

## 2 A Bare Bones Model

The demographic component of the model developed in this chapter consists primarily of a set of mutually exclusive and exhaustive categories into which members of a population may be classified and a set of parameters that specify birth rates, death rates and rates of movement between categories. Models of this sort have a long history in demography and related social sciences (Feeney 1973). They are generally linear, and their behavior is usually simple and well understood.

The essential epidemiological element of the model is the dependence of rates of new infection on the proportion of the population who are already infected. Deciding how this dependence should be specified is perhaps the single most important epidemiological aspect of the model. To explore the possibilities we develop in this chapter a simple “bare bones” version of our “minimalist” model that does not incorporate age or sexual activity status.

We study this model for two main reasons. First, to examine the sensitivity of long and short term model behaviour to assumptions about the scale of the demographic and epidemiological parameters, particularly looking at interactions and non-linear effects. Second, to get some clues about the useful scale of certain age-specific parameters in the full model for which we have no empirical evidence at present.

### Model specification

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We consider a population divided into two classes, uninfected and infected. The numbers of uninfected and infected persons at time  $t$  are denoted by  $Y(t)$  and  $Z(t)$ , respectively. Births are generated by a birth rate  $\mathbf{b}$  applied to the total population, infected as well as uninfected. Uninfected persons are subject to a mortality risk  $\mathbf{m}$  and a risk  $\mathbf{I}$  of new infection. Infected persons are subject to the same mortality risk as uninfected persons (the risk of death due to non-HIV-related causes) and to an additional mortality risk  $\mathbf{a}$  due to HIV-related causes.

The model is defined by three equations, two defining the change in numbers uninfected and infected over a single time period in terms of the parameters  $\mathbf{b}$ ,  $\mathbf{m}$ ,  $\mathbf{I}(t)$  and  $\mathbf{a}$ , and a third defining the dependence of  $\mathbf{I}(t)$  on the proportion of infected persons. The first two equations are as follows:

$$Y(t+1) = Y(t) \exp\{-[\mathbf{I}(t) + \mathbf{m}]\} + \mathbf{b}[Y(t) + Z(t)] \quad (1)$$

$$Z(t+1) = Z(t) \exp\{-[\mathbf{a} + \mathbf{m}]\} + Y(t) \frac{\mathbf{I}(t)}{\mathbf{I}(t) + \mathbf{m}} [1 - \exp\{-[\mathbf{I}(t) + \mathbf{m}]\}] \quad (2)$$

$Z(0)$  is assumed to be zero, to represent a baseline year in which the population is free from any infection.

The first of these equations may be read as saying that the number of uninfected persons at time  $t+1$  equals the number of uninfected persons present at time  $t$  who do not die or become infected by time  $t+1$  plus the number of births to the population between time  $t$  and time  $t+1$ . The second may be read as saying that the number of infected persons at time  $t$  equals the number of

infected persons at time  $t$  who do not die by time  $t + 1$ , whether of non-HIV-related or of HIV-related causes, plus the number of uninfected persons at time  $t$  who become infected between time  $t$  and time  $t + 1$ . The exponential expressions are standard mathematical demography for survival and multiple decrements (see Appendix to the main model design document).

The force of infection  $I(t)$  is assumed to have two additive components, an “endogenous” component proportional to current prevalence and an “exogenous” component independent of current prevalence. The endogenous component is the product of the proportion of infected persons and a factor consisting of two additive components. One of these components is time independent and always positive. This component represents the notion that reproductive sex carries a finite risk of HIV transmission in a population containing some infected sexually active individuals. The other component is time-dependent, and represents the idea that sexual behavior may involve different levels of risk. This risk may be lowered in response to the perceived threat of the epidemic by behavioural change (condom use, lower rates of partner change) or medical interventions (treatment of other STDs which may be transmission co-factors).

Writing  $P(t) = Y(t) + Z(t)$  for the total population at time  $t$ , the force of infection  $I(t)$  can be defined as:

$$I(t) = i(t) + [k + q(t)] \frac{Z(t)}{P(t)} \quad (3)$$

Here  $i(t)$  denotes the time dependent exogenous component,  $k > 0$  the time independent endogenous component and  $q(t)$  the time dependent endogenous component. Both  $i(t)$  and  $q(t)$  are non-negative, and may be set to zero for some or all of the projection period.

