998782 (ML H)	.1998660	.0000122
ASPMMSIM	b = -1	.2001172	.2000893 (ML H)	.2000776	.0000117
ASPSIM	c = 1.1	.2000429	.2000705 (ML G)	.2000668	.0000037
ASPMMSIM	c = 1.1	.1998566	.1998463 (ML G)	.1998346	.0000117
		---	---	---	---
Average (excl. c = 1.1)		.2000534	.2000534	.2000378	.0000156

It is seen that the values of the one-parameter and corresponding two-parameter maximum likelihood estimators are very close, but that in each of the nine simulations, the average value of the one-parameter maximum likelihood estimator is lower than that of the two-parameter maximum likelihood estimator.

To provide an unsophisticated comparison, Table 5.19 also shows averages, over the seven simulations in the table which use the rectangular hyperbolic distribution, of the estimates of the population value of q_x given by the one-parameter and two-parameter maximum likelihood estimators, and of the product limit estimator.

It will be seen that the average values, over the seven simulations, of the two-parameter maximum likelihood estimator and the product limit estimator are actually the same and that the average value of the two-parameter maximum likelihood estimator is greater than that of the one-parameter maximum likelihood estimator by .0000156 .

The fact that for these seven simulations the average value of the ML H estimator equals the average value of the unbiased product limit estimator does nothing to strengthen the previous tentative speculation, based on Tables 5.15 and 5.16, that the ML H may have a very slight positive bias.

However the fact that there seems to be a consistent tendency for the average value of the estimate given by the two-parameter maximum likelihood estimator to be very slightly greater than that given by the corresponding one-parameter maximum likelihood estimator is interesting, since it suggests the presence of a small amount of bias somewhere in the calculation of the two-parameter maximum likelihood estimator and/or the calculation of the one-parameter maximum likelihood estimator. However to keep matters in perspective, it should be noted that the difference between the values of the two estimators appears to be less than 0.01% of the value of q_x of 0.2 . Again, this possible bias is a feature which could be given further attention in subsequent research.

It is worth pointing out that, in the rectangular hyperbolic calculations, the values of the parameters a and b which are calculated, when the two-parameter maximum likelihood estimator is being determined, are those values for which the one-parameter maximum likelihood estimator and the log-estimator give the same value of q_x (being the values of the one-parameter maximum likelihood estimator and log-estimator given by equations (3.86) and (3.85) respectively in Section 3.16 for the appropriate value of b).

If the average value of the two-parameter maximum likelihood estimator differs slightly from that obtained when b is assumed at the value applicable in the population, this could suggest that the estimate of b obtained in the two-parameter calculation may be slightly biased, or alternatively, it may be the case that any random fluctuation in the estimated value of b, whether the fluctuation is positive or negative, has a tendency in either case to lead to an increase in the value of q_x estimated by the two-parameter maximum likelihood estimator.

Table 5.20 shows 95% confidence intervals for the mortality distribution parameters b or c. It can be seen that the population value of the parameter b for the rectangular hyperbolic mortality distribution appears to lie satisfactorily within the confidence interval in each case.

When we consider the population value of the parameter c for the Gompertz mortality distribution, we again find that it falls within the 95% confidence intervals, but there is a tendency for the value to lie towards an end of the confidence interval.

For both the simulations using the population value $c = 1.05$, this population value of c lies towards the lower limit of the interval, as is also the case for $c = 1.1$ where the **ASPSIM** program was used. In contrast however the population value of c lies, quite unambiguously, closer to the upper limit of the interval where the **ASPMMSIM** program was used with an assumed population value of $c = 1.1$.

Table 5.20 95% confidence intervals for the distribution parameter b or c where a two-parameter maximum likelihood estimator is used

Pop. distn. parameter	ASPSIM		ASPMMSIM	
	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	1.96319	2.02283	1.97374	2.03032
b = 1	0.96553	1.02262	0.95697	1.01223
b = 0	-0.02564	0.02960	-0.04755	0.01030
b = -1	-1.01845	-0.96391	-1.02729	-0.97178
c = 1.1	1.09834	1.11188	1.09060	1.10431
c = 1.05	1.04853	1.06153	1.04804	1.06183

To show more clearly these effects, Table 5.21 gives the distances of the upper and lower limits of each confidence interval from the population value of the mortality distribution parameter.

Table 5.21 Position of the 95% confidence limits relative to the population distribution parameter b or c where a two-parameter maximum likelihood estimator is used

Pop. distn. parameter	ASPSIM		ASPMMSIM	
	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	-0.03681	+0.02283	-0.02626	+0.03032
b = 1	-0.03447	+0.02262	-0.04303	+0.01223
b = 0	-0.02564	+0.02960	-0.04755	+0.01030
b = -1	-0.01845	+0.03609	-0.02729	+0.02822
c = 1.1	-0.00166	+0.01188	-0.00940	+0.00431
c = 1.05	-0.00147	+0.01153	-0.00196	+0.01183

Examination of the data printed out for each individual repetition of the simulation runs using the Gompertz population law does not give any indication of any program malfunction.

Intuitively, one might expect that the estimate of c would be positively biased since it might be anticipated that half the estimated values of c would be greater than 1.1 in a range from 1.1 up to ∞, while the other half of the estimated values of c would be less than 1.1,

occupying a range running from 1.1 down to 0.0, the compression of the second range suggesting that the average estimated value over both ranges might be positively biased.

A positive bias would mean that the population value of c = 1.1 would lie closer to the lower limit of the confidence interval, because the interval would be displaced to reflect the positive bias of the observations on which it is based.

Despite the apparently contrary indication provided by one simulation, the broad indication from the simulation outputs seems to be that the estimate of c might be subject to a positive bias. Obviously this is another area which could be clarified by further research.

It will be recalled that the attractive properties of maximum likelihood estimators do not in general include unbiasedness.

Table 5.22 gives an indication of the effectiveness of the approximate relationships (3.107) and (3.108) linking b and c. For each of the 12 simulations, it shows the distribution parameter b or c assumed to apply in the population, the value of the alternative parameter c or b which is approximately equivalent to this according to equations (3.107) and (3.108), and the values of b and c estimated by the maximum likelihood estimators of these parameters. It is seen that the values given by the approximate relationships agree well with the values estimated from the simulated data.

Table 5.22 Effectiveness of the approximate formulae linking b and c

Program	Distn para	Approx value of other para	mle of b	mle of c
ASPSIM	b = 2	c = 1.56250	1.99301	1.56950
ASPMMSIM	b = 2	c = 1.56250	2.00203	1.57152
ASPSIM	b = 1	c = 1.25000	.99407	1.25140
ASPMMSIM	b = 1	c = 1.25000	.98460	1.24993
ASPSIM	b = 0	c = 1.00000	.00198	1.00515
ASPMMSIM	b = 0	c = 1.00000	-.01862	1.00040
ASPSIM	b = -1	c = .80000	-.99118	.80368
ASPMMSIM	b = -1	c = .80000	-.99954	.80241
ASPSIM	c = 1.1	b = .42715	.43215	1.10511
ASPMMSIM	c = 1.1	b = .42715	.40015	1.09745
ASPSIM	c = 1.05	b = .21865	.22203	1.05503
ASPMMSIM	c = 1.05	b = .21865	.22018	1.05494

Table 5.23 shows the estimated standard deviations of single observed values of the two-parameter maximum likelihood estimators, the one-parameter maximum likelihood estimator and the product limit estimator.

Intuitively, one might expect that the largest standard deviations would apply to the product limit estimator since this estimator uses no extra information about the nature of the underlying mortality distribution and that the smallest standard deviations would apply to the one-parameter maximum likelihood estimator since this estimator assumes not only the form of the mortality distribution, but also the value of one distribution parameter. Further one might expect that the standard deviation applying to the two-parameter maximum likelihood estimators would lie in-between, since these assume the form of the mortality distribution, but not the value of any distribution parameters.

Also one might perhaps hypothesise that the standard deviation of the two-parameter maximum likelihood estimator which assumes the Gompertz distribution, when the rectangular hyperbolic distribution applies in the population, would be greater than that of the two-parameter maximum likelihood estimator which assumes the rectangular hyperbolic distribution, and vice versa.

Table 5.23 Estimated standard deviations of single observed values of the two-parameter maximum likelihood estimators, the one-parameter maximum likelihood estimator and the product limit estimator

(If needed, the mortality assumption is same as in the population).

Program	Distn para	product limit est	mle ML H	mle ML G	mle one-para
ASPSIM	b = 2	.0033495	.0031991	.0031845	.0031891
ASPMMSIM	b = 2	.0032227	.0031579	.0031417	(not calc)
ASPSIM	b = 1	.0033918	.0033345	.0033401	.0033168
ASPMMSIM	b = 1	.0032442	.0031285	.0031321	.0031164
ASPSIM	b = 0	.0033094	.0032441	.0032447	.0032295
ASPMMSIM	b = 0	.0034677	.0033512	.0033514	.0033516
ASPSIM	b = -1	.0033741	.0032678	.0032776	.0032840
ASPMMSIM	b = -1	.0034726	.0033605	.0033633	.0033604
ASPSIM	c = 1.1	.0033591	.0033254	.0033237	.0033309
ASPMMSIM	c = 1.1	.0031362	.0031294	.0031258	.0031309
ASPSIM	c = 1.05	.0034309	.0033483	.0033494	(not calc)
ASPMMSIM	c = 1.05	.0034279	.0032898	.0032829	(not calc)

The results of the simulations, as summarised in Table 5.23, only partially support these intuitive anticipations.

In each of the 12 simulations, it is true that the standard deviation of the product limit estimator is the largest of the four estimators tabulated. However in the case of the one-parameter maximum likelihood estimator, this estimator has the smallest standard deviation in only 4 of the 9 simulations where the one-parameter maximum likelihood estimator has been determined, has the largest standard deviation after the product limit estimator in 3 simulations, is sandwiched between the standard deviation of the ML H and ML G in one case and features in a virtual dead-heat between the ML H, ML G and one-parameter maximum likelihood estimator in the ninth case, one of the simulations for which $b = 0$.

It will be seen that the two-parameter maximum likelihood estimator which assumes the correct form of the mortality distribution in the population has a smaller standard deviation than the two-parameter maximum likelihood estimator which assumes the wrong form of the mortality distribution in 7 out of 10 relevant simulations, the two simulations for which $b = 0$ (ie $c = 1$) in the population having been excluded.

We may be basing our observations of these standard deviations on a sample which is too limited in size for the purpose, so that random effects are very dominant. Again perhaps further investigations might be undertaken, and practical considerations might dictate the use of faster computing equipment to allow a major increase in the volume of the simulations.

In Table V of each of the simulation printouts shown in Appendix II, the many values of the average observed q_x from Table I of the printouts are taken and the average observed value of the "ML H" or the "ML G" maximum likelihood estimator is deducted from each of them; the "ML H" or "ML G" value is used according to whether the simulation had assumed that the underlying population was subject to the rectangular hyperbolic mortality distribution or the Gompertz mortality distribution. However, with regard to the parameters b and c relating to the "ML H" and "ML G" estimators, the figures shown are simply repetitions of the values of the maximum likelihood estimators of the parameters.

As already stated in Section 5.10, the purpose of this was to give a strong visual impression of the degree to which the two-parameter maximum likelihood estimator concerned had agreed in its average value with the estimators in which the correct mortality distribution parameter had been assumed. Examination of Table V in the printouts confirms that the two-parameter maximum likelihood estimators have been very effective in estimating the population value of q_x without the assumption of a distribution parameter, and the

presentation of the results in Table V gives an effective visual impression of how the different estimates of q_x compare.

5.25 Examination of n-estimators

As explained in Section 4.27, the n-estimators were an embryonic form of the g-estimators in which the g-functions were limited to functions of the form:

$$(\mu_{x+t})^n \qquad \text{for any value of n.}$$

As previously explained, the n-estimators were given especial attention because it had been noted that, when the rectangular hyperbolic mortality distribution with an assumed value of b applied, a number of important estimators were obtained for particular values of n. It was subsequently realised that the g-function could be generalised so that virtually any estimator assuming a parametric mortality law could be produced.

The simulation programs were developed at a stage of the research when n-estimators were receiving maximum attention, before the generalisation to g-estimators had occurred, and therefore n-estimators featured heavily in the outputs of programs ASP, ASPMOM and ASPSIM. Programs ASP, ASPMOM and ASPSIM were designed to calculate n-estimators for n equal to -2, -1, 0, 1, 2 and 3. Programs ASP and ASPMOM also offer, among other things, the option to calculate this range of n-estimators for any assumed value of the parameter b, and further to calculate an n-estimator for any value of n and assumed value of b.

Table 5.24 shows average values of n-estimators determined from 4 simulations in which the population is assumed to be subject to the rectangular hyperbolic mortality distribution with b equal to 2, 1, 0 and -1. The n-estimators shown are for n equal to -2, -1, 0, 1, 2 and 3; the n-estimators shown incorporate the same mortality assumption as applies in the population. These results have been obtained using the program ASPSIM. For comparative purposes, average values of the product limit estimator and two-parameter maximum likelihood estimator are also shown, together with the average maximum likelihood estimate of the parameter b.

It must be stressed that the discussion in this Section considers only the case of the rectangular hyperbolic mortality distribution for both the population mortality and the mortality assumption in the estimator. Obviously estimators with the g-function in the form:

$$g(t,\phi) = (\mu_{x+t})^n$$

can be created assuming the Gompertz mortality distribution, but it is found that the one-parameter maximum likelihood estimator does not correspond to n = 1 as for the rectangular hyperbolic mortality distribution, but instead it corresponds to n = 0 and it coincides with the log-estimator.

In the printouts, the Gompertz one-parameter maximum likelihood estimator is shown in the line labelled "MLE" or "Max Likelihood" but is not an n-estimator with n = 1 as is the case for the other estimators shown in the same line (which assume the rectangular hyperbolic mortality distribution).

Table 5.24 Program ASPSIM: Average observed values of n-estimators, with other estimators for comparison

(n-estimators use the same mortality assumption as in the population).

	Mortality assumption in the population			
n-estimator	b = 2	b = 1	b = 0	b = -1
n = -2	.2002432	.1999178	.1998596	.1998811
n = -1 (Time)	.2002376	.1999102	.1998596	.1998762
n = 0 (log)	.2002303	.1999043	.1998596	.1998713
n = 1 (mle)	.2002207	.1999002	.1998596	.1998660
n = 2	.2002094	.1998977	.1998596	.1998607
n = 3	.2001960	.1998969	.1998596	.1998548
PL	.2002003	.1999971	.1999001	.1998418
ML H	.2002398	.1999161	.1998702	.1998782
est. of b	1.99301	.99407	.00198	-.99118

As can be verified from the simulation printouts (for program ASPSIM) reproduced in Appendix II, the 95% confidence intervals based on these estimators, and their corresponding estimated standard deviations, all contain the population value of q_x for every estimator summarised in Table 5.24 . Therefore all the n-estimators shown in Table 5.24 appear to be satisfactory if measured by this criterion.

Three of the simulations, for b = 2, b = 1 and b = -1, appear to indicate that the average

values of n-estimators appear to decrease as n increases over the range of n considered. For the case when b = 0, all the n-estimators shown give the same value because the g-function is constant over the year of age for all values of n.

The apparent tendency for the average value of n-estimators generally to decrease as n increases is perhaps another feature which would require confirmation through further investigation and the possibility must be borne in mind that the feature could be related to the particular assumptions common to all the simulations reported in this thesis.

It is interesting to note that Table 5.11 shows 3 further simulations assuming the rectangular hyperbolic mortality distribution in the population (from program **ASPMMSIM** which does not compute a full range of n-estimators) which are also consistent with the apparent tendency for the average value of n-estimators to decrease as n increases. This is seen if one examines the values shown in Table 5.11 for the time-count estimator (n = -1), the maximum likelihood estimator (n = 1) and the conventional estimator (n = 1/b).

