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# SPREAD OF HIV/AIDS-FUTURE PROSPECTS

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## Abstract

This study consists of a pure statistical model for estimating the rate of spread of Human Immunodeficiency Virus as well as AIDS with the help of available secondary data of Uttar Pradesh. Data on some applicable variables like year of test, age group, gender, mode of transmitting disease and the percentage which is positive while testing were analyzed. The Generating function approach ahs been used to solve the associated Birth Process model. A reduction from normal population is numerically noticed through the use of Birth Process model. It is found that the age group (30-39) is on the greatest risk as out of an assumed 10500 members of each group while the unsafe heterosexual relations are the biggest mode of transmitting disease.

**Key words**: Statistical Model, Estimation Heterosexual, HIV.

## 1. Introduction

AIDS is the most severe consequences of infection with the Human Immunodeficiency Virus (HIV). It is invariably fatal. The AIDS appeared as if from nowhere in the spring of 1981. It was actually first appeared in 1979 and was brought to the attention of the medical community in 1981.

It is the disease that is changing the human history. Many research groups in the world have produced models of varying degrees of complexities to describe the spread of HIV/AIDS epidemic. While the statistical models use the HIV/AIDS cases data for short term projections of HIV/AIDS cases by applying statistical extrapolation techniques such as growth curves, power index curves, log linear models on doubling times to the observed temporal curves of reported cases.

It is known that time, life and risks are three basics elements of stochastic processes. The study has made use of generating function approach to solve the associated birth process model. Data on related variables comprising year of test, route to transmission of disease, age group, gender as well as the percentage that tested positive were analyzed.

Brookmayer and Gail (1986) addressed the projection of the future number of people who will be diagnosed with AIDS. Brookmayer and Liao (1990) presented a paper on statistical modeling of the AIDS epidemic for forecasting health care needs. Joel and Frank (1990) have used HIV/AIDS back calculation regression model with linear inequality constraints to estimate cumulative adult/adolescent HIV infection. Crawford (1990) has projected a model for reduction in new AIDS incidence followed by a long slower resurge. Solomon and Wilson (1990) have showed the method of back projection to applied the incidence of HIV infection, extended to incorporate distribution changes due to treatment effect (AZT). Lee and Carter (1992) has used the time series methods to make long run forecasts with confidence intervals of age specific

mortality in the U S. Wu and Zhang (2002) introduced a class of semi parametric NLME models. A basis based approach is proposed to fit a model for study of long term HIV dynamics. The MTCT model of Waema (2002) and the improved SIA- model of Waema and Olowofeso (2005) are also taken as a guideline for the study.

## 2. Material and Methods

Relevant secondary data of HIV sero-positive of U.P from the duration of 2002-07 were used in the study. This is later classified on the basis of year of test, route to transmission of disease, age group, gender, population that reported for testing and percentage that tested positive. The deterministic model can be used for estimation of parameters and due to all taken care; the model should help in estimation of the infection concerning the different age groups, both sex and for different route of disease transmit ion.

### Formulation of Birth Process

Each new HIV infection is taking as an addition to the HIV/AIDS family. So the pure birth process from stochastic process is considered as follows:

Let the rate of birth within time interval (t,$t+\Delta t) = \lambda$

Probability of more than one event occurring in time interval (t,$t+\Delta t) = o(\Delta t)$

Probability of k events occurring in time t = $P_k$

The initial conditions are $P_0(0) = 1$, $P_k(0) = 0$, (k>0)

Let the probability of 1 birth or a new event will occur within time interval

(t,$t+\Delta t) = \lambda_k(t)\Delta t + o(\Delta t)$

Probability that no event occur within time interval (t,$t+\Delta t) = 1 - \lambda_k(t)\,\Delta t + o(\Delta t)$

Now considering two possible consecutive independent events,

$P_k(t,t+\Delta t) = [1 - \lambda_k(t)\,\Delta t + o(\Delta t)]\,P_k(t) + [\lambda_{k-1}(t)\,\Delta t + o(\Delta t)]\,P_{k-1}(t)\,o(\Delta t)$

$= [1 - \lambda_k(t)\,\Delta t]\,P_k(t) + [\lambda_{k-1}(t)\,\Delta t]\,P_{k-1}(t) + o(\Delta t)^3$

It is assumed that more than one person cannot be infected simultaneously from the same source at the same time,

Then $o(\Delta t) \to 0$

Hence $P_k(t,t+\Delta t) = [1 - \lambda_k(t)\,\Delta t]\,P_k(t) + [\lambda_{k-1}(t)\,\Delta t]\,P_{k-}$

$P_k(t,t+\Delta t) - P_k(t) = [-P_k(t)\,\lambda_k(t) + \lambda_{k-1}(t)\,P_{k-1}(t)]\,\Delta t$

$\Rightarrow \frac{Pk(t,t+\Delta t) - Pk(t)}{\Delta t} = [-P_k(t)\,\lambda_k(t) + \lambda_{k-1}(t)\,P_{k-1}(t)]$

Taking it as $\lim_{\Delta t \to 0} \frac{Pk(t,t+\Delta t) - Pk(t)}{\Delta t} = \frac{d}{dt} P_k(t)$

Then $P_k'(t) = [-P_k(t)\,\lambda_k(t) + \lambda_{k-1}(t)\,P_{k-1}(t)]$ (1)

Now since $\lambda = rate$ and k = population at time t; then,

Mean=k $\lambda$.

