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ON APPLICATION OF KALMAN FILTER METHOD TO HIV/AIDS EPIDEMIC

M . GEETHA
HEAD AND ASSISTANT PROFESSOR OF MATHEMATICS
PG DEPARTMENT OF MATHEMATICS
SARADHA GANGADHARAN COLLEGE
PONDICHERRY – 605004 , INDIA

MAIL ID : m.geetha_06@yahoo.co.in

Abstract:

The epidemic of HIV infection and AIDS is still growing and has been steadily raising the national rankings of causes of death. The composition of AIDS population is changing both in geographic area and risk group. The changing behaviour of the epidemic necessitates our better understandings of the disease and the ways of intervention. One of the tools to facilitate this task is by the use of modelling the natural history of the epidemic. In recent years many factors, including therapy and behavioural changes have modified the course of the HIV/AIDS epidemic. To include these modifications in HIV/AIDS models, a recessive estimation technique such as Kalman Filter is used. The Kalman Filter approach was applied to a simple differential model to describe the observed HIV/AIDS epidemic in the homo/bisexual male community.

Keywords: Epidemic, HIV/AIDS, Infectives

INTRODUCTION

Because the AIDS disease has rapidly become a very serious disease with enormous impact, there is an urgent need for more accurate predictions of the future course of the epidemic. Statistical and mathematical modeling of the AIDS epidemic can help provide an understanding of the key factors that propagate the epidemic and a quantitative forecast of the course of the AIDS disease under different situations.

Public health authorities must answer several questions in the monitoring, planning, and intervention aimed at controlling the HIV/AIDS epidemic. Epidemiological HIV/AIDS modeling can help to answer these questions by making projections of the epidemic into the future.

The aim of this paper is to explore the potential of the Kalman Filter techniques in assessing the changing HIV/AIDS epidemic by means of dynamic models. We used a simple model to describe the H I V / A I D S epidemic in the homo/bisexual male community and applied the Kalman technique to this model. The main feature of our H I V / A I D S model, Introduction to the Kalman filter method, specifies the conditions for applying this filter are discussed here.

The HIV/AIDS Model

The model used in this study was applied to the spread of HIV in the homo/bisexual male population. The population at risk is divided into groups of susceptibles (X), infectives (Y), and diseased (Z). To describe the incubation period, the infective group is subdivided into a series *n* subgroups, in each of which the resident time has a negative exponential distribution. Thus the incubation time is a gamma distribution. Concerning the mixing pattern, for simplification, we have assumed no preferential choice between partners. We have also assumed that the infected group is mixed homogeneously throughout the population at risk and that individuals already having AIDS do not contribute to the spread of the disease.

The dynamic of susceptibles is given by $\frac{dX}{dt} = \lambda - \mu.X - \psi(t).X$ (1)

Where $X(t)$ is the number of susceptibles at time t, μ is the emigration plus mortality rate in the absence of HIV infection, and λ the recruitment of susceptibles per year, λ was calculated to have a stationary population in the absence of HIV infection. The dynamic parameter $\psi(t)$ describes the force of infection for a susceptible individual and is the probability of becoming infected by randomly chosen sexual partners per year:

$$\psi(t) = \sum_{i=1}^{n} \gamma_{i.Y_i(t)} \Big/ N(t)$$

$$\text{With } N(t) = X(t) + \sum_{i=1}^{n} Y_i(t) \quad (2)$$

Where N(t) is the total number of sexually active individuals and γ_i is the average transmission rate. We assume as usual that $\gamma_i = \beta_i c$, where β_i is the transistion probability per partner and c is the average number of new partners per year.

The model equations for the infected group are

$$\frac{dY_i}{dt} = \psi(t).X - (k_i + \mu).Y_i \quad \text{for i=1}$$

$$\frac{dY_i}{dt} = k_{i-1}.Y_{i-1} - (k_i + \mu).Y_i \quad \text{for i=2,n,} \quad (3)$$

Where $Y_i(t)$ is the number of infectives in subgroup i at time t and k_i is the incubation rate of subgroup i. The average incubation time τ is given by

$$\tau = \sum_{i=1}^{n} \frac{1}{k_i} \quad (4)$$

Finally, the model equation for cumulated AIDS cases [Z(t)] is

$$\frac{dZ}{dt} = k_n . Y_n \quad (5)$$

The basic reproduction rate R_o is the average number of secondary infections generated by one primary case in a susceptible population (if R_o is less than one, no epidemic will occur; if R_o is greater than one, the infection will spread in the population). In a multistage model, in which the incubation time is subdivided into n sub periods with constant or variable transmission probability per partner (β_i) , the R_o is computed as

$$R_o = \sum_{i=1}^{n} \beta_i . c_i . \tau_i . (1 - q_i) \quad (6)$$

with $\tau_i$the mean time spent in stage i and q_i the probability of removal before an infective reaches stage i:

$$\tau_i = \frac{1}{k_i + \mu} \quad (7)$$

$(1-q_i) = 1$ for i=1

$$(1 - q_i) = \frac{k_i}{k_i + \mu}(1 - q_{i-1}) \quad \text{for i>1} \quad (8)$$

Application of the Kalman Filter Method

The Kalman filter provides a linear minimum error variance estimation of the state characterized by a state-space model. With respect to other recursive methods such as recursive least squares, the Kalman filter has the advantage of addressing uncertainties (or noises) in both the model and the data. Admitting a degree of confidence in the model and a degree of uncertainty in the observations, the filter seeks for the best compromise between the two sources of errors.