If this apparent tendency is a genuine feature, it does imply the presence of a small amount of bias in at least some of the n-estimators.

When the values of n-estimators as calculated for single runs are considered, and not values averaged over 500 runs, some interesting patterns are seen. (For reasons of brevity, printouts of single runs have not been included in this thesis.) If, in single runs, the n-estimators are calculated assuming for the parameter b the value estimated by maximum likelihood, it is found that the log-estimator (n-estimator with n = 0) and the one-parameter maximum likelihood estimator (n-estimator with n = 1) give identical values which is theoretically correct since this is the condition for determining the two-parameter maximum likelihood estimator, which is based on the maximum likelihood estimate of b. This has previously been discussed in Section 5.24 .

When, in single runs, one goes on to consider n equal to -2, -1, 2 and 3, it appears that, in roughly half the cases, the values of the n-estimators when n = 0 and n = 1 are minimum values, and that values increase as we go from n = 0 to n = -1 to n = -2, and from n = 1 to n = 2 to n = 3. In nearly all the other cases, this pattern appears to be inverted and the values for n = 0 and n = 1 are maximum values. However at least one case has been observed in which the values of the n-estimators increased from n = -2 to n = 0 and again from n = 1 to n = 3, although in the latter range the increase was the minimum measurable. A methodical study of this behaviour has not been undertaken, so that the possibility also of the values decreasing from n = -2 to n = 0 and again from n = 1 to n = 3 cannot be ruled out.

Thus it seems that the apparent tendency for the average value of n-estimators to decrease as n increases is not a reflection of the general behaviour of n-estimators in individual sets of data, as n increases, but is the net result of averaging the fluctuations over the many runs.

Table 5.25 shows estimated standard deviations of single observed values of n-estimators determined from the same 4 simulations considered in Table 5.24 in which the population is assumed to be subject to the rectangular hyperbolic mortality distribution with b equal to 2, 1, 0 and -1. As before, the n-estimators shown are for n equal to -2, -1, 0, 1, 2 and 3; again the n-estimators shown incorporate the same mortality assumption as applies in the population.

Table 5.25 Program ASPSIM: Estimated standard deviations of single observed values of n-estimators, with other estimators for comparison

(n-estimators use the same mortality assumption as in the population).

	Mortality assumption in the population			
n-estimator	b = 2	b = 1	b = 0	b = -1
n = -2	.0034197	.0033977	.0032295	.0033110
n = -1 (Time)	.0032798	.0033498	.0032295	.0032909
n = 0 (log)	.0031958	.0033305	.0032295	.0032781
n = 1 (mle)	.0031891	.0033168	.0032295	.0032840
n = 2	.0032315	.0033181	.0032295	.0032872
n = 3	.0033251	.0033280	.0032295	.0033226
PL	.0033495	.0033918	.0033094	.0033741
ML H	.0031991	.0033345	.0032441	.0032678
est. of b	.33341	.31914	.30881	.30492

It is seen that the estimated standard deviation of the product limit estimator is the largest in each simulation except for the n-estimator with n = 2 in the simulations where the population is subject to mortality with b = 2 and b = 1 . It is also seen that, apart from the simulation where the "constant μ" mortality law applies in the population, the standard deviations of the n-estimators appear to pass through a minimum value as n increases from -2 to 3. In two cases the minimum occurs for the one-parameter maximum likelihood estimator (n-estimator with n = 1) and in the other case it occurs for the log-estimator (n-estimator with n = 0).

It is interesting also to note how reasonably the estimated standard deviation of the two-parameter maximum likelihood estimator compares with the estimated standard deviations of the n-estimators, which unlike the two-parameter maximum likelihood estimator assume a value for one mortality distribution parameter.

5.26 Comparison of some estimators using fixed mortality assumptions

The application of traditional exposed-to-risk theory involves the estimation of q_x by calculating the conventional estimator always using the Balducci mortality assumption. For this of course, we calculate q_x using formulae involving the initial exposed-to-risk, as given for example by equation (1.12).

Table 5.26 shows, for the 12 simulations, the 95% confidence limits for the population q_x given by the "Balducci" conventional estimator.

Table 5.26 The "Balducci" conventional estimator:
95% confidence intervals for population q_x

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.2024408	.2030248	.2021294	.2027068
b = 1	.2014789	.2020843	.2017920	.2023605
b = 0	.2006245	.2012109	.2008948	.2015021
b = -1	.1995819	.2001706	.1997758	.2003848
c = 1.1	.2012137	.2018205	.2009778	.2015518
c = 1.05	.2011513	.2017599	.2010345	.2016317

It will be seen that the population value of q_x only falls within the confidence intervals in 2 out of the 12 simulations, namely where the Balducci mortality assumption applies in the underlying population.

For all the other simulations (in which the population force of mortality had a more positive gradient with increasing age), the estimated value of q_x is greater than the true value.

This suggests that, in these circumstances, the "Balducci" conventional estimator is positively biased.

This is contrary to the impression given in London (1988) where the "actuarial estimator" is defined by the "full data" formula (London 1988 page 128), which is of course the Balducci conventional estimator, and is subsequently stated to be negatively biased (London 1988 page 129) when "enders" are involved. In discussing the bias and consistency of this estimator, London refers to Breslow and Crowley (1974) who did not in fact consider the full data actuarial estimator (nor a model which admits the possibility that lives may enter observation after the beginning of the year of age) and to Broffitt (1984) whose simulation results involving the full data actuarial estimator *but excluding the possibility that lives may enter observation after the beginning of the year of age* are reasonably consistent with a negative bias. Broffitt considers just two population distributions: either a "level deaths" mortality distribution (associated with a similar censoring distribution) or a "constant μ" mortality distribution (also associated with a similar censoring distribution).

Broffitt also considers a model in which lives can enter observation after the beginning of the year of age, but the results are reported in a form which does not appear to allow bias to be identified as negative or positive. London also implies that there are other references which would apparently confirm that the full data actuarial estimator is negatively biased, but does not specify these.

As commented in Section 1.15, it seems likely that the bias of an estimator will be affected by the values of all the parameters involved in defining the environment in which it is applied, including the parameters governing entry and withdrawal, so that it is probably not enough to simply state without qualification that an estimator is positively biased or negatively biased.

Hoem (1984) advocates the estimation of q_x by applying the maximum likelihood estimator using the "constant μ" assumption. This combination of criterion and mortality assumption leads of course to the familiar estimator for μ involving the central exposed-to-risk as derived in Section 2.22 and as summarised later in this section in equation (5.3).

Table 5.27 shows, for the 12 simulations, the 95% confidence limits for the population q_x given by the "constant μ" maximum likelihood estimator.

It will be seen that the population value of q_x falls within the confidence intervals for 8 out of the 12 simulations, the exceptions being the 2 simulations assuming a Balducci mortality distribution in the population, and one each of the simulations assuming population mortality with b = 1 ("level deaths") and b = 2.

Table 5.27 The "constant μ" maximum likelihood estimator:
95% confidence intervals for population q_x

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.2001049	.2006730	.1997988	.2003577
b = 1	.1997951	.2003916	.2001078	.2006663
b = 0	.1995708	.2001485	.1998515	.2004510
b = -1	.1991585	.1997437	.1993544	.1999592
c = 1.1	.1998879	.2004810	.1996732	.2002330
c = 1.05	.1999527	.2005522	.1998394	.2004280

A better performance from the "constant μ" maximum likelihood estimator compared with the Balducci conventional estimator might be expected, given that the mortality distribution assumed in the estimator is generally less remote from that actually applying in the simulated population.

However it may also be the case that the use of the maximum likelihood criterion gives an estimator which copes better in the presence of a different mortality distribution to that assumed in the estimator, than is the case if the implication-A criterion is used to create a conventional estimator. Some insight into this possibility might be gained by examining the performance of the conventional estimator which incorporates the "constant μ" assumption and the maximum likelihood estimator which incorporates the Balducci assumption.

Table 5.28 shows, for the 12 simulations, the 95% confidence limits for the population q_x given by the "constant μ" conventional estimator. It will be recalled that the combination of this estimation method and mortality assumption leads to an equation for q_x requiring an iterative solution, as set out for example in equation (1.28). (It should not be confused with the familiar estimator just considered, involving the central exposed-to-risk, which arises when the maximum likelihood method is used in combination with the "constant μ" mortality assumption).

It is seen that the population value of q_x falls within the confidence intervals for 4 out of the 12 simulations, including the two simulations which assume a "constant μ" mortality distribution in the population (b = 0).

Table 5.28 The "constant μ" conventional estimator:
95% confidence intervals for population q_x

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.2013824	.2019571	.2010737	.2016456
b = 1	.2004263	.2010240	.2007353	.2012974
b = 0	.1995766	.2001567	.1998453	.2004434
b = -1	.1985417	.1991210	.1987303	.1993344
c = 1.1	.2001617	.2007613	.1999276	.2004931
c = 1.05	.2000969	.2007000	.1999821	.2005729

Table 5.29 shows, for the 12 simulations, the 95% confidence limits for the population q_x given by the Balducci maximum likelihood estimator. This estimator also requires an iterative calculation, which can be achieved using equations (3.61) and (3.63) with b = -1 inserted.

Table 5.29 The Balducci maximum likelihood estimator:
95% confidence intervals for population q_x

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.1986417	.1992012	.1983379	.1988841
b = 1	.1989611	.1995502	.1992680	.1998227
b = 0	.1993486	.1999253	.1996415	.2002364
b = -1	.1995723	.2001598	.1997770	.2003781
c = 1.1	.1993949	.1999817	.1992050	.1997580
c = 1.05	.1995945	.2001868	.1994800	.2000647

It is seen that the population value of q_x falls within the confidence intervals for 5 out of the 12 simulations, including the two simulations which assume a Balducci mortality distribution in the population (b = -1).

These observations will now be summarised: when a conventional estimator is used, the population value of q_x falls within the confidence intervals for 2 out of the 12 simulations if the Balducci mortality assumption is made and within the confidence intervals for 4 out of the 12 simulations if the "constant μ" mortality assumption is made; if a maximum likelihood estimator is used, the population value of q_x falls within the confidence intervals for 5 out of the 12 simulations if the Balducci mortality assumption is made and within the confidence intervals for 8 out of the 12 simulations if the "constant μ" mortality assumption is made.

The apparent conclusion to be drawn from these simulations appears to be that, not only is a better performance obtained when the "constant μ" assumption is made and not the Balducci assumption, as might be expected given that the mortality distribution assumed in the estimator will then be generally less remote from that actually applying in the population, but also the maximum likelihood estimator appears to cope better in the presence of a different mortality distribution to that assumed in the estimator, than does the conventional estimator. However it must be borne in mind that these results may vary if the common assumptions underlying all the simulations are altered, or if different mortality assumptions are made in association with the maximum likelihood criterion or the implication-A criterion (which leads to the conventional estimator).

Thus it appears that, in terms of performance, the "constant μ" maximum likelihood estimator is to be preferred in general application to the "Balducci" conventional estimator. However, it is interesting to speculate whether there are any other estimators making a fixed mortality assumption which might be used in preference to the "constant μ" maximum likelihood estimator or the "Balducci" conventional estimator. It will be noted that both of the latter estimators are also time-count estimators, which accounts for the simplicity of their evaluation, ie involving the counting of exposure time.

This may suggest that the time-count estimator assuming the Gompertz distribution with $c = 1.1$ might provide a further improvement in general performance, by virtue of its more generally realistic mortality assumption.

Table 5.30 shows, for the 12 simulations, the 95% confidence limits for the population q_x given by the "Gompertz 1.1" time-count estimator. (The calculation of this estimator is summarised in equations (5.4) and (5.5) which follow shortly).

It will be seen that the population value of q_x falls within the confidence intervals for 11 of the 12 simulations, the sole exception being one of the simulations assuming a population mortality distribution with $b = 2$.

Table 5.30 The "Gompertz 1.1" time-count estimator:
95% confidence intervals for population q_x

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.1995646	.2001340	.1992578	.1998174
b = 1	.1995263	.2001222	.1998389	.2003995
b = 0	.1995622	.2001431	.1998498	.2004514
b = -1	.1994150	.2000038	.1996151	.2002199
c = 1.1	.1997669	.2003612	.1995608	.2001197
c = 1.05	.1998876	.2004870	.1997749	.2003636

However it may be the case that this better performance of the "Gompertz 1.1" time-count estimator compared with, say, the "constant μ" maximum likelihood estimator is obtained at the cost of a more complicated estimation calculation. This aspect will now be examined.

The "constant μ" maximum likelihood estimator is calculated as follows:

$$\mu = \frac{D}{\sum_N (t_i - s_i)}, \qquad \text{where} \quad q_x = 1 - e^{-\mu} \tag{5.3}$$

The "Gompertz 1.1" time-count estimator is calculated as follows (with c = 1.1):

$$B' = \frac{\sum_D \frac{1}{c^{t_i}}}{\sum_N (t_i - s_i)} \qquad \text{where} \quad \mu_{x+t} = B'c^{x+t} \tag{5.4}$$

and

$$q_x = 1 - h^{c-1} \qquad \text{where} \quad h = \exp\left(-\frac{B'}{\log c}\right) \tag{5.5}$$

It will be seen that the "Gompertz 1.1" time-count estimator is slightly more complicated to calculate than the "constant μ" maximum likelihood estimator, as indicated by formulae (5.3), (5.4) and (5.5) but with modern aids to calculation the differences, and in particular the adjustments required to the deaths in calculating the numerator of B', do not seem to represent a complication of any great significance.

It is also interesting to examine the general performance of the maximum likelihood

estimator with the fixed assumption of the Gompertz distribution with c = 1.1 .

Table 5.31 shows, for the 12 simulations, the 95% confidence limits for the population q_x given by the "Gompertz 1.1" maximum likelihood estimator. (The calculation of this estimator is summarised in equations (5.6) and (5.7) which follow shortly).

Table 5.31 The "Gompertz 1.1" maximum likelihood estimator: 95% confidence intervals for population q_x

Pop. distn.	ASPSIM		ASPMMSIM	
parameter	Lower limit	Upper limit	Lower limit	Upper limit
b = 2	.1999895	.2005586	.1996832	.2002441
b = 1	.1996788	.2002745	.1999915	.2005501
b = 0	.1994496	.2000308	.1997341	.2003312
b = -1	.1990348	.1996207	.1992315	.1998352
c = 1.1	.1997689	.2003647	.1995545	.2001146
c = 1.05	.1998342	.2004333	.1997210	.2003094

It is seen that the population value of q_x falls within the confidence intervals for 10 of the 12 simulations, the exceptions being the 2 simulations assuming a Balducci population mortality distribution.

We will consider whether the calculations involved in evaluating this estimator are more or less complicated than those needed to evaluate the "Gompertz 1.1" time-count estimator.

The "Gompertz 1.1" maximum likelihood estimator is calculated as follows (with c = 1.1):

$$B' = \frac{D}{\frac{1}{\log c}\sum_{N}(c^{t_i} - c^{s_i})} \quad \text{where} \quad \mu_{x+t} = B'c^{x+t} \tag{5.6}$$

and

$$q_x = 1 - h^{c-1} \quad \text{where} \quad h = \exp\left(-\frac{B'}{\log c}\right) \tag{5.7}$$

It can be seen that the calculation of the "Gompertz 1.1" maximum likelihood estimator is more complicated than that of the "Gompertz 1.1" time-count estimator, adjustments being

involved in the calculation of the "exposed-to-risk" of all lives, as shown in formula (5.6) .

Obviously there would be no problem if the data and calculations were dealt with on the computer. The calculations would be straightforward to program, particularly as an iterative method is not involved.

