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Modeling Secondary Level of HIV Contact Tracing:

Its Impact on HIV Intervention

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Abstract.

Universal HIV testing program has currently been suggested for elimination of HIV

epidemic in Africa, although not without practical issues in its costs and full

implementation. A mathematical model is proposed which contains two levels of

detection of HIV-infectives through contact tracing of known infectives in addition to

detections through other means, e.g., random testing. Boundary disease-free equilibria

and unique positive equilibrium are obtained. Simulations using Cuban contact

tracing data were performed to illustrate that: (1) contact tracing is an important

intervention measure which might be less effective than random screening but

perhaps more cost-effective, and hence are ideal for large-scale intervention programs in developing countries; (2) by adding a secondary level of contact tracing to the model, the basic disease transmission dynamics might be significantly changed where, depending on the parameter values, the prevalence level of the epidemic at the time of implementation of contact tracing program might become crucial in determining whether the measure will be effective in preventing disease infections and in its eventual eradication. Our results indicate that contact tracing for detection of HIV infectives could be suitably used to remedy inadequacies in universal HIV testing program and to design timely and effective intervention measures.

Keywords: Cuba, contact tracing, intervention, random screening, universal testing.

中文摘要

我們提出一個數學模型包含兩層透過已知愛滋病感染者的接觸者追蹤
(contact tracing)，檢驗出新愛滋病感染者，以及其他的檢驗方法如隨機測
試。我們獲得了無疾病平衡點和唯一有疾病平衡點的結果，並進行古巴接
觸者追蹤資料的模擬，來說明：

(1) 接觸者追蹤是一個重要的干預方法，也許比隨機篩檢較不有效，但或
許是較有成本效益的。而且在開發中的國家中，大規模的干預計畫是適合
的。

(2) 藉由在模型上增加一個接觸者追蹤的第二層已知愛滋病感染者的接觸
者追蹤，可能顯著改變基本的疾病傳輸動態，對防止疾病傳染和在它最後
的根除上有極重要性。

我們的結果顯示已知愛滋病感染者的接觸者追蹤可能適合地用在補救在
HIV 隨機篩檢之不足，是個有效的干涉措施。

關鍵字：古巴，接觸者追蹤，干預措施，隨機篩檢。
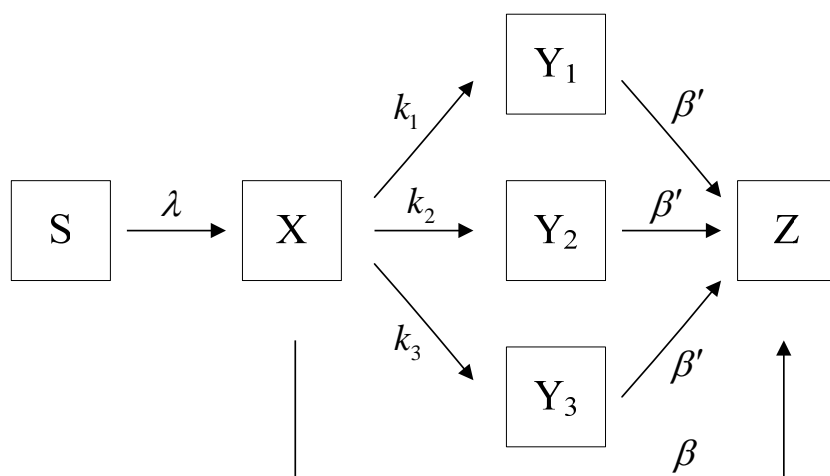
1. The Model

Fig. 1 Model flowchart

We consider a compartmental model as diagramed in Fig 1. The model variables are

given below:

$S(t)$ is the susceptible population.

$X(t)$ is the number of HIV-infected persons that do not know they are infected at time

t.

$Y_1(t)$ is the number of HIV-infected persons that are known by the health authority to

be infected at time t and were detected in a random type search.

$Y_2(t)$ is the number of HIV-infected persons that are known by the health authority to

be infected at time t and were detected at the first level of contact tracing as past

contacts (or sexual partners) of Y_1.

$Y_3(t)$ is the number of HIV-infected persons that are known by the health authority to

be infected at time t and were detected at the second level of contact tracing as past

contacts of Y_2.

Z(t) is the number of persons with AIDS at time t.

The model parameters are listed below:

λ : the rate of recruitment of new HIV-infected persons infected by X(t).

k_1 : the rate at which the unknown HIV-infected persons are detected by the system, independently of other HIV-positive persons (through "random" screening).

k_2 : the rate at which the unknown HIV-infected persons are detected by the system through contact of Y_1.

k_3 : the rate at which the unknown HIV-infected persons are detected by the system through contact of Y_2.

β : the rate at which the undetected HIV-positive persons develop AIDS.

β' : the rate at which the detected HIV-positive persons develop AIDS.

μ : the mortality rate of the sexually active population.

μ' : the mortality rate of the population with AIDS.

Following previous modeling work (e.g. de Arazoza & Lounes, 2002; Hsieh *et al*., 2005; Lounes *et al*., 2008), we assume a constant recruitment rate λ of new infectives, infected by infectives who did not know they were infected. The assumption of linear rate of recruitment of new HIV-infected persons infected by X(t), λ X, is based on our background setting of Cuba, where the prevalence is low. More

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precisely, it can be considered as a linear approximation of standard incidence, $\lambda\,XS/(S+X+Y_1+Y_2+Y_3)$, when the total number of HIV-infectives, $X+Y_1+Y_2+Y_3$, is small compared with S. We also assume linear detection rates by contact tracing, k_2 and k_3, where a certain fraction of previous contacts of a known infective is successively traced and tested to be HIV-positive. A class of linear and nonlinear functions for detection via contact tracing was considered in Hsieh et al (2005), the nonlinear detection by contact tracing term we used in this model is the one found to be give best fit for Cuban HIV data. Moreover, estimates for k_2 were also obtained in Hsieh et al. (2005).

We also assume that the infection by detected infectives is negligible when compared with infection rate by the unknown infectives, since it was estimated in de Arazoza & Lounes (2002), using Cuban HIV/AIDS data between 1986-2000, that the infection rate by the known infectives in Cuba is only around 5.79% (SD=3.55) of that of unknown infectives. We also ignore the contact tracing at the third level and after, since the tertiary levels of detections are comparatively small. Moreover, we assume a nonlinear detection rate which was determined to be the best among a class of linear and nonlinear rates studied in Hsieh *et al.* (2005), also by fitting Cuban HIV/AIDS data.

The model dynamics is described by the following system, with the time unit in

years:

$$\frac{dS}{dt} = \Lambda - \left(\lambda + \mu\right)X$$

$$\frac{dX}{dt} = \left(\lambda - \mu - \beta - k_1\right)X - k_2 Y_1 X / (X + Y_1 + Y_2 + Y_3)$$
$$\qquad - k_3 Y_2 X / (X + Y_1 + Y_2 + Y_3),$$

$$\frac{dY_1}{dt} = k_1 X - \left(\mu + \beta'\right)Y_1, \qquad\qquad\qquad (2.1)$$

$$\frac{dY_2}{dt} = k_2 Y_1 X / (X + Y_1 + Y_2 + Y_3) - \left(\mu + \beta'\right)Y_2,$$

$$\frac{dY_3}{dt} = k_3 Y_2 X / (X + Y_1 + Y_2 + Y_3) - \left(\mu + \beta'\right)Y_3,$$

$$\frac{dZ}{dt} = \beta X + \beta'\left(Y_1 + Y_2 + Y_3\right) - \mu' Z.$$

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