The state of the population and the scale of the infection force at time  $t+1$  can thus be derived from the state at time  $t$ , and by repeated application of the equations we can obtain the state at any time from a definition of starting conditions at time  $t = 0$ .

Prevalence of HIV at a point in time  $t$  is simply the proportion of the total population infected, the ratio  $Z(t)/P(t)$ , and is found directly from the values of  $Y(t)$  and  $Z(t)$  given by equations (1-2). Incidence in the time interval  $t$  to  $t+1$  is defined as new infections divided by the population at risk at the beginning of the interval, i.e. the HIV negative  $Y(t)$ . New infections are given by the second term on the right in equation (2), dividing this through by  $Y(t)$  shows us that incidence can be calculated from the values of the forces of infection  $I(t)$  and mortality  $m$ :

$$\text{incidence} = \frac{I(t)}{I(t) + m} [1 - \exp\{-[I(t) + m]\}]$$

## Experimentation

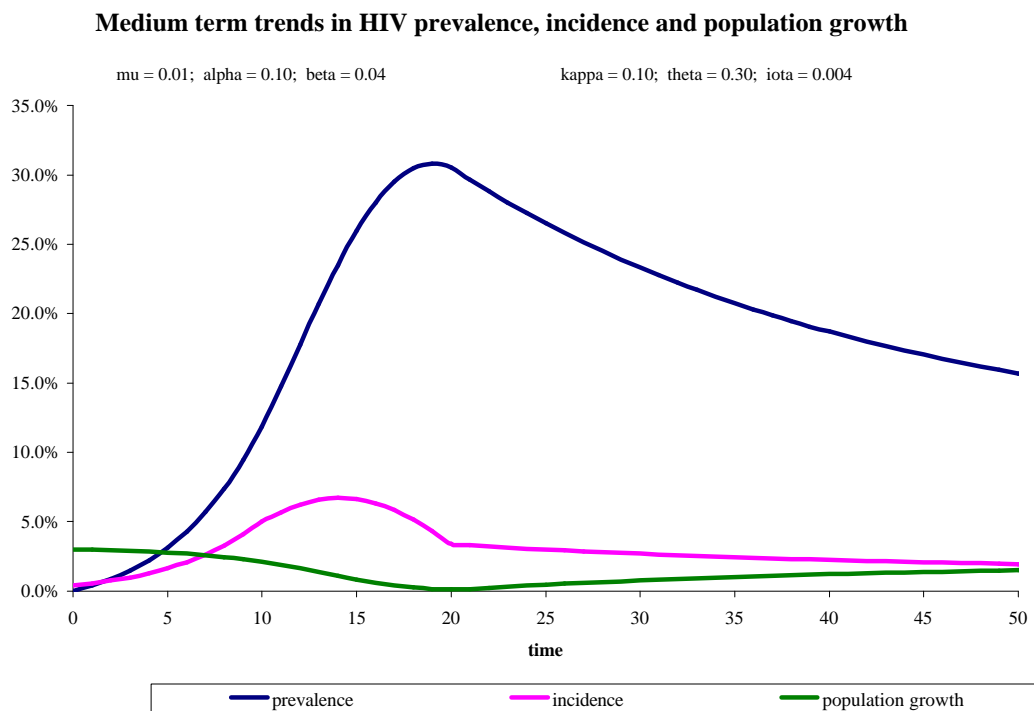
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We experiment with various forms for the components of  $I(t)$  to understand what they imply for the short and long term behaviour of incidence and prevalence and how they interact with one another. A default set of parameter values is chosen for the demographic and epidemiological parameters, to tie in with the demographic circumstances of “typical” East African populations, and to yield an epidemic trend in which prevalence peaks within 20 years of the base year and then subsides to a non-zero stable endemic prevalence.