On balance, one can argue that the "Gompertz 1.1" time-count estimator is marginally to be preferred to the "Gompertz 1.1" maximum likelihood estimator, since it performs slightly better in the simulations and is somewhat simpler to calculate. And, as we have seen, the performance of the "Gompertz 1.1" time-count estimator appears better in our simulations than the "constant μ" maximum likelihood estimator, and it is only marginally more complicated to calculate.

5.27 Effect of making wrong mortality assumptions in estimators

In the previous section, we considered the performances of certain estimators which make fixed mortality assumptions when they are applied to populations in which other mortality assumptions apply. Predictably it was found that a disparity between the mortality law applicable in the population and that assumed by the estimator leads to a reduction in performance as measured by the frequency with which supposed 95% confidence intervals based on the estimator contained the population value of q_x. The reduced frequency with which such intervals contain the population value of q_x reflects the bias introduces into the estimator by the discrepancy in the mortality law.

A more comprehensive view of this effect can be obtained by studying the simulation printouts contained in Appendix II, which show for each simulation the values of estimators for a range of mortality assumptions, together with estimated standard deviations and confidence intervals.

As an example, let us consider the printout for Simulation 2A (Appendix II) which is based on the results of 500 runs of the program **ASPSIM** where the mortality law in the population is "level deaths" ie the rectangular hyperbolic mortality distribution with $b = 1$.

A key to the abbreviations used in the printouts is provided in Appendix II.

It is seen that the population value of q_x falls within the confidence interval for all estimators which assume the "level deaths" ($b = 1$) mortality law.

However when the rectangular hyperbolic mortality distribution with $b = 2$ is assumed, only

the confidence interval based on the log-estimator contains the population q_x.

When the "constant μ" assumption (b = 0) is made, the confidence interval based on the "constant μ" maximum likelihood estimator, and all the coincident n-estimators, contains the population q_x but the confidence intervals based on the conventional estimator or the implication-B estimator do not.

When the Balducci assumption (b = -1) is made, none of the estimators provide "95%" confidence intervals which contain the population q_x.

When the "Gompertz 1.1" assumption is made (c = 1.1), the confidence intervals based on the one-parameter maximum likelihood estimator (which is also the log-estimator) and the time-count estimator contain the population q_x, as does very marginally that based on the implication-B estimator, whereas the confidence interval based on the conventional estimator does not. The "Gompertz 1.1" assumption lies approximately somewhere between the b = 1 and b = 0 assumption; indeed the approximate formulae (3.107) and (3.108) linking b and c indicate that a value of b = 0.42715 corresponds approximately to c = 1.1 when $q_x = 0.2$.

Further examination of the Simulation 2A printout shows that the average observed values of the conventional estimator and the implication-B estimator appear to decrease monotonically as b increases over the range from b = -1 to b = 2; this suggests that there is likely to be a value of b which, if assumed in the estimator, will produce an estimator with zero bias, and that the absolute value of the bias increases as the assumed value of b diverges from this value, either positively or negatively, within the range considered.

The simplest interpretation of the behaviour of the value of any of the rectangular hyperbolic n-estimators shown for Simulation 2A, as b varies from b = -1 to b = 2, is that there is a turning point which is either a maximum or minimum in the range b = -1 to b = 2.

Thus for example, on the simplest interpretation, the average observed values of the time-count estimator and log-estimator appear to reach a minimum somewhere between b = 0 and b = 2, while for example the average observed value of the one-parameter maximum likelihood estimator appears to reach a maximum somewhere between b = -1 and b = 1.

One must bear in mind the dangers of interpreting the behaviour of a function from just four measurements of the function: the function could behave with more subtlety than can be portrayed by this small number of measurements. However it seems unlikely that the averaging of 500 individual runs in each simulation would produce a function that behaves

with greater subtlety than the simple turning point that has been hypothesised here.

It is interesting that nearly all the rectangular hyperbolic n-estimators in the other runs of **ASPSIM** (Simulations 1A, 3A, 4A, 5A, 6A) appear to exhibit the same behaviour. The one slight exception is Simulation 4A where the population is assumed to obey the Balducci mortality assumption ($b = -1$) and the average observed values of the log-estimator, one-parameter maximum likelihood estimator and the n-estimators with $n = 2$ and $n = 3$ all appear broadly to decrease in the range $b = -1$ to $b = 2$.

Most probably a turning point does occur but falls either outside the range $b = -1$ to $b = 2$ or just within its edges. The behaviour of the figures may suggest that, for this simulation, a minimum in the average observed value of the log-estimator occurs in the region of $b = 2$ and that, for the other three estimators, a maximum occurs in the region of, or below, $b = -1$.

It will be noted that in the range considered for the value of b which is assumed in the estimator, namely $b = -1$ to $b = 2$, the corresponding average observed values of the log-estimator ($n = 0$) change relatively little. Larger changes, but still relatively modest, are shown by the one-parameter maximum likelihood estimator ($n = 1$) and the time-count estimator ($n = -1$) perhaps with the one-parameter maximum likelihood estimator being marginally superior. When $n = -2$, $n = 2$ and $n = 3$ are considered, the average observed values of the estimators appear broadly to change more significantly over the range of b considered, as b changes.

A relatively modest change in the values of an estimator as the assumption in the estimator concerning b changes, indicates that the estimator should perform relatively robustly if the wrong assumption for b is made. These simulations seem to suggest that, within the range of b discussed, the log-estimator, the one-parameter maximum likelihood estimator and the time-count estimator should perform quite favourably in this regard. The conventional estimator, whose bias appears to change monotonically with changes in b, appears to behave less favourably in this regard over the range considered, and this perhaps sheds further light on the results of the comparisons made in Section 5.26 between the Balducci conventional estimator and the "constant μ" maximum likelihood estimator.

The values of the implication-B estimator are broadly similar to those of the conventional estimator and so the general comments relating to the conventional estimator apply also to the implication-B estimator.

The n-estimators with $n = -2$, $n = 2$ and $n = 3$ appear to perform satisfactorily if the correct value of b is assumed, but the more the value of n diverges from the values $n = -1$, 0 or

n = 1, the less robust the estimators appear in coping with a wrong assumption of the value of b.

Of course in interpreting these simulation results, it must again be borne in mind that one particular set of assumptions has been used throughout with regard to the number of lives in the investigation, the number and entry point of "new entrants", the rate of mortality, the rate of withdrawals and the distribution of withdrawals, and that variation in these details might cause modification in the observed behaviour of estimators and possibly in the comparative performance of different estimators. There are so many parameters defining the scenario of the investigation that it would require a more extensive piece of research to investigate the effects of varying them all.

It is also of interest to consider how the method of moments estimator and the conventional estimator compare when the mortality assumption made in the estimator differs from that applicable in the population. Table 5.32 shows the difference between the average observed values of the conventional estimator and the method of moments estimator for the 24 pairs of mortality assumptions, applying in the population and assumed in the estimators, that were observed in the six simulations using program ASPMMSIM.

Table 5.32 Program ASPMMSIM:
Average observed values of conventional estimator minus method of moments estimator

Popn. distn.	Parameter assumed in estimator			
parameter	b = 1	b = 0	b = -1	c = 1.1
b = 2	.0001484	.0002855	.0004195	.0002279
b = 1	.0000005	.0001415	.0002791	.0000820
b = 0	-.0001425	.0000015	.0001414	-.0000598
b = -1	-.0002766	-.0001311	.0000101	-.0001934
c = 1.1	-.0000903	.0000517	.0001902	-.0000088
c = 1.05	-.0001138	.0000294	.0001688	-.0000313

It is seen that the absolute difference between the average observed values of the conventional estimator and the method of moments estimator increases as the disparity between the mortality assumption applying in the population and the mortality assumption assumed in the estimator increases. It is of further interest to investigate whether the value given by the conventional estimator or the value given by the method of moments estimator is likely to be closer to the true population value when there is a disparity between the

mortality assumption applying in the population and the mortality assumption assumed in the estimator.

Tables 5.33 and 5.34 show the differences between the average observed values of the conventional estimator and the product limit estimator and between the average observed values of the method of moments estimator and the product limit estimator respectively. The product limit estimator has been adopted as a virtually unbiased estimator of the true population rate of mortality so that, if because of random fluctuations the simulated data is not exactly representative of the population distribution, the effect of these fluctuations on the estimated values of q_x will hopefully be largely eliminated in the comparisons of the respective estimators with the product limit estimator, which would not be the case if the population value of q_x were used.

Table 5.33 Program ASPMMSIM:
Average observed values of conventional estimator minus product limit estimator

Popn. distn.	Parameter assumed in estimator			
parameter	b = 1	b = 0	b = -1	c = 1.1
b = 2	.0006788	.0015031	.0025616	.0011162
b = 1	.0000248	.0008520	.0019118	.0004635
b = 0	-.0008332	-.0000084	.0010458	-.0003973
b = -1	-.0019070	-.0010848	-.0000369	-.0014742
c = 1.1	-.0004709	.0003537	.0014082	-.0000350
c = 1.05	-.0005714	.0002541	.0013097	-.0001349

Table 5.34 Program ASPMMSIM:
Average observed values of method of moments estimator minus product limit estimator

Popn. distn.	Parameter assumed in estimator			
parameter	b = 1	b = 0	b = -1	c = 1.1
b = 2	.0005304	.0012176	.0021421	.0008883
b = 1	.0000243	.0007105	.0016327	.0003815
b = 0	-.0006907	-.0000099	.0009044	-.0003375
b = -1	-.0016304	-.0009537	-.0000470	-.0012808
c = 1.1	-.0003806	.0003020	.0012180	-.0000262
c = 1.05	-.0004576	.0002247	.0011409	-.0001036

It is seen that, when there is a disparity between the mortality assumption applying in the population and the mortality assumption assumed in the estimator, the average observed value of the method of moments estimator is slightly closer to the average observed value of the product limit estimator than is the average observed value of the conventional estimator, the disparity from the average product limit estimator value in the case of the method of moments estimator being of the order of 80–85% of that applicable in the case of the conventional estimator, and always of the same sign in the simulations.

Thus we can conclude that, when the mortality assumption in the estimator is the same as that applicable in the population, the values of the conventional estimator and the method of moments estimator are extremely close, and that when there is a disparity between the mortality assumption applying in the population and the mortality assumption assumed in the estimator, the two estimators behave in a broadly similar way although the method of moments estimator appears to give a value of q_x which is slightly closer to the true population value of q_x, than the conventional estimator, but not spectacularly so. It is also of interest that the two estimators seem likely to be biased in the same direction, ie either both negatively biased or both positively biased.

It must be borne in mind that fairly extreme values of mortality and withdrawal rates have been considered, deliberately to emphasize any effects. Also, it must again be remembered that the possibility exists that these conclusions could be subject to modification if the common assumptions underlying all the simulations were varied.

5.28 Evidence of bias in estimators incorporating the correct mortality assumption

Examination of the 95% confidence intervals indicates that, for all the estimators calculated from the simulated data which assume a one-parameter mortality law, bias is not discernible against the background of random fluctuations when the correct mortality assumption has been made (with the inconsequential exception of the approximated "operational moment relations" estimators suggested by Hoem (1984), as discussed in Section 5.20). Of course it must be borne in mind that modification of the parameters assumed for all the simulations could modify this situation, and in particular a reduction in the numbers of lives observed during the year of age, n_1 and n_2. This appears a pertinent area for further research.

However some subtle effects have been noted in the simulation results which would tend to imply the existence of low levels of bias even when the correct mortality assumption has been made; this implication arises where it is noted that one method of estimation appears to give values that tend to be higher than values given by another method, even when both calculations incorporate the correct mortality assumption.

In particular, it has been noted that, in the simulations, the average observed values of n-estimators incorporating the correct mortality assumption showed an apparent tendency to decrease as n increased (see Section 5.25). (It will be recalled that n-estimators are g-estimators in which the g-function takes the form $(\mu_{x+t})^n$, as discussed in Section 4.27).

However, the actual amount of possible bias implied by these simulation results is very small, so that any such bias is not readily apparent from examination of the 95% confidence intervals, the random fluctuations being dominant. This is an area where further simulation studies could be undertaken to seek additional evidence.

5.29 Tailpiece: the anachronistic "direct method"

In 1986, the Institute of Actuaries introduced the "direct method" into its examination syllabuses. As described in Puzey (1986), the "direct method" involves the use of a computer to count initial or central exposed-to-risk directly, and it could be argued that this is an anachronism, representing the use of late twentieth century technology to carry out methods evolved to meet the computational limitations of the nineteenth century. These computational limitations have to a great extent been swept away, so that there is no computational reason to continue using the Balducci assumption to estimate q_x, nor indeed the "constant μ" assumption to estimate μ_x or m_x.

If the data is available on computer in a form which allows the "direct method" to be carried out, there is available a number of arguably more attractive methods of analysis, including a number of the methods discussed in this chapter. Some of these estimators make relatively few additional computational demands, for example the time-count and maximum likelihood estimators for the Gompertz assumption with an assumed value of c, and the product limit estimator.

As discussed in Section 5.26, the Gompertz time-count and maximum likelihood estimators, with c assumed equal to 1.1, appear to provide simple but effective estimators which generally appear to give better estimates than the two traditional estimators based on deaths divided by initial or central exposed-to-risk. As a further refinement, the value assumed for c could of course be chosen from knowledge of populations similar to that under investigation.

In Section 5.23, it was noted that the virtually unbiased product limit estimator appeared to be an attractive alternative to any of the estimators which required the assumption of a one-parameter mortality law, at least at the sample sizes considered in the simulations. Further investigations would be advisable to see whether a reduction in sample size would

affect this comparison; possibly the use of fewer observations could make a mortality assumption more important.

Data prepared for the "direct method" would almost certainly be suitable for the non-iterative calculation of the product limit estimator, an estimator which hitherto has been omitted from the syllabus of the Institute of Actuaries, doubtless because it was not suitable for use with large volumes of data before the computer became available.

There are further approaches, some of which involve more complex and invariably iterative calculations, such as the two-parameter maximum likelihood estimators. However the two-parameter maximum likelihood estimators in particular also extract additional information from the data about the mortality distribution, and they may be considered attractive for this reason. They also avoid the consequences of making a poor choice of an assumed distribution parameter.

The inclusion in 1986 of the "direct method" as the only computer based approach in the syllabus of the Institute of Actuaries might be seen as an illustration of "exposures per life" having gained an unjustified grip on the thinking of actuaries, a possibility pointed out in Section 2.7.

London (1983) implied that "the actuarial tradition of expressing estimated rates as the ratio of observed decrements to a measure of exposure" had tended to exclude other procedures from consideration by actuaries.

Modern computing technology offers the opportunity to escape from the prison of using only traditional exposed-to-risk methods to estimate mortality rates from observed data, and perhaps the simulations discussed in this chapter give an indication of some of the attractive alternatives.

CHAPTER VI

Conclusions

6.1 Introduction

Conclusions arising from the work will be given under six broad headings:

The alleged flaw in the conventional estimator

Further aspects of the conventional estimator and aspects of other estimators

The rectangular hyperbolic mortality distribution

Two-parameter mortality rate estimators

A general theory of mortality rate estimators

Areas for further research

6.2 The alleged flaw in the conventional estimator

The conventional estimator appears to have an acceptable theoretical basis giving results which would be similar to those given by a method of moments estimator, if it could actually be calculated, when the correct mortality assumption is made. This conclusion is based on the following considerations:

(a) An analysis of the mechanics of the calculations of the conventional estimator and the method of moments estimator has been presented in Section 2.10 from which it can be seen that the two estimators would be likely to produce similar values when the correct mortality assumption is being made.

(b) A new rationale of the method of calculating the conventional estimator has been identified in Section 2.18 which does not rely on explaining the estimator as a modified, or even degraded, version of the method of moments estimator, and which as shown in Section 2.20 is analogous to the calculation of a money-weighted rate of

return in a financial transaction. This new rationale appears intuitively attractive.