Now let $\lambda_k = k\,\lambda$.

Then eq.(1) becomes $P_k'(t) = -k\,\lambda\,(t)\,P_k(t) + (k-1)\lambda(t)\,P_{k-1}(t)$ for k>1 (2)

For k=1, it changes as

$P'_1(t) = -\lambda(t) P_1(t) + 0$

$\therefore$ eq. (2) exists for $k \geq 1$

I.e. $P'_k(t) = -k\lambda(t) P_k(t) + (k-1)\lambda(t) P_{k-1}(t)$ (3)

To solve eq. (3) considering the probability generating function (p.g.f) approach,

$G_x(s, t) = \sum_{k=1}^{\infty} Pk(t) s^k$

Multiplying (3) by $s^k$ and summing over k to have,

$\sum_{k=1}^{\infty} P'_K(t) s^k = -\lambda \sum_{k=1}^{\infty} k P_k(t) s^k + \lambda \sum_{k=1}^{\infty} (k-1) P_{k-1}(t) s^k$ (4)

Now let

$G_x(s, t) = \sum_{k=1}^{\infty} Pk(t) s^k$ (5)

Then $\frac{\partial}{\partial t} G_x(s, t) = \sum_{k=1}^{\infty} Pk(t) s^k$ (6)

And $\frac{\partial}{\partial s} G_x(s, t) = \sum_{k=1}^{\infty} k\, Pk(t) s^{k-1}$ (7)

Multiplying (7) by $\lambda s$ and $\lambda s^2$ in succession and get,

$$\lambda s \frac{\partial}{\partial s} G_x(s, t) = \lambda \sum_{k=1}^{\infty} k\, Pk(t) \quad (8)$$

$$\lambda s^2 \frac{\partial}{\partial s} G_x(s, t) = \lambda \sum_{k=1}^{\infty} (k-1) Pk(t) s^{k+1} \quad (9)$$

Since the two consecutive probabilities $P_k$ and $P_{k-1}$ have been considered from the beginning,

Then let $k \rightarrow k-1$ in (9) to have,

$$\lambda s^2 \frac{\partial}{\partial s} G_x(s, t) = \lambda \sum_{k=1}^{\infty} (k-1) Pk-1(t) s^k \quad (10)$$

Putting (6), (8) and (10) in eqn.(4),

Becomes $$\frac{\partial}{\partial t} G_x(s, t) = -\lambda s \frac{\partial}{\partial s} G_x(s, t) + \lambda s^2 \frac{\partial}{\partial s} G_x(s, t) \quad (11)$$

Eqn. (11) is a linear probability differential equation with auxiliary equations

$$\frac{dt}{1} = \frac{ds}{\lambda s(1-s)} = \frac{dGx(s,t)}{0}$$

To get the solution, first consider:

$$\frac{dt}{1} = \frac{dGx(s,t)}{0}$$

$$\Rightarrow \int dGx(s,t) = \int 0\, dt$$

$$\Rightarrow Gx(s,t) = c \quad (1^{st} \text{ sol.})$$

Then consider

$$\frac{dt}{1} = \frac{ds}{\lambda s(1-s)}$$

$$\Rightarrow \int \lambda\, dt = \int \frac{ds}{s(1-s)}$$

This will be solved by partial fraction, and get:

$$\lambda t + c1 = \log_n s - \log_n (1-s) + c_2$$

$$\lambda t = \log_n \frac{cs}{(1-s)}$$

Or $\frac{(1-s)}{s} e^{\lambda t} = c$ ($2^{nd}$ sol.)

Hence the general solution is- $$Gx(s,t) = x\left(\left(\frac{(1-s)}{s}\right) e^{\lambda t t}\right) \quad (12)$$

Equation (12) shows the most general solution for birth process and this forms the birth process model that can be used to estimate the number of infected person after (t) time interval when the rate of infection($\lambda$) and initial population (k) are known.