Table 1: Default parameter values

Parameter	Default value(s)	Notes
$m$	0.01	the right order of magnitude for crude death rates in East Africa before the HIV epidemic
$a$	0.1	mortality of the HIV infected about 10 times that of the uninfected, mean survival time after infection 10 years
$b$	0.04	the right order of magnitude for crude birth rates in East Africa, together with CDR above gives 3% pa growth
$i(t)$	0.004 constant over time	combined with $k = 0.1$ gives an endemic prevalence level of about 10%
$k$	0.1	gives desired level and shape to prevalence trends in “Ugandan” epidemic in combination with selected $q(t)$ and $i(t)$ values
$q(t)$	0.3 decreasing to 0.0 between years 10 and 20	combined with $k = 0.1$ gives a peak prevalence level of about 30% at around 20 years after the baseline

Figure 1: Default epidemic trends



We may note some basic properties of the model which are obvious from the defining equations above:

- prevalence will never rise above zero unless  $i(t) > 0$  at some time  $t$
- endemic prevalence will remain above zero if  $i(t) > 0$  for all  $t > T$

Some properties of the model may be discovered by allowing the parameters to vary, one at a time through a wide set of possible values, and monitoring the effect this has on one possible outcome measure – endemic prevalence, which we define for convenience sake as prevalence measured 250 years from the base year. This definition is used not because it is realistic to project for such a long time into the future, but just because 250 years is sufficient for stability to develop in almost all the simulations we have investigated. This investigation shows us that:

- high mortality from causes other than HIV has no discernible effect on endemic HIV prevalence
- high HIV-related mortality has a powerful negative effect on endemic HIV prevalence, because of the combined effect of shorter survival time directly lowering prevalence for a given incidence, and the indirect effect of lower prevalence lowering incidence
- high fertility has a strong negative effect on prevalence, because it supplies new HIV negative individuals to bolster the uninfected population
- exogenous risk, if applied constantly throughout the time period of the projection, has a strong positive effect on prevalence. However, if it is used just at time  $t = 0$  to “kick start” the system and then set to zero it has no effect on endemic prevalence
- the time independent component of endogenous risk has a very strong positive effect on endogenous prevalence - it may well be the most important determinant among the model parameters, though it is hard to say what are the sensible and realistic limits between which we should allow it to vary, since it represents the net effect of all the prevalence dependent factors which determine the “irreducible” force of infection.
- The time dependent component of endogenous risk, which we use to represent a possible combined behavioural response to the epidemic, by allowing it to decline to zero after an early high, has no detectable effect on long-term endemic prevalence. We also looked at the effects of changing the time window in which this variable is reduced to zero, but as long as this process occurs within the first 50 years of the projection cycle, it has no effect on endemic prevalence measured at 250 years.

The results of these sensitivity analyses are displayed in figure 2, which shows the generating parameters on the x axis on a logarithmic scale, so that their “natural” ranges of variation appear more-or-less comparable.

Figure 2:

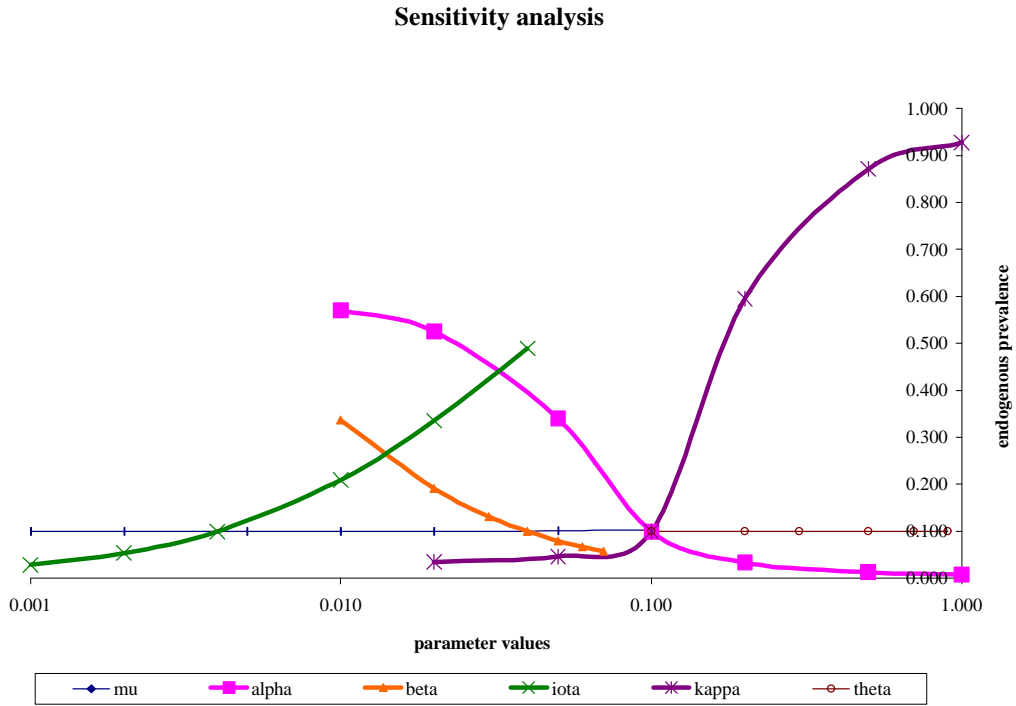
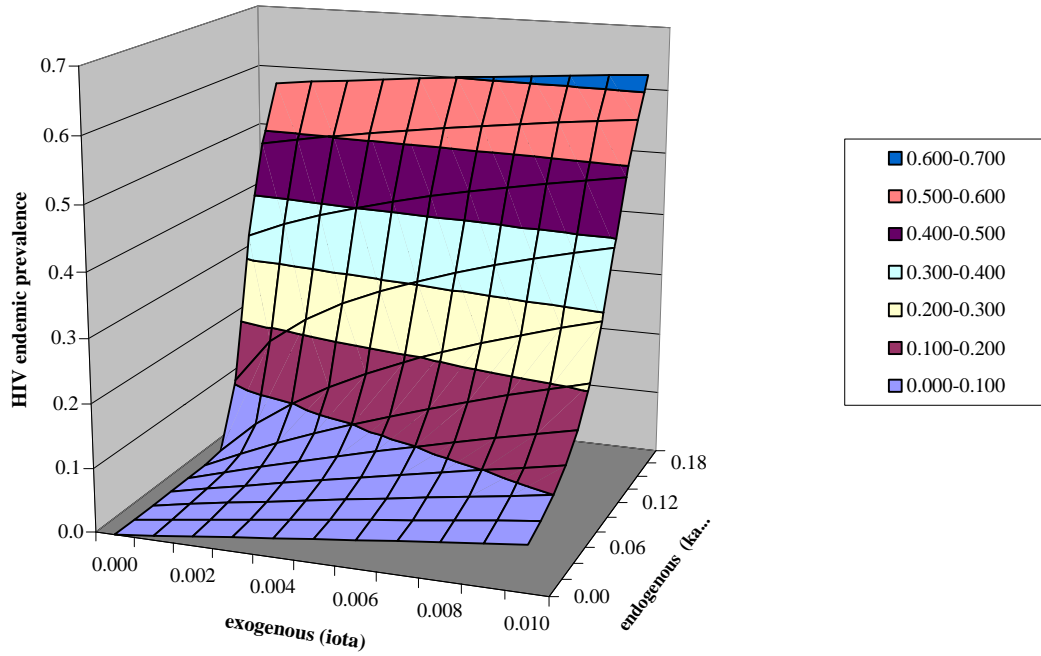


Figure 3:

**Interaction between endogenous and exogenous components of infection force**



We also examined interactions between several pairs of parameters – one of the more interesting results is shown in figure 3. This shows evidence of non-linear effects when we look at the simultaneous variation in the (constant) exogenous and endogenous components of the force of infection. We see that even if the exogenous component is kept at zero throughout the projection (after the initial impulse is given at time  $t = 0$ ), a large enough value of a constant of proportionality acting on prevalence will ensure that the epidemic does not die back completely. This can occur even if we do not stipulate any additional large behavioural effect ( $\theta$ ) which can be reduced substantially in the early years of the epidemic.