(c) The simulation studies reported in Chapter 5 suggest that the performance of the conventional estimator is satisfactory and is not compromised by alleged theoretical flaws as suggested by Hoem (1984). The performance of the conventional estimator in the simulations is discussed in particular in Sections 5.19, 5.21, 5.23, 5.26 and 5.27. It must be borne in mind that, because of the volume of analysis that would be required, it has not been possible to consider the effect of changing some parameters governing the simulated scenarios, but it is felt that further research covering other parameter values is unlikely to require revision of these conclusions.

It is therefore concluded that Hoem (1984) is wrong to describe the conventional estimator as flawed.

6.3 Further aspects of the conventional estimator and aspects of other estimators

Further conclusions of note relating to the conventional estimator or other estimators are the following:

(a) Simulation studies suggest that even when the wrong mortality assumption is made, the results given by the conventional estimator are just marginally more biased than those that would be given by a method of moments estimator (see Section 5.27).

(b) Simulation studies reported in Section 5.26 do suggest however that the "constant μ" maximum likelihood estimator may generally perform somewhat better than the Balducci conventional estimator under the mortality distributions likely to be encountered in practice, which will generally be different to those assumed in the estimator, and that this is due not only to the mortality assumption in the estimator but also to the statistical criterion used. This would confirm the recommendations of Hoem (1984) and of Roberts (1987) that the "constant μ" maximum likelihood estimator be used in preference to the Balducci conventional estimator, although the argument preceding the recommendation in Hoem (1984), that the conventional estimator is theoretically flawed, is not accepted.

(c) Simulation studies also suggest that the time-count estimator, developed in this thesis, is likely, when the Gompertz mortality law with $c = 1.1$ is assumed, to perform even better than the "constant μ" maximum likelihood estimator under the mortality distributions likely to be encountered in practice with little sacrifice of computational simplicity (see Section 5.26). A further refinement would be to choose

the value for c using knowledge of populations similar to that under investigation. Also in the simulation studies, the maximum likelihood estimator assuming the Gompertz law with c equal to 1.1 performed almost as well as the corresponding time-count estimator and is only marginally more complicated to calculate (see Section 5.26).

(d) The "direct method", in which a computer is used to count traditional exposed-to-risk directly, to the exact day, is argued to be a poor use of computer technology as, it is contended, there are more attractive estimators, including those mentioned in the previous paragraph, that can be calculated with a computer using data in a format similar to that required for the "direct method" (see Section 5.29).

(e) In the course of the research relating to the conventional estimator, consideration was also given to the calculation of exposed-to-risk by means of "exposures per life". As summarised in Section 2.7, this examination has readily confirmed the view that the exposure which an *individual* life receives under such systems cannot be expected to have a rational explanation in terms of the behaviour of that life, as also commented for example by Batten (1978) in connection with "prospective existings".

(f) Examination of the 95% confidence intervals suggests that, for all the estimators studied in the simulations which assume a one-parameter mortality law, bias is not discernible against the background of random fluctuations when the correct mortality assumption has been made (with one inconsequential exception, discussed in paragraph (j) below), although comparisons of average estimator values do give some subtle indications that bias of relatively trivial levels could be present in some estimators (see Section 5.28). Of course it must be borne in mind that a reduction in the numbers of lives observed during the year of age might alter the conclusion that bias is generally unimportant when the correct mortality assumption is made.

(g) In the course of research into the conventional estimator, a related estimator of mainly theoretical interest was evolved and designated the "implication-B" estimator (see Section 2.14). The simulation studies indicate that the implication-B estimator performs satisfactorily (see Sections 5.22, 5.23 and 5.27).

(h) The log-estimator is a further estimator developed in this thesis (see Sections 3.16 and 4.8); the log-estimator performs well in the simulation studies (see Sections 5.22, 5.23, 5.25 and 5.27).

(i) In general, simulation studies suggest that the maximum likelihood estimator, log-estimator and time-count estimator may be more robust, if the wrong mortality

assumption is made, than in general the conventional estimator or the implication-B estimator (see Section 5.27).

(j) It is argued in Sections 1.9 and 2.9 that the approximated "operational moment relations" estimators of q_x, suggested by Hoem (1984), are unsatisfactory as the inherent approximation will introduce a negative bias and, indeed, simulation studies using the correct mortality assumption in the estimator have confirmed the presence of a marked negative bias (see Section 5.20).

(k) It is shown in Section 2.24 that an alternative rationale for the derivation of a maximum likelihood estimator of a mortality parameter can be obtained which involves the reconciliation of the rates of change, with respect to changes in the mortality parameter, of the numbers of lives entering and leaving the mortality investigation.

(l) Extension of the analogy between the calculation of the conventional estimator and a money-weighted rate of return shows that the calculation of the product limit estimator can be viewed as analogous to that of a time-weighted rate of return (see Section 2.20).

6.4 The rectangular hyperbolic mortality distribution

A valuable conclusion, discussed in Chapter 3, is that it is possible to formulate the rectangular hyperbolic mortality distribution:

$$\mu_{x+t} = \frac{1}{a - bt}$$

which is a two-parameter mortality law embracing three well-known mortality assumptions as special cases, namely the uniform distribution of deaths assumption, the "constant μ" assumption and the Balducci assumption.

Use of this law enables the equations defining a number of estimators to be expressed in simple and generalised forms.

6.5 Two-parameter mortality rate estimators

The rectangular hyperbolic mortality distribution allows the development of a new

maximum likelihood estimator involving two parameters, one relating to the general level of the mortality rates and the other relating to the general shape of the mortality curve (see Section 3.16) and this estimator has performed satisfactorily in the simulation studies (as discussed in Section 5.24). A tenuous and slightly ambiguous suggestion of minor positive bias may have been due to random effects.

The two-parameter maximum likelihood estimator based on the Gompertz mortality law has also been considered (see Section 3.17) and in the simulations there were indications of minor negative bias that appeared more distinct and unambiguous in certain circumstances than the tenuous indications of slight positive bias mentioned above in the case of the two-parameter rectangular hyperbolic maximum likelihood estimator (see Section 5.24).

The attractions of these two-parameter estimators include the features that they require a very minimal assumption about the mortality law applicable in the population and that one of the parameters relates in general terms to the *shape* of the mortality curve over the year of age; this latter feature is not provided by any mortality rate estimator requiring the assumption of a one-parameter mortality law, nor indeed by the product limit estimator.

6.6 A general theory of mortality rate estimators

Perhaps the most important conclusion in this thesis is that it is possible to develop a general theory of mortality rate estimators which permits most, if not all, mortality rate estimators assuming a parametric mortality law to be derived by a common method (see Section 4.1 and subsequent sections).

An important implication of this theory is that all estimators derived by its application, assuming a one-parameter mortality law, are asymptotically unbiased if the correct assumption about the mortality distribution in the population has been made (see Section 4.13).

The general theory has permitted new or previously unrecognised mortality rate estimators to be identified, such as the time-count estimator assuming the Gompertz mortality law for a given value of c (see Section 4.9), and the log-estimator for various assumptions (see Section 4.8).

Also, the general theory allows the mortality assumptions under which estimators based on different statistical criteria give identical values to be identified. For example it can be readily seen (Section 4.7) that, if the uniform distribution of deaths is assumed, the conventional estimator and the maximum likelihood estimator are identical, a result first

identified earlier in the thesis by more laborious means (Section 2.23).

6.7 Areas for further research

As summarised in the previous section, an important theoretical result presented in this thesis is that all estimators, assuming a one-parameter mortality law, which can be produced using the general theory are asymptotically unbiased when the correct mortality law has been assumed (Section 4.13). As noted in Section 4.13, an even more powerful result would be that such estimators are also consistent under these circumstances, but preliminary investigations suggest that such a proof, if indeed these estimators have this property of consistency, would be analytically more demanding than the comparatively simple proof of asymptotic unbiasedness presented in Section 4.13. As stated in Section 4.13, it is intended that further research will be undertaken to obtain such a proof, if the property of consistency does indeed apply to these estimators.

There are a number of areas in which further simulation studies would be likely to yield important new insights or clarify uncertainties remaining from the present studies. Fortunately, the availability of ever faster personal computers at moderate cost makes it possible to carry out further simulations using considerably higher numbers of runs than was possible previously, and the increase in the number of runs should allow more clear-cut distinctions to be drawn between genuine effects on the one hand and random fluctuations on the other. The use of greatly increased numbers of runs should also allow the standard deviations of estimator values to be better estimated.

As has been previously pointed out, all the simulation studies reported in Chapter 5 have been conducted assuming the same values for certain parameters, namely the following values as quoted in Section 5.14:

$q_x = 0.2$	$w_x = 0.4$	$r = 3$
$n_1 = 10000$	$n_2 = 10000$	no. of runs = 500

Clearly the conclusions drawn in Chapter 5 would be broadened by investigations into the effects of changing the values of q_x, w_x, r, n_1 and n_2, although it is felt that the conclusions presented in Chapter 5 about the relative behaviour of the estimators are likely to remain broadly valid over a wide range of values of these parameters.

It would be especially instructive to investigate whether bias in the estimates of q_x becomes an important issue, when the estimator incorporates the correct mortality assumption, if smaller numbers of lives are observed, ie when smaller values of n_1 and n_2 apply.

In Section 5.23, it was noted that the virtually unbiased product limit estimator appeared to be an attractive alternative to any of the estimators which required the assumption of a one-parameter mortality law, at least at the sample sizes considered in the simulations.

Further simulation studies could show whether a reduction in sample size would affect this comparison; possibly the use of fewer observations could make a mortality assumption more important.

The simulations reported in Chapter 5 did not include the use of g-estimators where the g-function involved the factor $\frac{1}{P(t)}$, because these estimators had not been considered at the time the simulations were planned and the programs written. Simulation studies, extended to cover this group of estimators, should be considered to facilitate comparisons of these estimators with those previously studied. These studies would also cast light on the extent of the negative bias which is inherent in these estimators of q_x, even when the correct mortality assumption has been made, and on the circumstances, if any, in which this bias is sufficiency severe to be a serious difficulty.

In the discussion of n-estimators calculated from the simulated data and incorporating the correct mortality assumption, it was noted that their average observed values showed an apparent tendency to decrease as n increased (see Section 5.25). This is another area where further simulations could be of great value, in order to confirm that this apparent tendency, with its important implications concerning bias, is genuine and to investigate whether the effect is modified by changes in the assumed parameters.

A number of apparent effects were noted in Section 5.24, in connection with the estimation of q_x using the two-parameter maximum likelihood estimators assuming the rectangular hyperbolic mortality distribution ("ML H") and the Gompertz mortality distribution ("ML G"), and further investigations were suggested. Thus, the following apparent phenomena were highlighted for further investigation:

(a) For a given set of mortality data, the value of q_x given by the ML H estimator was greater than the value given by the ML G estimator *in all but a very small number of cases*, the exceptions occurring when the population mortality corresponded to $b = 0$ and $c = 1$.

(b) There appeared to be a clear effect that the ML G estimator was subject to a distinct negative bias when used with populations subject to a mortality distribution of a distinctly rectangular hyperbolic shape (that is, with b of the order -1, 1, 2 when $q_x = 0.2$). There was also speculation that the ML H estimator might be subject to a slight positive bias, although the evidence was tenuous and a little ambiguous.

(c) There appeared to be a consistent tendency for the average value of the ML H estimator to be very slightly greater than that given by the corresponding one-parameter maximum likelihood estimator.

(d) The values of c estimated in evaluating the ML G estimator appeared to be positively biased.

Also comparisons of the standard deviations of the ML H estimator, the ML G estimator, the one-parameter maximum likelihood estimator and the product limit estimator yielded results in which a consistent pattern was not clear, and it would be interesting to repeat the investigation using simulations based on greatly increased numbers of runs, which would reduce the random effects in measuring the standard deviations.

As noted in Section 5.9, the construction of the two programs **ASPMOM** and **ASPMMSIM** would make it possible to study the derivation of mortality rates from a year of age in which there is a single fixed duration of entry and a single fixed duration of non-death exit applicable to all lives. It would be instructive to conduct simulations to study the degree to which bias occurs in these circumstances when the estimator incorporates the correct mortality assumption, and to identify the parameters which are particularly important in determining the extent of such bias.

In Section 4.30, brief attention was given to the extension of the "general theory" to the estimation of the parameters where a multiple-parameter mortality law applies in the population. There may be scope for further research here, to develop theory and make applications.

Despite the detail of the research reported in this thesis, there clearly remain many intriguing uncertainties still to be resolved. The availability of ever faster personal computers at modest cost provides the actuarial researcher with unprecedented opportunities, that previous generations could only have dreamt of, to investigate the mysteries of mortality rate estimation.

APPENDIX I

Derivation of Miscellaneous Results for the Rectangular Hyperbolic Mortality Distribution

A1.1 Introducing the rectangular hyperbolic mortality distribution

Firstly we will state the formulae for μ_{x+t} under respectively the "level deaths", "constant μ" and Balducci assumptions, from which it will be seen that these are all particular cases of the more general rectangular hyperbolic mortality distribution.

(a) Level Deaths Assumption

This is most conveniently stated as:

$$ {}_tq_x = t*q_x \qquad (0 \leq t \leq 1) \tag{A1.1} $$

which leads to the result:

$$ \mu_{x+t} = \frac{q_x}{1 - t*q_x} = \frac{1}{\frac{1}{q_x} - t} \qquad (0 \leq t \leq 1) \tag{A1.2} $$

(b) Constant μ Assumption

Obviously this can be directly stated as:

$$ \mu_{x+t} = \text{constant} \tag{A1.3} $$

(c) Balducci Assumption

This is most conveniently stated as:

$$ {}_{1-t}q_{x+t} = (1-t)*q_x \qquad (0 \leq t \leq 1) \tag{A1.4} $$

which leads to the result:

$$\mu_{x+t} = \frac{q_x}{1 - (1 - t)*q_x} = \frac{1}{\frac{1 - q_x}{q_x} + t} \qquad (0 \leq t \leq 1) \qquad \text{(A1.5)}$$

Clearly, we can express all of these results in the general form:

$$\mu_{x+t} = \frac{1}{a - bt} \qquad (0 \leq t \leq 1) \qquad \text{(A1.6)}$$

where immediately we can see that:

$$a = \frac{1}{\mu_x} \qquad \text{(A1.7)}$$

and we have:

b = −1 for the "Balducci" assumption

b = 0 for the "constant μ" assumption

b = 1 for the "level deaths" assumption.

A1.2 Expression for q_x when $b \neq 0$

We will now derive an expression for q_x under the rectangular hyperbolic distribution in terms of a and b, for $b \neq 0$.