The differential equations of the model can easily be incorporated into a state-space framework:

$$\frac{dx(t)}{dt} = f[x(t), \theta(t), t] + \xi(t) \quad (9)$$

$$y(t) = h[x(t), t] + \eta(t) \quad (10)$$

Equation (9) is the state equation, where f is a nonlinear function that expresses the relations between the state variables, and Equation (10) is the observation equation, where h describes the relations between the state variables and observations. In Equations (9) and (10), *x(t)* is the vector of state variables *{X(t),Y(t),Z(t)}, O(t)* is the vector of model parameters $\{\gamma_i, k_i\}$, *y(t)* is the vector of observations (cumulative AIDS cases reported), and ξ (t) and , η (t) are the vectors of system and observation noises. The Kalman filter method assumes that ξ (t) and , η (t) are Gaussian white noises, ξ (t) having zero mean and a variance-covariance matrix *Q(t)* and , η (t) having zero mean and a variance-covariance matrix *R(t).*

The model presented in Previous Section was used with four subgroups of infectives (n = 4). The four subgroups had the same negative exponential distribution of residence time (k_i= k for all i), the same infectiousness, and the same mean contact rate ($\gamma_i = \gamma$ for all i). The emigration plus mortality rate μ was estimated from the mean period of active life (18-60 years). For R_0, with constant transmission rate and constant incubation rate, Equation (6) is reduced to

$$R_o = \frac{\gamma}{k+\mu}\sum_{i=1}^{n}\left(\frac{k}{k+\mu}\right)^{i-1} \quad (11)$$

To match the model predictions with the observations, the Kalman filter requires: (i) the model inputs; (ii) the variance of the system error; (iii) the variance of the observation error, and (iv) the initial estimate of the state-parameter covariance matrix. These four points are discussed below:

(i) Initial values of the parameters {γ, k}: The initial values were estimated by least squares on the basis of data before 1985, using the Marquardt algorithm. In this early phase of the epidemic, the assumption of a model with constant parameters is reasonable.

(ii) System noise: The system noise ξ (t) represents all the unknown influences (simplifications in the model structure as well as uncertainties in inputs and parameters). Its variance-covariance matrix is a measure of the uncertainty of the model. It is assumed that the system noise at time t_i for i≠k.

In the present study, we expressed the variance of the state- parameter as

$$\sigma_{x_i}^2 = (\alpha_{x_i}\ x_i)^2,$$
$$\sigma_{p_i}^2 = (\alpha_{\theta_i}\ p_i)^2, \quad (12)$$

Where x and p are the state and parameter vectors, and $\sigma_{x_i}^2$ and $\sigma_{p_i}^2$ are the variances of states *{X, Y, Z }* and of parameters { γ, k }, respectively. The α_i's, which define the noise parameters, are scalars. Thus the variance-covariance matrix *Q(t)* of the system noise is defined as

$$Q(t) = \begin{bmatrix} \sigma_x^2 & 0 & 0 & 0 & 0 \\ 0 & \sigma_y^2 & 0 & 0 & 0 \\ 0 & 0 & \sigma_z^2 & 0 & 0 \\ 0 & 0 & 0 & \sigma_\gamma^2 & 0 \\ 0 & 0 & 0 & 0 & \sigma_k^2 \end{bmatrix} \quad (13)$$

(iii) Observation noise: η(t) represents the uncertainty associated with the observations. According to previous results, the variance of the observations was assumed to be

$$\sigma_y^2 = (\alpha_{R1}\ y)^2,$$
$$\sigma_y^2 = (\alpha_{R2}\ y)^2 \quad (14)$$

and the variance-covariance matrix *R(t)* of the observation noise was defined as

$$R(t) = \left[\sigma_y^2\right] \quad (15)$$

where y was the reported cumulated AIDS cases and σ_y^2 its variance. The two different periods were distinguished because more than 98% of the cases were reported.

(iv) Initial value of the state-parameter covariance matrix P(0|0): This matrix represents the uncertainty of the initial conditions of the state-parameter vector. The uncertainty of the initial conditions of the state-parameter vector was assumed to be cross uncorrelated and only the diagonal term was estimated. We assumed that P(0|0) had the simple form.

$$P(0|0) = \alpha_p \, Q(0) \qquad (16)$$

It should be noted that the effect of the initial variance-covariance matrix P(0|0) on the estimations of the state-parameter variables gradually decreases.

Conclusion

In this work, we have investigated the use of the Kalman filter in assessing the H I V / A I D S dynamics. We highlighted a noticeable change in some parameters of major epidemiological significance (average transmission rate, mean incubation rate, and basic reproduction rate), most probably because of prevention, changes in sexual behaviour, and the gradual introduction of treatment for infected individuals, including antiretroviral therapy and prophylaxis for opportunistic infections.

The Kalman approach offers a "data-based" understanding of the model dynamics.*A priori* assumptions in building the model are kept to a minimum, and additional parameter modifications are progressively introduced into the model by tuning the dynamics with the data, taking into account noises in the observations and uncertainty in the model equations. This approach allows assessment of the time-evolution of the major epidemiological parameters in the absence of appropriate external data sources and possible consequences of intervention measures. This qualitative information on the evolution of the parameters is of interest to policy-makers in controlling the epidemic and in health-care planning.

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