Figure 4

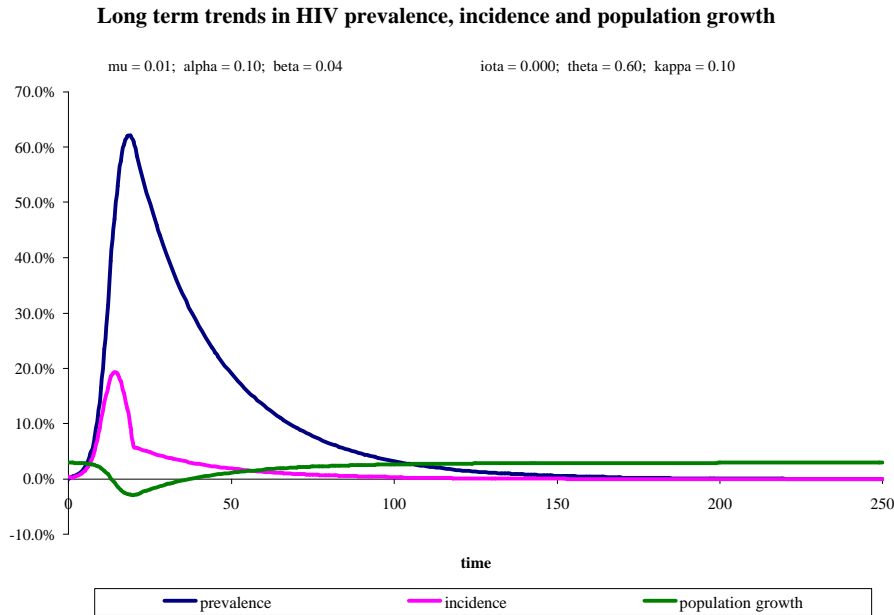
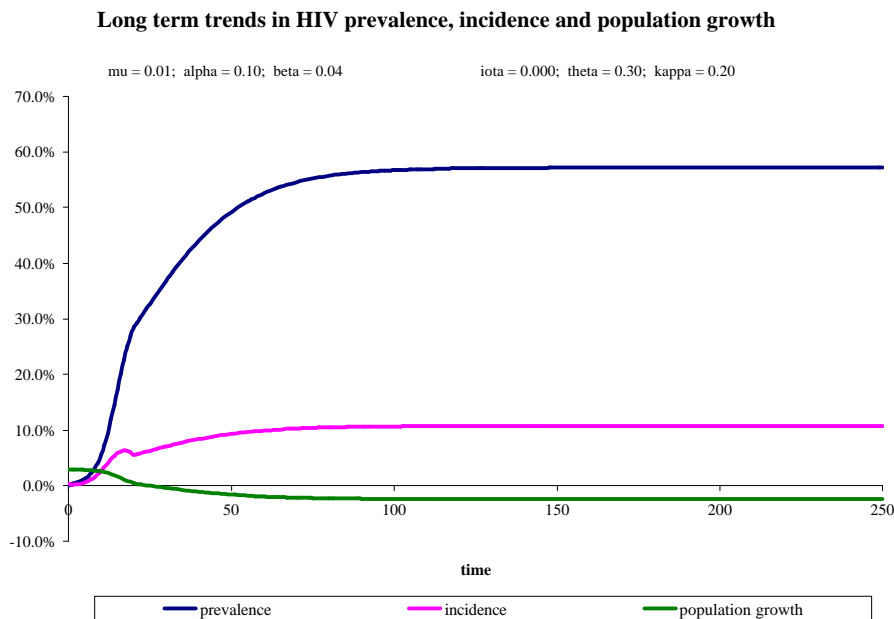


Figure 5



The default parameter values illustrated in figure 1 were chosen for their ability to generate the “peak and plateau” shape which is thought to be characteristic of certain kinds of epidemics. But the model is sufficiently flexible to allow us to describe many distinct patterns. Figures 4 and 5 illustrate two of these – one shows an epidemic in which prevalence rises to a considerably higher level in the short term than in the default scenario illustrated in figure 1, but then drops back down to virtually zero because of the rapid fall in the behavioural change component of the infection force. The second shows an epidemic in which prevalence attains a stable endemic level without reaching a preliminary peak. The graphs have been extended to 250 years to show convergence to stability in these two cases.

### **Approximate endemic solution – supplied by Marc Artzrouni**

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Marc Artzrouni suggested the following method for obtaining an approximate value for the endemic prevalence from a knowledge of the values of the stable input parameters, without performing the actual projection. The solution assumes that the time stable forces of change ( $m, a, i$ , and  $k$ ) are small enough to be able to use approximations of the sort

$$\exp(-a) \cong 1 - a$$

This would certainly be valid for the kinds of values of  $m, i$ , and  $k$  which are likely to be encountered in practice, the only doubt which might arise would concern the force of AIDS mortality,  $a$ , which might be of the order of 0.1, but even this would only produce an error of the order of 0.005

Writing  $p$  for endemic prevalence, the key equilibrium relationships are:

$$I = i + k \cdot p \tag{4}$$

since for suitably small  $I$  and  $m$ , the incidence rate is the same as the force of infection, and this is the expression for the endemic incidence.

$$r = b - m - a \cdot p \tag{5}$$

$$r = -(I + m) + \frac{b}{1 - p} \tag{6}$$

Equation (5) arises from a consideration of stable growth in the whole population, equation (6) from considering the annual stable growth in the number of uninfected individuals.