In general:

$$q_x = 1 - \exp\left(- \int_0^1 \mu_{x+t}\, dt\right) \qquad \text{(A1.8)}$$

Let us consider the integral:

$$\int_0^1 \mu_{x+t}\, dt = \int_0^1 \frac{dt}{a - bt} = \frac{1}{-b} \int_0^1 \frac{dt}{t - \frac{a}{b}}$$

$$= - \frac{1}{b} \left[\log \left(t - \frac{a}{b}\right) \right]_0^1$$

$$= - \frac{1}{b} \log \left(\frac{a - b}{a}\right) \qquad \text{(A1.9)}$$

$$\Rightarrow \qquad q_x = 1 - \exp \left(\frac{1}{b} \log \left(\frac{a - b}{a}\right)\right) \qquad \text{(A1.10)}$$

$$\Rightarrow \qquad q_x = 1 - (1 - \tfrac{b}{a})^{\frac{1}{b}} \tag{A1.11}$$

A1.3 Expression for q_x when $b = 0$

When $b = 0$, we have:

$$q_x = 1 - e^{-\mu} = 1 - e^{\frac{-1}{a}} \tag{A1.12}$$

which also follows from:

$$q_x = \lim_{b \to 0} (1 - (1 - \tfrac{b}{a})^{\frac{1}{b}}) \tag{A1.13}$$

A1.4 Expressions for the parameter a in terms of b and q_x

We also have from equations (A1.11) and (A1.12) :

$$a = \frac{b}{1 - (1 - q_x)^b} \qquad \text{when } b \neq 0 \tag{A1.14}$$

$$a = \frac{-1}{\log (1 - q_x)} \qquad \text{when } b = 0 \tag{A1.15}$$

A1.5 Expressions for the parameters a and b in terms of μ_x and μ_{x+1}

A pair of expressions for a and b that can be useful in some applications are:

$$a = \frac{1}{\mu_x} \quad , \quad b = \frac{1}{\mu_x} - \frac{1}{\mu_{x+1}} \tag{A1.16}$$

These follow immediately from:

$$\mu_{x+t} = \frac{1}{a - bt} \qquad (0 \leq t \leq 1) \tag{A1.17}$$

A1.6 Concerning the second differential coefficient of l_{x+t}

We will now obtain the following results:

$$\frac{d^2 l_{x+t}}{dt^2} > 0 \qquad \text{for } b < 1 \tag{A1.18}$$

$$\frac{d^2 l_{x+t}}{dt^2} < 0 \qquad \text{for } b > 1 \tag{A1.19}$$

We know from life contingencies that:

$$\mu_{x+t} = -\frac{1}{l_{x+t}} \frac{dl_{x+t}}{dt} \tag{A1.20}$$

$$\Rightarrow \qquad \frac{dl_{x+t}}{dt} = -l_{x+t}\mu_{x+t} \tag{A1.21}$$

$$\Rightarrow \qquad \frac{d^2 l_{x+t}}{dt^2} = -\frac{dl_{x+t}}{dt}\mu_{x+t} - l_{x+t}\frac{d\mu_{x+t}}{dt}$$

$$= l_{x+t}(\mu_{x+t})^2 - l_{x+t}\frac{d\mu_{x+t}}{dt} \tag{A1.22}$$

But since:

$$\mu_{x+t} = \frac{1}{a - bt} \tag{A1.23}$$

we have:

$$\frac{d\mu_{x+t}}{dt} = \frac{b}{(a - bt)^2} \tag{A1.24}$$

$$\Rightarrow \qquad \frac{d^2 l_{x+t}}{dt^2} = (1 - b) * \frac{l_{x+t}}{(a - bt)^2} \tag{A1.25}$$

from which the results follow.

A1.7 Expressions for ${}_{t-s}p_{x+s}$

We will now obtain the following results:

for $b \neq 0$:

$${}_{t-s}p_{x+s} = \left(\frac{a - bt}{a - bs}\right)^{\frac{1}{b}} = \left(\frac{\mu_{x+s}}{\mu_{x+t}}\right)^{\frac{1}{b}} \tag{A1.26}$$

for $b = 0$:

$${}_{t-s}p_{x+s} = e^{\frac{-(t-s)}{a}} = e^{-(t-s)\mu} = (p_x)^{t-s} . \tag{A1.27}$$

Now
$$ {}_{t-s}p_{x+s} = \frac{{}_tp_x}{{}_sp_x} \tag{A1.28} $$

Firstly we will consider the case when $b \neq 0$. Now:

$$ {}_tp_x = \exp\left(-\int_0^t \mu_{x+r}\, dr\right) \tag{A1.29} $$

Let us consider the integral:

$$ \int_0^t \mu_{x+r}\, dr = \int_0^t \frac{dr}{a - br} = \frac{1}{-b}\int_0^t \frac{dr}{r - \frac{a}{b}} $$

$$ = -\frac{1}{b}\left[\log\left(r - \frac{a}{b}\right)\right]_0^t $$

$$ = -\frac{1}{b}\log\left(\frac{a - bt}{a}\right) \tag{A1.30} $$

$$ \Rightarrow \quad {}_tp_x = \exp\left(\frac{1}{b}\log\left(\frac{a - bt}{a}\right)\right) $$

$$ \Rightarrow \quad = \left(1 - \frac{b}{a}t\right)^{\frac{1}{b}} \tag{A1.31} $$

$$ \Rightarrow \quad {}_{t-s}p_{x+s} = \frac{{}_tp_x}{{}_sp_x} = \left(\frac{a - bt}{a - bs}\right)^{\frac{1}{b}} = \left((a - bt)*\frac{1}{a - bs}\right)^{\frac{1}{b}} = \left(\frac{\mu_{x+s}}{\mu_{x+t}}\right)^{\frac{1}{b}} \tag{A1.32} $$

remembering that:

$$ \mu_{x+r} = \frac{1}{a - br}. \tag{A1.33} $$

When $b = 0$, μ_{x+t} is constant and life contingencies tells us:

$$ {}_{t-s}p_{x+s} = e^{-(t-s)\mu} \tag{A1.34} $$

$$ \Rightarrow \quad {}_{t-s}p_{x+s} = (p_x)^{t-s} \tag{A1.35} $$

and since in general a is the reciprocal of μ_x, we also have:

$$ {}_{t-s}p_{x+s} = e^{\frac{-(t-s)}{a}} \tag{A1.36} $$

A1.8 Concerning l_{x+r}

Further results follow:

For $b \neq 0$:
$$ {}_{t-s}p_{x+s} = \frac{l_{x+t}}{l_{x+s}} = \left(\frac{\mu_{x+s}}{\mu_{x+t}}\right)^{\frac{1}{b}} \tag{A1.37} $$

so that:

$$l_{x+r} \propto (\frac{1}{\mu_{x+r}})^{\frac{1}{b}} \tag{A1.38}$$

where x is a given integer and $0 \leq r \leq 1$.

And for $b = 0$:

$${}_{t-s}p_{x+s} = \frac{l_{x+t}}{l_{x+s}} = e^{-(t-s)\mu} = \frac{e^{-\mu t}}{e^{-\mu s}} \tag{A1.39}$$

so that:

$$l_{x+r} \propto e^{-\mu r} \tag{A1.40}$$

where x is a given integer and $0 \leq r \leq 1$.

A1.9 Expression for m_x in terms of μ_x and μ_{x+1}

We will now derive an expression for m_x in terms of μ_x and μ_{x+1}:

$$m_x = \frac{q_x}{\int_0^1 {}_t p_x \, dt} = \frac{1 - p_x}{\int_0^1 {}_t p_x \, dt} \tag{A1.41}$$

Let us consider the integral:

$$\begin{aligned} \int_0^1 {}_t p_x \, dt &= \int_0^1 (1 - \tfrac{b}{a}t)^{\frac{1}{b}} \, dt \\ &= \left[\frac{-a}{b} * \frac{(1 - \frac{b}{a}t)^{\frac{1}{b}+1}}{(\frac{1}{b} + 1)} \right]_0^1 \\ &= (\frac{a}{1 + b}) * (1 - (1 - \tfrac{b}{a})^{\frac{1}{b}+1}) \end{aligned} \tag{A1.42}$$

Using expression (A1.42) and the following result, which follows from equation (A1.31):

$$p_x = (1 - \tfrac{b}{a})^{\frac{1}{b}} \tag{A1.43}$$

we have:

$$m_x = \frac{1 - (1 - \frac{b}{a})^{\frac{1}{b}}}{1 - (1 - \frac{b}{a})^{\frac{1}{b}+1}} * (\frac{b}{a} + \frac{1}{a}) \qquad \text{(A1.44)}$$

Substituting for a and b using the expressions:

$$a = \frac{1}{\mu_x} \quad , \quad b = \frac{1}{\mu_x} - \frac{1}{\mu_{x+1}} \qquad \text{(A1.45)}$$

leads to the result:

$$m_x = \frac{1 - (\frac{\mu_x}{\mu_{x+1}})^{\frac{\mu_x \mu_{x+1}}{\mu_{x+1} - \mu_x}}}{1 - (\frac{\mu_x}{\mu_{x+1}})^{(\frac{\mu_x \mu_{x+1}}{\mu_{x+1} - \mu_x} + 1)}} * (1 + \mu_x - \frac{\mu_x}{\mu_{x+1}}) \qquad \text{(A1.46)}$$

APPENDIX II

The printouts of the simulation output

Key to the printouts of the simulation outputs:

A2.1 ASPSIM Table I

Table I shows, for the simulation concerned, the average of the 500 values of q_x calculated for each estimator.

Table I of **ASPSIM** shows for assumptions b = 2, b = 1 ("Level deaths"), b = 0 ("Constant μ") and b = -1 (Balducci) of the rectangular hyperbolic mortality distribution, values of the following estimators:

"Hoem"	:	Hoem's approximated "operational moment relations" estimators (for b = 1 or b = -1 only)
"ImpB"	:	the Implication-B estimator
"Conv"	:	the conventional estimator
"n=-2"	:	the n-estimator for n = -2
"Time"	:	the time-count estimator (the n-estimator for n = -1)
"Log"	:	the log-estimator (the n-estimator for n = 0)
"MLE"	:	the maximum likelihood estimator (the n-estimator for n = 1)
"n=2"	:	the n-estimator for n = 2
"n=3"	:	the n-estimator for n = 3

Table I of **ASPSIM** also shows for assumption c = 1.1 of the Gompertz mortality distribution, values of the following estimators:

"ImpB"	:	the Implication-B estimator
"Conv"	:	the conventional estimator
"Time"	:	the time-count estimator
"MLE"	:	the maximum likelihood estimator

In addition Table I shows values of the following estimators:

"PL" : the product limit estimator

"ML H" : the value of q_x, assuming the rectangular hyperbolic mortality distribution, calculated from the maximum likelihood estimators of both a and b, ie the two-parameter maximum likelihood estimator of q_x assuming the rectangular hyperbolic mortality distribution.

"parameter b" : the maximum likelihood estimator of b, assuming the rectangular hyperbolic mortality distribution, (and used in calculating "ML H").

"ML G" : the value of q_x, assuming the Gompertz mortality distribution, calculated from the maximum likelihood estimators of both a and b, ie the two-parameter maximum likelihood estimator of q_x assuming the Gompertz mortality distribution.

"parameter c" : the maximum likelihood estimator of c, assuming the Gompertz mortality distribution, (and used in calculating "ML G").

A2.2 ASPSIM Table II

Table II shows, for the simulation concerned, the estimated standard deviation of each estimator. It must be emphasised that the standard deviation shown is for a single observed value of the estimator concerned, and not for the average of 500 observed values. The latter standard deviation may be obtained by dividing the corresponding figure shown in Table II for a single observed value by the square root of 500.

The figures are presented in a similar layout to that used in Table I of ASPSIM. It will be noted that the item "sd of para b" in the printouts gives the standard deviation of the maximum likelihood estimator of the parameter b calculated when the rectangular hyperbolic mortality distribution is assumed, and that the item "sd of para c" gives the standard deviation of the maximum likelihood estimator of the parameter c calculated when the Gompertz mortality distribution is assumed .

A2.3 ASPSIM Tables III and IV

These tables show respectively the lower limit and upper limit of the confidence intervals for the population value of q_x based on each of the estimators calculated in the simulation concerned.

For each estimator, the limits have been obtained by respectively subtracting or adding twice the estimated standard deviation of the average observed value from/to the average observed value of the estimator, the latter figure being that shown in Table I. The estimated standard deviation of the average observed value is obtained by taking the standard deviation of a single observed value, as given in Table II, by the square root of 500.

Lower and upper limits for the population parameters b and c based on the values estimated in connection with the "ML H" and "ML G" estimators are also shown, and similarly calculated.

The distribution of the average observed value of each estimator will be very close to a normal distribution so that the confidence interval based on the addition/subtraction of two standard deviations will be a 95% confidence interval.

A2.4 ASPSIM Table V

In Table V, the many values of the average observed q_x from Table I are taken and the average observed value of the "ML H" or the "ML G" maximum likelihood estimator is deducted from each of them; the "ML H" or "ML G" value is used according to whether the simulation had assumed that the underlying population was subject to the rectangular hyperbolic mortality distribution or the Gompertz mortality distribution. However, with regard to the parameters b and c relating to the "ML H" and "ML G" estimators, the figures shown are simply repetitions of the values of the maximum likelihood estimators of the parameters.

A2.5 ASPMMSIM Tables I–V

The general principles upon which the output is presented for the ASPMMSIM tables are similar to those used for the ASPSIM tables. The descriptions of the estimators in the tables are less abbreviated than in the ASPSIM tables and in general should need no additional explanation.

It will be noted that a reduced number of estimators are dealt with, although the "method of moments" estimator (calculated using simulated values of "τ_i" and applying equations (1.36), (1.37) and (5.2)) is now included.

It will also be noted that estimators which make the $b = 2$ assumption under the

rectangular hyperbolic mortality distribution are also omitted.

The main purpose of the ASPMMSIM program was to allow comparison of the "method of moments" estimator with other mortality rate estimators. This estimator was not incorporated into the ASPSIM program due to the more complex simulation procedure which it required, which among other things could have lengthened the time taken by a run.

A2.6 The printouts

The printouts of the simulation outputs now follow.

Program: ASPSIM A S Puzey 1990

Mortality distribution : Rectangular hyperbolic

Mortality rate : 0.20 Distn parameter : 2.00

Withdrawal rate : 0.40 Random deaths/wdls

No of lives exposed from beginning of year : 10000

No of lives exposed from duration 3 months : 10000

No of runs : 500

TABLE I - Average observed q

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1981701		0.2000149		
ImpB	0.2002303	0.2007837	0.2015292	0.2024830	*	0.2011793
Conv	0.2002258	0.2008413	0.2016698	0.2027328	*	0.2012816
n=-2	0.2002432	0.1989462	0.2003889	0.2047307		
Time	0.2002376	0.1995725	0.2003889	0.2027328	*	0.1998493
Log	0.2002303	0.2002050	0.2003889	0.2007952		
MLE	0.2002207	0.2008413	0.2003889	0.1989215	*	0.2002741
n= 2	0.2002094	0.2014794	0.2003889	0.1971138		
n= 3	0.2001960	0.2021164	0.2003889	0.1953730		
PL	0.2002003					
ML H	0.2002398	parameter b =	1.99301			
ML G	0.2000295	parameter c =	1.56950			

TABLE II - Standard deviation of observed q

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.0031140		0.0031681		
ImpB	0.0031951	0.0032043	0.0032292	0.0032659	*	0.0032230
Conv	0.0031801	0.0032052	0.0032129	0.0032647	*	0.0032246
n=-2	0.0034197	0.0032067	0.0031756	0.0033663		
Time	0.0032798	0.0031893	0.0031756	0.0032647	*	0.0031831
Log	0.0031958	0.0031903	0.0031756	0.0031892		
MLE	0.0031891	0.0032052	0.0031756	0.0031278	*	0.0031812
n= 2	0.0032315	0.0032289	0.0031756	0.0030817		
n= 3	0.0033251	0.0032761	0.0031756	0.0030527		
PL	0.0033495					
ML H	0.0031991	sd of para b =	0.33341			
ML G	0.0031845	sd of para c =	0.11785			

TABLE III - Confidence interval for q - lower limit

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1978916		0.1997315		
ImpB	0.1999445	0.2004972	0.2012404	0.2021908	*	0.2008910
Conv	0.1999414	0.2005547	0.2013824	0.2024408	*	0.2009932
n=-2	0.1999373	0.1986594	0.2001049	0.2044296		
Time	0.1999443	0.1992873	0.2001049	0.2024408	*	0.1995646
Log	0.1999445	0.1999196	0.2001049	0.2005100		
MLE	0.1999355	0.2005547	0.2001049	0.1986417	*	0.1999895
n= 2	0.1999204	0.2011906	0.2001049	0.1968381		
n= 3	0.1998986	0.2018234	0.2001049	0.1951000		
PL	0.1999008					
ML H	0.1999537	para b lower limit =		1.96319		
ML G	0.1997447	para c lower limit =		1.55896		

TABLE IV - Confidence interval for q - upper limit

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1984487		0.2002983		
ImpB	0.2005161	0.2010703	0.2018181	0.2027751	*	0.2014676
Conv	0.2005103	0.2011280	0.2019571	0.2030248	*	0.2015700
n=-2	0.2005491	0.1992330	0.2006730	0.2050318		
Time	0.2005310	0.1998578	0.2006730	0.2030248	*	0.2001340
Log	0.2005161	0.2004903	0.2006730	0.2010805		
MLE	0.2005059	0.2011280	0.2006730	0.1992012	*	0.2005586
n= 2	0.2004984	0.2017682	0.2006730	0.1973894		
n= 3	0.2004934	0.2024094	0.2006730	0.1956461		
PL	0.2004999					
ML H	0.2005260	para b upper limit =		2.02283		
ML G	0.2003143	para c upper limit =		1.58004		

TABLE V - Diff wrt two-para Rect Hyper/Gompertz MLE

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		-0.0020697		-0.0002249		
ImpB	-0.0000095	0.0005439	0.0012894	0.0022431	*	0.0009395
Conv	-0.0000140	0.0006015	0.0014299	0.0024929	*	0.0010418
n=-2	0.0000034	-0.0012936	0.0001491	0.0044909		
Time	-0.0000022	-0.0006673	0.0001491	0.0024929	*	-0.0003905
Log	-0.0000095	-0.0000349	0.0001491	0.0005554		
MLE	-0.0000191	0.0006015	0.0001491	-0.0013183	*	0.0000342
n= 2	-0.0000304	0.0012396	0.0001491	-0.0031261		
n= 3	-0.0000439	0.0018766	0.0001491	-0.0048668		
PL	-0.0000395					
ML H	0.0000000	parameter b =		1.99301		
ML G	-0.0002103	parameter c =		1.56950		

Program: ASPMMSIM A S Puzey 1990

Mortality distribution : Rectangular hyperbolic

Mortality rate : 0.20 Distn parameter : 2.00

Withdrawal rate : 0.40 Random deaths/wdls

No of lives exposed from beginning of year : 10000

No of lives exposed from duration 3 months : 10000

No of runs : 500

TABLE I - Average observed q

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1978693		0.1997061		
Meth of Moments	0.2003869	0.2010741	0.2019986	*	0.2007448
Implication-B	0.2004692	0.2012104	0.2021590	*	0.2008619
Conventional	0.2005353	0.2013596	0.2024181	*	0.2009727
Max Likelihood	0.2005353	0.2000782	0.1986110	*	0.1999636
Time-count	0.1992587	0.2000782	0.2024181	*	0.1995376
Product Limit	0.1998565				
MLE - Rect Hyper	0.1999311	parameter b =	2.00203		
MLE - Gompertz	0.1997198	parameter c =	1.57152		

TABLE II - Standard deviation of observed q

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.0030913		0.0031549		
Meth of Moments	0.0031628	0.0031925	0.0032162	*	0.0031794
Implication-B	0.0031666	0.0031849	0.0032129	*	0.0031787
Conventional	0.0031699	0.0031972	0.0032279	*	0.0031987
Max Likelihood	0.0031699	0.0031245	0.0030529	*	0.0031354
Time-count	0.0031133	0.0031245	0.0032279	*	0.0031281
Product Limit	0.0032227				
MLE - Rect Hyper	0.0031579	sd of para b =	0.31630		
MLE - Gompertz	0.0031417	sd of para c =	0.11245		

TABLE III - Confidence interval for q - lower limit

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1975928		0.1994239		
Meth of Moments	0.2001040	0.2007885	0.2017109	*	0.2004604
Implication-B	0.2001859	0.2009256	0.2018716	*	0.2005776
Conventional	0.2002518	0.2010737	0.2021294	*	0.2006866
Max Likelihood	0.2002518	0.1997988	0.1983379	*	0.1996832
Time-count	0.1989803	0.1997988	0.2021294	*	0.1992578
Product Limit	0.1995682				
MLE - Rect Hyper	0.1996486	para b lower limit =	1.97374		
MLE - Gompertz	0.1994388	para c lower limit =	1.56146		

TABLE IV - Confidence interval for q - upper limit

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1981458		0.1999883		
Meth of Moments	0.2006698	0.2013596	0.2022862	*	0.2010292
Implication-B	0.2007524	0.2014953	0.2024464	*	0.2011462
Conventional	0.2008188	0.2016456	0.2027068	*	0.2012588
Max Likelihood	0.2008188	0.2003577	0.1988841	*	0.2002441
Time-count	0.1995372	0.2003577	0.2027068	*	0.1998174
Product Limit	0.2001447				
MLE - Rect Hyper	0.2002136	para b upper limit =	2.03032		
MLE - Gompertz	0.2000008	para c upper limit =	1.58157		

TABLE V - Diff wrt two-para Rect Hyper/Gompertz MLE

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	-0.0020618		-0.0002250		
Meth of Moments	0.0004558	0.0011430	0.0020675	*	0.0008137
Implication-B	0.0005381	0.0012793	0.0022279	*	0.0009308
Conventional	0.0006042	0.0014285	0.0024870	*	0.0010416
Max Likelihood	0.0006042	0.0001471	-0.0013201	*	0.0000325
Time-count	-0.0006724	0.0001471	0.0024870	*	-0.0003935
Product Limit	-0.0000746				
MLE - Rect Hyper	0.0000000	parameter b =	2.00203		
MLE - Gompertz	-0.0002113	parameter c =	1.57152		

Program: ASPSIM A S Puzey 1990

Mortality distribution : Rectangular hyperbolic

Mortality rate : 0.20 Distn parameter : 1.00

Withdrawal rate : 0.40 Random deaths/wdls

No of lives exposed from beginning of year : 10000

No of lives exposed from duration 3 months : 10000

No of runs : 500

TABLE I - Average observed q

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1972628		0.1990980		
ImpB	0.1993401	0.1998990	0.2006481	0.2016034	*	0.2002952
Conv	0.1992846	0.1999002	0.2007251	0.2017816	*	0.2003370
n=-2	0.2025719	0.1999178	0.2000934	0.2030889		
Time	0.2012300	0.1999102	0.2000934	0.2017816	*	0.1998242
Log	0.1999213	0.1999043	0.2000934	0.2005026		
MLE	0.1986622	0.1999002	0.2000934	0.1992556	*	0.1999766
n= 2	0.1974661	0.1998977	0.2000934	0.1980431		
n= 3	0.1963426	0.1998969	0.2000934	0.1968673		
PL	0.1999971					
ML H	0.1999161	parameter b =	0.99407			
ML G	0.1998588	parameter c =	1.25140			

TABLE II - Standard deviation of observed q

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.0032410		0.0032984		
ImpB	0.0033098	0.0033267	0.0033520	0.0033806	*	0.0033551
Conv	0.0033008	0.0033168	0.0033417	0.0033842	*	0.0033420
n=-2	0.0036617	0.0033977	0.0033347	0.0034573		
Time	0.0034804	0.0033498	0.0033347	0.0033842	*	0.0033310
Log	0.0033581	0.0033305	0.0033347	0.0033377		
MLE	0.0032704	0.0033168	0.0033347	0.0032932	*	0.0033302
n= 2	0.0032352	0.0033181	0.0033347	0.0032639		
n= 3	0.0032632	0.0033280	0.0033347	0.0032486		
PL	0.0033918					
ML H	0.0033345	sd of para b =	0.31914			
ML G	0.0033401	sd of para c =	0.08901			

TABLE III - Confidence interval for q - lower limit

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1969729		0.1988030		
ImpB	0.1990441	0.1996015	0.2003483	0.2013010	*	0.1999951
Conv	0.1989894	0.1996035	0.2004263	0.2014789	*	0.2000381
n=-2	0.2022444	0.1996139	0.1997951	0.2027797		
Time	0.2009187	0.1996106	0.1997951	0.2014789	*	0.1995263
Log	0.1996209	0.1996064	0.1997951	0.2002040		
MLE	0.1983697	0.1996035	0.1997951	0.1989611	*	0.1996788
n= 2	0.1971768	0.1996009	0.1997951	0.1977512		
n= 3	0.1960507	0.1995992	0.1997951	0.1965767		
PL	0.1996938					
ML H	0.1996178	para b lower limit =		0.96553		
ML G	0.1995600	para c lower limit =		1.24344		

TABLE IV - Confidence interval for q - upper limit

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1975527		0.1993930		
ImpB	0.1996362	0.2001966	0.2009479	0.2019058	*	0.2005953
Conv	0.1995799	0.2001968	0.2010240	0.2020843	*	0.2006359
n=-2	0.2028994	0.2002217	0.2003916	0.2033982		
Time	0.2015413	0.2002099	0.2003916	0.2020843	*	0.2001222
Log	0.2002216	0.2002022	0.2003916	0.2008011		
MLE	0.1989547	0.2001968	0.2003916	0.1995502	*	0.2002745
n= 2	0.1977555	0.2001945	0.2003916	0.1983351		
n= 3	0.1966345	0.2001945	0.2003916	0.1971579		
PL	0.2003005					
ML H	0.2002143	para b upper limit =		1.02262		
ML G	0.2001576	para c upper limit =		1.25936		

TABLE V - Diff wrt two-para Rect Hyper/Gompertz MLE

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		-0.0026533		-0.0008181		
ImpB	-0.0005759	-0.0000170	0.0007320	0.0016873	*	0.0003791
Conv	-0.0006314	-0.0000159	0.0008091	0.0018655	*	0.0004209
n=-2	0.0026558	0.0000017	0.0001773	0.0031729		
Time	0.0013139	-0.0000058	0.0001773	0.0018655	*	-0.0000918
Log	0.0000052	-0.0000118	0.0001773	0.0005865		
MLE	-0.0012539	-0.0000159	0.0001773	-0.0006604	*	0.0000606
n= 2	-0.0024499	-0.0000184	0.0001773	-0.0018729		
n= 3	-0.0035734	-0.0000192	0.0001773	-0.0030488		
PL	0.0000811					
ML H	0.0000000	parameter b =		0.99407		
ML G	-0.0000573	parameter c =		1.25140		

Program: ASPMMSIM A S Puzey 1990

Mortality distribution : Rectangular hyperbolic

Mortality rate : 0.20 Distn parameter : 1.00

Withdrawal rate : 0.40 Random deaths/wdls

No of lives exposed from beginning of year : 10000

No of lives exposed from duration 3 months : 10000

No of runs : 500

TABLE I - Average observed q

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1975446		0.1993852		
Meth of Moments	0.2001887	0.2008749	0.2017971	*	0.2005459
Implication-B	0.2001860	0.2009369	0.2018946	*	0.2005838
Conventional	0.2001892	0.2010164	0.2020762	*	0.2006279
Max Likelihood	0.2001892	0.2003871	0.1995454	*	0.2002708
Time-count	0.2002093	0.2003871	0.2020762	*	0.2001192
Product Limit	0.2001644				
MLE - Rect Hyper	0.2002110	parameter b =	0.98460		
MLE - Gompertz	0.2001542	parameter c =	1.24993		

TABLE II - Standard deviation of observed q

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.0030346		0.0030919		
Meth of Moments	0.0031250	0.0031412	0.0031742	*	0.0031379
Implication-B	0.0031230	0.0031404	0.0031824	*	0.0031366
Conventional	0.0031164	0.0031419	0.0031781	*	0.0031298
Max Likelihood	0.0031164	0.0031222	0.0031005	*	0.0031224
Time-count	0.0031459	0.0031222	0.0031781	*	0.0031338
Product Limit	0.0032442				
MLE - Rect Hyper	0.0031285	sd of para b =	0.30893		
MLE - Gompertz	0.0031321	sd of para c =	0.08673		

TABLE III - Confidence interval for q - lower limit

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1972732		0.1991087		
Meth of Moments	0.1999092	0.2005939	0.2015131	*	0.2002652
Implication-B	0.1999067	0.2006560	0.2016100	*	0.2003033
Conventional	0.1999105	0.2007353	0.2017920	*	0.2003480
Max Likelihood	0.1999105	0.2001078	0.1992680	*	0.1999915
Time-count	0.1999279	0.2001078	0.2017920	*	0.1998389
Product Limit	0.1998742				
MLE - Rect Hyper	0.1999312	para b lower limit =	0.95697		
MLE - Gompertz	0.1998740	para c lower limit =	1.24217		

TABLE IV - Confidence interval for q - upper limit

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1978160		0.1996618		
Meth of Moments	0.2004682	0.2011558	0.2020810	*	0.2008265
Implication-B	0.2004653	0.2012178	0.2021793	*	0.2008643
Conventional	0.2004679	0.2012974	0.2023605	*	0.2009078
Max Likelihood	0.2004679	0.2006663	0.1998227	*	0.2005501
Time-count	0.2004906	0.2006663	0.2023605	*	0.2003995
Product Limit	0.2004546				
MLE - Rect Hyper	0.2004908	para b upper limit =	1.01223		
MLE - Gompertz	0.2004343	para c upper limit =	1.25768		

TABLE V - Diff wrt two-para Rect Hyper/Gompertz MLE

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	-0.0026664		-0.0008258		
Meth of Moments	-0.0000223	0.0006639	0.0015860	*	0.0003349
Implication-B	-0.0000250	0.0007259	0.0016836	*	0.0003728
Conventional	-0.0000218	0.0008053	0.0018652	*	0.0004169
Max Likelihood	-0.0000218	0.0001761	-0.0006656	*	0.0000598
Time-count	-0.0000017	0.0001761	0.0018652	*	-0.0000918
Product Limit	-0.0000466				
MLE - Rect Hyper	0.0000000	parameter b =	0.98460		
MLE - Gompertz	-0.0000568	parameter c =	1.24993		

ASPSIM

$b = 0$ & $c = 1$

Program: ASPSIM A S Puzey 1990

Mortality distribution : Rectangular hyperbolic

Mortality rate : 0.20 Distn parameter : 0.00

Withdrawal rate : 0.40 Random deaths/wdls

No of lives exposed from beginning of year : 10000

No of lives exposed from duration 3 months : 10000

No of runs : 500

TABLE I - Average observed q

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1964406		0.1982689		
ImpB	0.1985442	0.1991098	0.1998642	0.2008233	*	0.1995079
Conv	0.1984284	0.1990440	0.1998666	0.2009177	*	0.1994781
n=-2	0.2049535	0.2009277	0.1998596	0.2015705		
Time	0.2022599	0.2002926	0.1998596	0.2009177	*	0.1998526
Log	0.1996729	0.1996643	0.1998596	0.2002727		
MLE	0.1972203	0.1990440	0.1998596	0.1996369	*	0.1997402
n= 2	0.1949204	0.1984341	0.1998596	0.1990129		
n= 3	0.1927845	0.1978364	0.1998596	0.1984019		
PL	0.1999001					
ML H	0.1998702	parameter b =	0.00198			
ML G	0.1998620	parameter c =	1.00515			

TABLE II - Standard deviation of observed q

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.0031252		0.0031933		
ImpB	0.0032021	0.0032152	0.0032401	0.0032767	*	0.0032353
Conv	0.0031956	0.0032156	0.0032429	0.0032781	*	0.0032427
n=-2	0.0036401	0.0033362	0.0032295	0.0033244		
Time	0.0034177	0.0032974	0.0032295	0.0032781	*	0.0032473
Log	0.0032528	0.0032416	0.0032295	0.0032371		
MLE	0.0031427	0.0032156	0.0032295	0.0032237	*	0.0032487
n= 2	0.0030966	0.0032027	0.0032295	0.0032001		
n= 3	0.0030736	0.0031901	0.0032295	0.0032056		
PL	0.0033094					
ML H	0.0032441	sd of para b =	0.30881			
ML G	0.0032447	sd of para c =	0.06988			