Endemic prevalence is then given by the “valid” root of the quadratic equation

$$(a - k)p^2 + (k - a - b - i)p + i = 0 \tag{7}$$

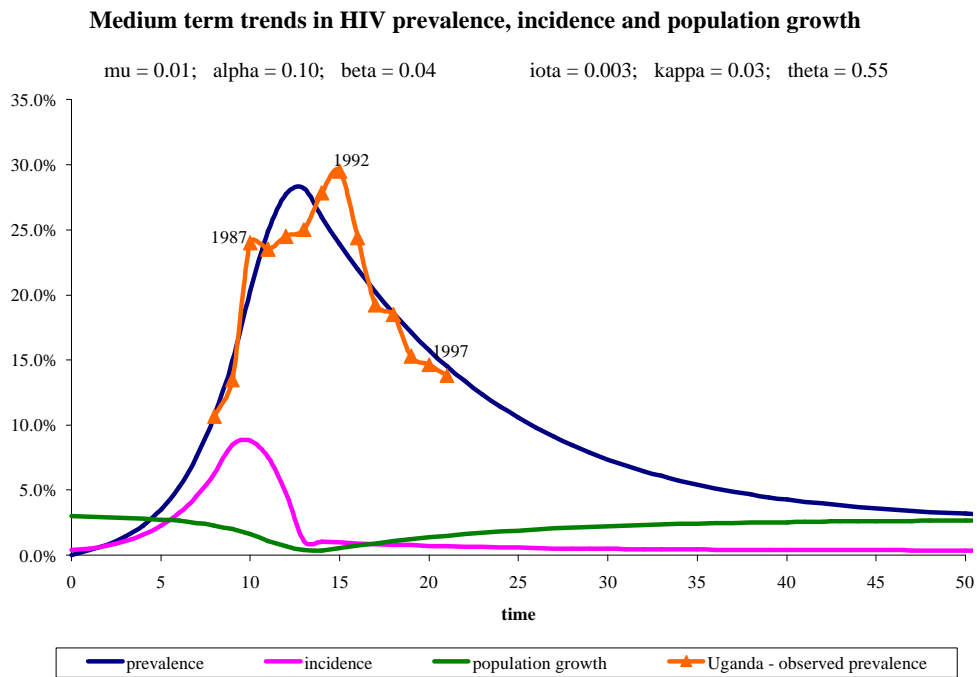
where by valid we mean that prevalence must be a proportion. The endemic incidence rate and stable population growth rate can be calculated from the prevalence using equations (4) and (5).

We have tried this approximation for various combinations of model parameters, and it seems to work very well.

## Fitting to real data

The bare bones model can easily be fitted to an empirical time series of prevalence data. Figure 6 shows a fitting to prevalence data from Uganda, for 1985 to 1998. Our recommended procedure is to fix the fertility and mortality parameters ( $m$ ,  $a$ ,  $b$ ) at plausible levels, and to choose a notional “zero year” for the start of the epidemic based on knowledge of the history of the epidemic in that population, and by a rough backward extrapolation of available data. A little experimentation with the values of the timing window for the behavioural change component can quickly help to locate the prevalence turning points in roughly the right years. A general function minimization routine can then be used to find the values of the components of the force of infection ( $i$ ,  $k$ ,  $q$ ) for which the differences between observed and fitted prevalence values are the smallest.

Figure 6



In the case of Uganda, the model achieves a respectable fit to the time series data on prevalence, and suggests convergence to an endemic prevalence level of about 2.5%. Looking at the size of the components of the force of infection, it is striking that in order to produce such a rapid decline as has apparently been observed in Uganda, it would be necessary for that part of the prevalence dependent component which can be eliminated to be almost 20 times the size of the fixed component, and we speculate that the elimination of this excess risk would have taken place over the remarkably short time period of just 4 years (corresponding to calendar years 1984 to 1988).