TABLE III - Confidence interval for q - lower limit

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1961611		0.1979833		
ImpB	0.1982578	0.1988222	0.1995744	0.2005302	*	0.1992186
Conv	0.1981426	0.1987564	0.1995766	0.2006245	*	0.1991881
n=-2	0.2046280	0.2006293	0.1995708	0.2012731		
Time	0.2019543	0.1999977	0.1995708	0.2006245	*	0.1995622
Log	0.1993820	0.1993743	0.1995708	0.1999832		
MLE	0.1969392	0.1987564	0.1995708	0.1993486	*	0.1994496
n= 2	0.1946435	0.1981476	0.1995708	0.1987267		
n= 3	0.1925096	0.1975511	0.1995708	0.1981152		
PL	0.1996041					
ML H	0.1995801	para b lower limit =		-0.02564		
ML G	0.1995718	para c lower limit =		0.99890		

TABLE IV - Confidence interval for q - upper limit

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1967202		0.1985545		
ImpB	0.1988306	0.1993974	0.2001540	0.2011164	*	0.1997973
Conv	0.1987143	0.1993316	0.2001567	0.2012109	*	0.1997681
n=-2	0.2052791	0.2012261	0.2001485	0.2018678		
Time	0.2025656	0.2005875	0.2001485	0.2012109	*	0.2001431
Log	0.1999639	0.1999542	0.2001485	0.2005622		
MLE	0.1975014	0.1993316	0.2001485	0.1999253	*	0.2000308
n= 2	0.1951974	0.1987206	0.2001485	0.1992991		
n= 3	0.1930594	0.1981218	0.2001485	0.1986886		
PL	0.2001961					
ML H	0.2001604	para b upper limit =		0.02960		
ML G	0.2001522	para c upper limit =		1.01140		

TABLE V - Diff wrt two-para Rect Hyper/Gompertz MLE

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		-0.0034296		-0.0016013		
ImpB	-0.0013260	-0.0007604	-0.0000061	0.0009530	*	-0.0003623
Conv	-0.0014418	-0.0008262	-0.0000036	0.0010474	*	-0.0003921
n=-2	0.0050833	0.0010574	-0.0000106	0.0017002		
Time	0.0023897	0.0004224	-0.0000106	0.0010474	*	-0.0000176
Log	-0.0001973	-0.0002060	-0.0000106	0.0004025		
MLE	-0.0026499	-0.0008262	-0.0000106	-0.0002333	*	-0.0001300
n= 2	-0.0049498	-0.0014361	-0.0000106	-0.0008573		
n= 3	-0.0070858	-0.0020338	-0.0000106	-0.0014684		
PL	0.0000298					
ML H	0.0000000	parameter b =		0.00198		
ML G	-0.0000082	parameter c =		1.00515		

Program: ASPMMSIM A S Puzey 1990

Mortality distribution : Rectangular hyperbolic

Mortality rate : 0.20 Distn parameter : 0.00

Withdrawal rate : 0.40 Random deaths/wdls

No of lives exposed from beginning of year : 10000

No of lives exposed from duration 3 months : 10000

No of runs : 500

TABLE I - Average observed q

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1967082		0.1985416		
Meth of Moments	0.1994620	0.2001428	0.2010571	*	0.1998152
Implication-B	0.1993816	0.2001374	0.2010986	*	0.1997808
Conventional	0.1993195	0.2001443	0.2011985	*	0.1997554
Max Likelihood	0.1993195	0.2001512	0.1999390	*	0.2000326
Time-count	0.2006023	0.2001512	0.2011985	*	0.2001506
Product Limit	0.2001527				
MLE - Rect Hyper	0.2001689	parameter b =	-0.01862		
MLE - Gompertz	0.2001608	parameter c =	1.00040		

TABLE II - Standard deviation of observed q

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.0032275		0.0033031		
Meth of Moments	0.0033314	0.0033561	0.0033864	*	0.0033506
Implication-B	0.0033131	0.0033444	0.0033866	*	0.0033466
Conventional	0.0033265	0.0033437	0.0033954	*	0.0033454
Max Likelihood	0.0033265	0.0033516	0.0033260	*	0.0033379
Time-count	0.0033942	0.0033516	0.0033954	*	0.0033634
Product Limit	0.0034677				
MLE - Rect Hyper	0.0033512	sd of para b =	0.32343		
MLE - Gompertz	0.0033514	sd of para c =	0.07255		

TABLE III - Confidence interval for q - lower limit

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1964196		0.1982461		
Meth of Moments	0.1991641	0.1998427	0.2007542	*	0.1995155
Implication-B	0.1990853	0.1998383	0.2007957	*	0.1994815
Conventional	0.1990220	0.1998453	0.2008948	*	0.1994562
Max Likelihood	0.1990220	0.1998515	0.1996415	*	0.1997341
Time-count	0.2002987	0.1998515	0.2008948	*	0.1998498
Product Limit	0.1998425				
MLE - Rect Hyper	0.1998691	para b lower limit = -0.04755			
MLE - Gompertz	0.1998611	para c lower limit = 0.99391			

TABLE IV - Confidence interval for q - upper limit

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1969969		0.1988370		
Meth of Moments	0.1997600	0.2004430	0.2013600	*	0.2001148
Implication-B	0.1996780	0.2004366	0.2014015	*	0.2000801
Conventional	0.1996170	0.2004434	0.2015021	*	0.2000546
Max Likelihood	0.1996170	0.2004510	0.2002364	*	0.2003312
Time-count	0.2009059	0.2004510	0.2015021	*	0.2004514
Product Limit	0.2004628				
MLE - Rect Hyper	0.2004686	para b upper limit = 0.01030			
MLE - Gompertz	0.2004606	para c upper limit = 1.00689			

TABLE V - Diff wrt two-para Rect Hyper/Gompertz MLE

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	-0.0034606		-0.0016273		
Meth of Moments	-0.0007068	-0.0000260	0.0008882	*	-0.0003537
Implication-B	-0.0007872	-0.0000314	0.0009297	*	-0.0003881
Conventional	-0.0008494	-0.0000245	0.0010296	*	-0.0004135
Max Likelihood	-0.0008494	-0.0000176	-0.0002299	*	-0.0001362
Time-count	0.0004334	-0.0000176	0.0010296	*	-0.0000183
Product Limit	-0.0000162				
MLE - Rect Hyper	0.0000000	parameter b = -0.01862			
MLE - Gompertz	-0.0000080	parameter c = 1.00040			

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Program:              ASPSIM              A S Puzey 1990
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Mortality distribution :  Rectangular hyperbolic

Mortality rate  : 0.20    Distn parameter :  -1.00

Withdrawal rate : 0.40    Random deaths/wdls

No of lives exposed from beginning of year  :   10000

No of lives exposed from duration  3 months :   10000

No of runs :    500
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TABLE I - Average observed q

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1954472		0.1972679		
ImpB	0.1975774	0.1981507	0.1989112	0.1998741	*	0.1985506
Conv	0.1973951	0.1980113	0.1988314	0.1998762	*	0.1984423
n=-2	0.2072675	0.2017938	0.1994511	0.1998811		
Time	0.2031334	0.2005076	0.1994511	0.1998762	*	0.1997094
Log	0.1992417	0.1992458	0.1994511	0.1998713		
MLE	0.1956173	0.1980113	0.1994511	0.1998660	*	0.1993277
n= 2	0.1922715	0.1968074	0.1994511	0.1998607		
n= 3	0.1892030	0.1956365	0.1994511	0.1998548		
PL	0.1998418					
ML H	0.1998782	parameter b =	-0.99118			
ML G	0.1998187	parameter c =	0.80368			

TABLE II - Standard deviation of observed q

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.0031375		0.0032023		
ImpB	0.0032182	0.0032281	0.0032481	0.0032915	*	0.0032532
Conv	0.0032060	0.0032176	0.0032384	0.0032909	*	0.0032453
n=-2	0.0038145	0.0034277	0.0032714	0.0033110		
Time	0.0035214	0.0033498	0.0032714	0.0032909	*	0.0032919
Log	0.0032850	0.0032701	0.0032714	0.0032781		
MLE	0.0031445	0.0032176	0.0032714	0.0032840	*	0.0032754
n= 2	0.0030452	0.0031771	0.0032714	0.0032872		
n= 3	0.0029957	0.0031515	0.0032714	0.0033226		
PL	0.0033741					
ML H	0.0032678	sd of para b =	0.30492			
ML G	0.0032776	sd of para c =	0.05476			

TABLE III - Confidence interval for q - lower limit

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1951666		0.1969815		
ImpB	0.1972895	0.1978620	0.1986206	0.1995797	*	0.1982596
Conv	0.1971083	0.1977235	0.1985417	0.1995819	*	0.1981520
n=-2	0.2069263	0.2014872	0.1991585	0.1995849		
Time	0.2028184	0.2002079	0.1991585	0.1995819	*	0.1994150
Log	0.1989478	0.1989533	0.1991585	0.1995781		
MLE	0.1953360	0.1977235	0.1991585	0.1995723	*	0.1990348
n= 2	0.1919991	0.1965232	0.1991585	0.1995667		
n= 3	0.1889351	0.1953546	0.1991585	0.1995576		
PL	0.1995400					
ML H	0.1995859	para b lower limit =		-1.01845		
ML G	0.1995256	para c lower limit =		0.79878		

TABLE IV - Confidence interval for q - upper limit

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1957279		0.1975543		
ImpB	0.1978652	0.1984395	0.1992017	0.2001685	*	0.1988416
Conv	0.1976818	0.1982991	0.1991210	0.2001706	*	0.1987326
n=-2	0.2076087	0.2021003	0.1997437	0.2001772		
Time	0.2034483	0.2008072	0.1997437	0.2001706	*	0.2000038
Log	0.1995355	0.1995382	0.1997437	0.2001645		
MLE	0.1958986	0.1982991	0.1997437	0.2001598	*	0.1996207
n= 2	0.1925439	0.1970916	0.1997437	0.2001547		
n= 3	0.1894710	0.1959184	0.1997437	0.2001520		
PL	0.2001436					
ML H	0.2001705	para b upper limit =		-0.96391		
ML G	0.2001119	para c upper limit =		0.80858		

TABLE V - Diff wrt two-para Rect Hyper/Gompertz MLE

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		-0.0044310		-0.0026103		
ImpB	-0.0023008	-0.0017275	-0.0009671	-0.0000041	*	-0.0013276
Conv	-0.0024831	-0.0018669	-0.0010468	-0.0000020	*	-0.0014359
n=-2	0.0073893	0.0019155	-0.0004272	0.0000029		
Time	0.0032552	0.0006294	-0.0004272	-0.0000020	*	-0.0001688
Log	-0.0006365	-0.0006325	-0.0004272	-0.0000069		
MLE	-0.0042609	-0.0018669	-0.0004272	-0.0000122	*	-0.0005505
n= 2	-0.0076067	-0.0030708	-0.0004272	-0.0000175		
n= 3	-0.0106752	-0.0042417	-0.0004272	-0.0000234		
PL	-0.0000364					
ML H	0.0000000	parameter b =		-0.99118		
ML G	-0.0000595	parameter c =		0.80368		

Program: ASPMMSIM A S Puzey 1990

Mortality distribution : Rectangular hyperbolic

Mortality rate : 0.20 Distn parameter : -1.00

Withdrawal rate : 0.40 Random deaths/wdls

No of lives exposed from beginning of year : 10000

No of lives exposed from duration 3 months : 10000

No of runs : 500

TABLE I - Average observed q

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1956406		0.1974654		
Meth of Moments	0.1984868	0.1991635	0.2000702	*	0.1988364
Implication-B	0.1983497	0.1991121	0.2000775	*	0.1987512
Conventional	0.1982102	0.1990324	0.2000803	*	0.1986430
Max Likelihood	0.1982102	0.1996568	0.2000776	*	0.1995333
Time-count	0.2007204	0.1996568	0.2000803	*	0.1999175
Product Limit	0.2001172				
MLE - Rect Hyper	0.2000893	parameter b =	-0.99954		
MLE - Gompertz	0.2000280	parameter c =	0.80241		

TABLE II - Standard deviation of observed q

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.0032541		0.0033200		
Meth of Moments	0.0033509	0.0033728	0.0034018	*	0.0033673
Implication-B	0.0033527	0.0033615	0.0034070	*	0.0033599
Conventional	0.0033420	0.0033771	0.0034041	*	0.0033578
Max Likelihood	0.0033420	0.0033810	0.0033604	*	0.0033750
Time-count	0.0034330	0.0033810	0.0034041	*	0.0033808
Product Limit	0.0034726				
MLE - Rect Hyper	0.0033605	sd of para b =	0.31032		
MLE - Gompertz	0.0033633	sd of para c =	0.05508		

TABLE III - Confidence interval for q - lower limit

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1953495		0.1971685		
Meth of Moments	0.1981871	0.1988618	0.1997659	*	0.1985352
Implication-B	0.1980499	0.1988115	0.1997727	*	0.1984506
Conventional	0.1979113	0.1987303	0.1997758	*	0.1983427
Max Likelihood	0.1979113	0.1993544	0.1997770	*	0.1992315
Time-count	0.2004133	0.1993544	0.1997758	*	0.1996151
Product Limit	0.1998066				
MLE - Rect Hyper	0.1997887	para b lower limit = -1.02729			
MLE - Gompertz	0.1997272	para c lower limit = 0.79748			

TABLE IV - Confidence interval for q - upper limit

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1959316		0.1977624		
Meth of Moments	0.1987865	0.1994651	0.2003744	*	0.1991376
Implication-B	0.1986496	0.1994128	0.2003822	*	0.1990517
Conventional	0.1985092	0.1993344	0.2003848	*	0.1989434
Max Likelihood	0.1985092	0.1999592	0.2003781	*	0.1998352
Time-count	0.2010274	0.1999592	0.2003848	*	0.2002199
Product Limit	0.2004278				
MLE - Rect Hyper	0.2003899	para b upper limit = -0.97178			
MLE - Gompertz	0.2003288	para c upper limit = 0.80733			

TABLE V - Diff wrt two-para Rect Hyper/Gompertz MLE

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	-0.0044487		-0.0026239		
Meth of Moments	-0.0016025	-0.0009259	-0.0000191	*	-0.0012529
Implication-B	-0.0017396	-0.0009772	-0.0000119	*	-0.0013382
Conventional	-0.0018791	-0.0010570	-0.0000090	*	-0.0014463
Max Likelihood	-0.0018791	-0.0004325	-0.0000117	*	-0.0005560
Time-count	0.0006310	-0.0004325	-0.0000090	*	-0.0001719
Product Limit	0.0000279				
MLE - Rect Hyper	0.0000000	parameter b = -0.99954			
MLE - Gompertz	-0.0000613	parameter c = 0.80241			

Program: ASPSIM A S Puzey 1990

Mortality distribution : Gompertz

Mortality rate : 0.20 Distn parameter : 1.10

Withdrawal rate : 0.40 Random deaths/wdls

No of lives exposed from beginning of year : 10000

No of lives exposed from duration 3 months : 10000

No of runs : 500

TABLE I - Average observed q

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1970107		0.1988452		
ImpB	0.1991164	0.1996802	0.2004341	0.2013941	*	0.2000789
Conv	0.1990203	0.1996365	0.2004615	0.2015171	*	0.2000730
n=-2	0.2041458	0.2007134	0.2001844	0.2024533		
Time	0.2020465	0.2003527	0.2001844	0.2015171	*	0.2000641
Log	0.2000084	0.1999933	0.2001844	0.2005945		
MLE	0.1980564	0.1996365	0.2001844	0.1996883	*	0.2000668
n= 2	0.1962090	0.1992832	0.2001844	0.1988009		
n= 3	0.1944795	0.1989348	0.2001844	0.1979344		
PL	0.2000429					
ML H	0.2000870	parameter b =		0.43215		
ML G	0.2000705	parameter c =		1.10511		

TABLE II - Standard deviation of observed q

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.0032380		0.0033061		
ImpB	0.0033126	0.0033286	0.0033486	0.0033847	*	0.0033470
Conv	0.0033058	0.0033293	0.0033518	0.0033922	*	0.0033454
n=-2	0.0036331	0.0033803	0.0033158	0.0034688		
Time	0.0034541	0.0033549	0.0033158	0.0033922	*	0.0033220
Log	0.0033411	0.0033352	0.0033158	0.0033307		
MLE	0.0032820	0.0033293	0.0033158	0.0032807	*	0.0033309
n= 2	0.0032701	0.0033276	0.0033158	0.0032487		
n= 3	0.0032852	0.0033443	0.0033158	0.0032356		
PL	0.0033591					
ML H	0.0033254	sd of para b =		0.31157		
ML G	0.0033237	sd of para c =		0.07570		

TABLE III - Confidence interval for q - lower limit

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1967211		0.1985495		
ImpB	0.1988201	0.1993825	0.2001346	0.2010914	*	0.1997796
Conv	0.1987246	0.1993387	0.2001617	0.2012137	*	0.1997738
n=-2	0.2038208	0.2004110	0.1998879	0.2021430		
Time	0.2017375	0.2000526	0.1998879	0.2012137	*	0.1997669
Log	0.1997096	0.1996950	0.1998879	0.2002966		
MLE	0.1977628	0.1993387	0.1998879	0.1993949	*	0.1997689
n= 2	0.1959165	0.1989856	0.1998879	0.1985103		
n= 3	0.1941856	0.1986356	0.1998879	0.1976450		
PL	0.1997424					
ML H	0.1997896	para b lower limit =		0.40428		
ML G	0.1997733	para c lower limit =		1.09834		

TABLE IV - Confidence interval for q - upper limit

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1973003		0.1991409		
ImpB	0.1994127	0.1999779	0.2007336	0.2016968	*	0.2003783
Conv	0.1993160	0.1999343	0.2007613	0.2018205	*	0.2003723
n=-2	0.2044708	0.2010157	0.2004810	0.2027635		
Time	0.2023554	0.2006528	0.2004810	0.2018205	*	0.2003612
Log	0.2003073	0.2002916	0.2004810	0.2008924		
MLE	0.1983499	0.1999343	0.2004810	0.1999817	*	0.2003647
n= 2	0.1965015	0.1995809	0.2004810	0.1990915		
n= 3	0.1947733	0.1992339	0.2004810	0.1982238		
PL	0.2003433					
ML H	0.2003845	para b upper limit =		0.46001		
ML G	0.2003678	para c upper limit =		1.11188		

TABLE V - Diff wrt two-para Rect Hyper/Gompertz MLE

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		-0.0030598		-0.0012253		
ImpB	-0.0009541	-0.0003903	0.0003636	0.0013236	*	0.0000084
Conv	-0.0010503	-0.0004341	0.0003910	0.0014466	*	0.0000025
n=-2	0.0040753	0.0006428	0.0001139	0.0023827		
Time	0.0019759	0.0002822	0.0001139	0.0014466	*	-0.0000065
Log	-0.0000621	-0.0000772	0.0001139	0.0005240		
MLE	-0.0020142	-0.0004341	0.0001139	-0.0003822	*	-0.0000037
n= 2	-0.0038615	-0.0007873	0.0001139	-0.0012696		
n= 3	-0.0055911	-0.0011358	0.0001139	-0.0021361		
PL	-0.0000276					
ML H	0.0000165	parameter b =		0.43215		
ML G	0.0000000	parameter c =		1.10511		

Program: ASPMMSIM A S Puzey 1990

Mortality distribution : Gompertz

Mortality rate : 0.20 Distn parameter : 1.10

Withdrawal rate : 0.40 Random deaths/wdls

No of lives exposed from beginning of year : 10000

No of lives exposed from duration 3 months : 10000

No of runs : 500

TABLE I - Average observed q

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1967706		0.1986043		
Meth of Moments	0.1994760	0.2001586	0.2010746	*	0.1998304
Implication-B	0.1994264	0.2001801	0.2011392	*	0.1998247
Conventional	0.1993857	0.2002103	0.2012648	*	0.1998216
Max Likelihood	0.1993857	0.1999531	0.1994815	*	0.1998346
Time-count	0.2001370	0.1999531	0.2012648	*	0.1998403
Product Limit	0.1998566				
MLE - Rect Hyper	0.1998616	parameter b =	0.40015		
MLE - Gompertz	0.1998463	parameter c =	1.09745		

TABLE II - Standard deviation of observed q

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.0030594		0.0031228		
Meth of Moments	0.0031432	0.0031612	0.0031862	*	0.0031390
Implication-B	0.0031423	0.0031657	0.0031900	*	0.0031480
Conventional	0.0031263	0.0031612	0.0032085	*	0.0031525
Max Likelihood	0.0031263	0.0031292	0.0030915	*	0.0031309
Time-count	0.0031403	0.0031292	0.0032085	*	0.0031244
Product Limit	0.0031362				
MLE - Rect Hyper	0.0031294	sd of para b =	0.31446		
MLE - Gompertz	0.0031258	sd of para c =	0.07667		

TABLE III - Confidence interval for q - lower limit

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1964970		0.1983250		
Meth of Moments	0.1991949	0.1998758	0.2007896	*	0.1995496
Implication-B	0.1991453	0.1998969	0.2008539	*	0.1995432
Conventional	0.1991061	0.1999276	0.2009778	*	0.1995396
Max Likelihood	0.1991061	0.1996732	0.1992050	*	0.1995545
Time-count	0.1998562	0.1996732	0.2009778	*	0.1995608
Product Limit	0.1995761				
MLE - Rect Hyper	0.1995817	para b lower limit =	0.37203		
MLE - Gompertz	0.1995667	para c lower limit =	1.09060		

TABLE IV - Confidence interval for q - upper limit

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1970443		0.1988836		
Meth of Moments	0.1997572	0.2004413	0.2013596	*	0.2001112
Implication-B	0.1997074	0.2004632	0.2014245	*	0.2001063
Conventional	0.1996653	0.2004931	0.2015518	*	0.2001036
Max Likelihood	0.1996653	0.2002330	0.1997580	*	0.2001146
Time-count	0.2004179	0.2002330	0.2015518	*	0.2001197
Product Limit	0.2001371				
MLE - Rect Hyper	0.2001415	para b upper limit =	0.42828		
MLE - Gompertz	0.2001258	para c upper limit =	1.10431		

TABLE V - Diff wrt two-para Rect Hyper/Gompertz MLE

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	-0.0030756		-0.0012420		
Meth of Moments	-0.0003702	0.0003123	0.0012283	*	-0.0000159
Implication-B	-0.0004199	0.0003338	0.0012930	*	-0.0000215
Conventional	-0.0004606	0.0003641	0.0014185	*	-0.0000247
Max Likelihood	-0.0004606	0.0001068	-0.0003647	*	-0.0000117
Time-count	0.0002908	0.0001068	0.0014185	*	-0.0000060
Product Limit	0.0000103				
MLE - Rect Hyper	0.0000154	parameter b =	0.40015		
MLE - Gompertz	0.0000000	parameter c =	1.09745		

Program: ASPSIM A S Puzey 1990

Mortality distribution : Gompertz

Mortality rate : 0.20 Distn parameter : 1.05

Withdrawal rate : 0.40 Random deaths/wdls

No of lives exposed from beginning of year : 10000

No of lives exposed from duration 3 months : 10000

No of runs : 500

TABLE I - Average observed q

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1969525		0.1987902		
ImpB	0.1990537	0.1996199	0.2003761	0.2013382	*	0.2000199
Conv	0.1989535	0.1995718	0.2003985	0.2014556	*	0.2000092
n=-2	0.2047883	0.2010488	0.2002525	0.2022570		
Time	0.2023843	0.2005511	0.2002525	0.2014556	*	0.2001873
Log	0.2000695	0.2000582	0.2002525	0.2006661		
MLE	0.1978692	0.1995718	0.2002525	0.1998906	*	0.2001337
n= 2	0.1958025	0.1990935	0.2002525	0.1991315		
n= 3	0.1938807	0.1986250	0.2002525	0.1983905		
PL	0.2002401					
ML H	0.2002021	parameter b =	0.22203			
ML G	0.2001921	parameter c =	1.05503			

TABLE II - Standard deviation of observed q

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.0032604		0.0033147		
ImpB	0.0033281	0.0033392	0.0033534	0.0033930	*	0.0033486
Conv	0.0033389	0.0033421	0.0033712	0.0034026	*	0.0033643
n=-2	0.0036931	0.0034155	0.0033514	0.0034715		
Time	0.0035100	0.0033791	0.0033514	0.0034026	*	0.0033507
Log	0.0033688	0.0033533	0.0033514	0.0033493		
MLE	0.0033001	0.0033421	0.0033514	0.0033109	*	0.0033489
n= 2	0.0032665	0.0033446	0.0033514	0.0032865		
n= 3	0.0032660	0.0033427	0.0033514	0.0032631		
PL	0.0034309					
ML H	0.0033483	sd of para b =	0.31446			
ML G	0.0033494	sd of para c =	0.07266			

TABLE III - Confidence interval for q - lower limit

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1966609		0.1984938		
ImpB	0.1987561	0.1993213	0.2000761	0.2010347	*	0.1997204
Conv	0.1986549	0.1992729	0.2000969	0.2011513	*	0.1997083
n=-2	0.2044580	0.2007433	0.1999527	0.2019465		
Time	0.2020704	0.2002489	0.1999527	0.2011513	*	0.1998876
Log	0.1997682	0.1997582	0.1999527	0.2003665		
MLE	0.1975741	0.1992729	0.1999527	0.1995945	*	0.1998342
n= 2	0.1955104	0.1987944	0.1999527	0.1988375		
n= 3	0.1935885	0.1983260	0.1999527	0.1980986		
PL	0.1999333					
ML H	0.1999026	para b lower limit =		0.19390		
ML G	0.1998925	para c lower limit =		1.04853		

TABLE IV - Confidence interval for q - upper limit

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		0.1972442		0.1990867		
ImpB	0.1993514	0.1999186	0.2006760	0.2016416	*	0.2003194
Conv	0.1992522	0.1998708	0.2007000	0.2017599	*	0.2003101
n=-2	0.2051187	0.2013543	0.2005522	0.2025675		
Time	0.2026983	0.2008533	0.2005522	0.2017599	*	0.2004870
Log	0.2003708	0.2003581	0.2005522	0.2009657		
MLE	0.1981644	0.1998708	0.2005522	0.2001868	*	0.2004333
n= 2	0.1960947	0.1993927	0.2005522	0.1994254		
n= 3	0.1941728	0.1989240	0.2005522	0.1986823		
PL	0.2005470					
ML H	0.2005015	para b upper limit =		0.25015		
ML G	0.2004917	para c upper limit =		1.06153		

TABLE V - Diff wrt two-para Rect Hyper/Gompertz MLE

	b=2	Level Dths	Const Mu	Balducci	*	Gompz
Hoem		-0.0032396		-0.0014019		
ImpB	-0.0011384	-0.0005722	0.0001840	0.0011460	*	-0.0001722
Conv	-0.0012386	-0.0006203	0.0002064	0.0012635	*	-0.0001829
n=-2	0.0045962	0.0008567	0.0000604	0.0020649		
Time	0.0021922	0.0003590	0.0000604	0.0012635	*	-0.0000048
Log	-0.0001226	-0.0001339	0.0000604	0.0004740		
MLE	-0.0023229	-0.0006203	0.0000604	-0.0003015	*	-0.0000584
n= 2	-0.0043896	-0.0010986	0.0000604	-0.0010606		
n= 3	-0.0063114	-0.0015671	0.0000604	-0.0018016		
PL	0.0000480					
ML H	0.0000100	parameter b =		0.22203		
ML G	0.0000000	parameter c =		1.05503		

Program: ASPMMSIM A S Puzey 1990

Mortality distribution : Gompertz

Mortality rate : 0.20 Distn parameter : 1.05

Withdrawal rate : 0.40 Random deaths/wdls

No of lives exposed from beginning of year : 10000

No of lives exposed from duration 3 months : 10000

No of runs : 500

TABLE I - Average observed q

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1968364		0.1986719		
Meth of Moments	0.1995658	0.2002481	0.2011643	*	0.1999198
Implication-B	0.1995016	0.2002569	0.2012180	*	0.1999008
Conventional	0.1994520	0.2002775	0.2013331	*	0.1998885
Max Likelihood	0.1994520	0.2001337	0.1997724	*	0.2000152
Time-count	0.2004334	0.2001337	0.2013331	*	0.2000692
Product Limit	0.2000234				
MLE - Rect Hyper	0.2000854	parameter b =	0.22018		
MLE - Gompertz	0.2000749	parameter c =	1.05494		

TABLE II - Standard deviation of observed q

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.0031818		0.0032464		
Meth of Moments	0.0032693	0.0032910	0.0033180	*	0.0032981
Implication-B	0.0032699	0.0032956	0.0033169	*	0.0032834
Conventional	0.0032694	0.0033031	0.0033381	*	0.0032905
Max Likelihood	0.0032694	0.0032904	0.0032683	*	0.0032897
Time-count	0.0033248	0.0032904	0.0033381	*	0.0032908
Product Limit	0.0034279				
MLE - Rect Hyper	0.0032898	sd of para b =	0.33021		
MLE - Gompertz	0.0032829	sd of para c =	0.07705		

TABLE III - Confidence interval for q - lower limit

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1965518		0.1983816		
Meth of Moments	0.1992734	0.1999538	0.2008676	*	0.1996248
Implication-B	0.1992091	0.1999621	0.2009213	*	0.1996071
Conventional	0.1991595	0.1999821	0.2010345	*	0.1995942
Max Likelihood	0.1991595	0.1998394	0.1994800	*	0.1997210
Time-count	0.2001360	0.1998394	0.2010345	*	0.1997749
Product Limit	0.1997168				
MLE - Rect Hyper	0.1997912	para b lower limit=	0.19065		
MLE - Gompertz	0.1997813	para c lower limit=	1.04804		

TABLE IV - Confidence interval for q - upper limit

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	0.1971209		0.1989623		
Meth of Moments	0.1998583	0.2005425	0.2014611	*	0.2002148
Implication-B	0.1997941	0.2005516	0.2015147	*	0.2001945
Conventional	0.1997444	0.2005729	0.2016317	*	0.2001828
Max Likelihood	0.1997444	0.2004280	0.2000647	*	0.2003094
Time-count	0.2007308	0.2004280	0.2016317	*	0.2003636
Product Limit	0.2003300				
MLE - Rect Hyper	0.2003797	para b upper limit=	0.24972		
MLE - Gompertz	0.2003686	para c upper limit=	1.06183		

TABLE V - Diff wrt two-para Rect Hyper/Gompertz MLE

	Level Dths	Const Mu	Balducci	*	1.1 Gompz
Hoems Adjusted	-0.0032386		-0.0014030		
Meth of Moments	-0.0005091	0.0001732	0.0010894	*	-0.0001552
Implication-B	-0.0005733	0.0001819	0.0011431	*	-0.0001741
Conventional	-0.0006230	0.0002026	0.0012582	*	-0.0001864
Max Likelihood	-0.0006230	0.0000588	-0.0003026	*	-0.0000597
Time-count	0.0003584	0.0000588	0.0012582	*	-0.0000057
Product Limit	-0.0000516				
MLE - Rect Hyper	0.0000105	parameter b =	0.22018		
MLE - Gompertz	0.0000000	parameter c =	1.05494		

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