## 3. Results and Discussions

The well known Birth process model-

$$P_k(t) = -k\lambda(t) P_k(t) + (k-1)\lambda(t) P_{k-1}(t)$$

Combined with the obtained partial differential equation:-

$$\frac{\partial}{\partial t} G_x(s, t) + \lambda s(1-s) \frac{\partial}{\partial s} G_x(s, t) = 0$$

With the solution of this partial differential equation, the general solution of Birth Process Model is:-

$$Gx(s,t) = x\left(\left(\frac{(1-s)}{s}\right) e^{\lambda t t}\right)$$

## Empirical Illustrations

$\lambda = rate$ of HIV infection; s= initial population

t = time of testing (say 1 year); $Gx(s,t)$=Population getting infected

| Year | Age | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | < 14 | 15-19 | 20-24 | 25-29 | 30-39 | 40-49 | 50+ | others |
| 2002 | 0.60 | 0.13 | 1.18 | 2.60 | 5.01 | 1.79 | 0.60 | 0.05 |
| 2003 | 0.44 | 0.15 | 0.96 | 1.98 | 4.32 | 1.63 | 0.33 | 0.01 |
| 2004 | 0.50 | 0.13 | 0.88 | 1.58 | 3.81 | 1.28 | 0.35 | 0.00 |
| 2005 | 0.71 | 0.12 | 0.81 | 2.06 | 4.29 | 1.62 | 0.42 | 0.00 |
| 2006 | 0.79 | 0.12 | 0.93 | 2.04 | 5.22 | 1.91 | 0.56 | 0.01 |
| 2007 | 0.64 | 0.08 | 0.62 | 1.43 | 3.52 | 1.42 | 0.38 | 0.01 |
| Total | 0.61 | 0.12 | 0.89 | 1.95 | 4.36 | 1.61 | 0.44 | 0.01 |

**Table 1: Percentage of infection among tested individual**

Thus started with the age group (0-14),

$\lambda$ =0.61

t=1

s=10500

$$Gx(10500,1) = x((\frac{(1-10500)}{10500})\, e^{(0.61)1}) = -1.84 \sim 1$$

(Negativity implies reduction from normal population)
Thus after 1 year one people will get infected from the population provided that the rate of infection and population remain constant.

## Illustrations according to the age group

**Age group (less than 14):** Estimated number of infection $Gx(s,t)$ with respect to time.

$\lambda$ =0.61

s=10500

| T | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | $\sum_{t=1}^{10} Gx(s,t)$=969 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| $Gx(s,t)$ | 1 | 3 | 5 | 11 | 21 | 38 | 71 | 131 | 242 | 445 | |

Thus within 10 years approx. 969 individuals would have got infected in the age group ( less than 14) among the 10500 population of less than 14 years while the rate of infection ($\lambda$ =0.61) remains constant. It is also shown by means of the following figure.

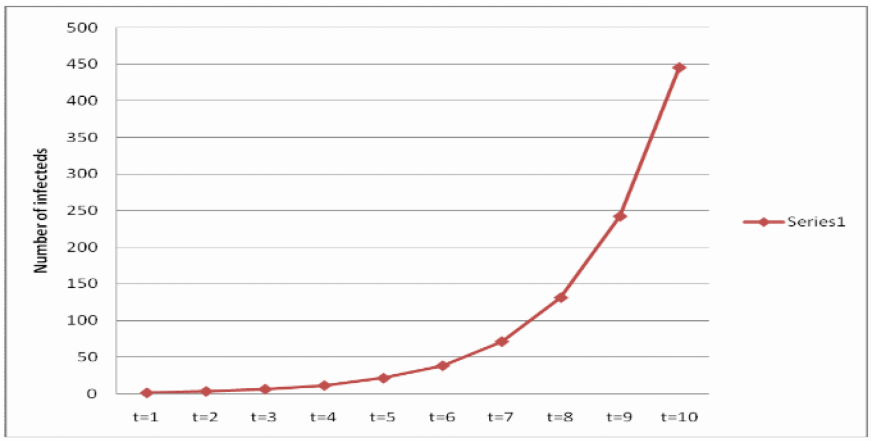


Table 2 shows the similar calculations for all the other observed age groups.

| **Age Groups** | less than 14 | 15-19 | 20-24 | 25-29 | 30-39 | 40-49 | 50+ | others |
|---|---|---|---|---|---|---|---|---|
| **rate of infection (λ)** | 0.61 | 0.12 | 0.89 | 1.95 | 4.36 | 1.61 | 0.44 | 0.01 |
| **Estimation** | 969 | 16 | 12432 | 17154 (up to 5 yrs.) | 6124 (up to 2 yrs.) | 15678 | 226 | 10 |

**Table 2: Estimated no. of infected individuals for different age groups**

It is observed from Table 2 that within a period of 10 years approx. the highest infection rate ($\lambda$ =4.36) is in the age-group 30-39 followed by $\lambda$ =1.95 in the age group 25-29, $\lambda$ =1.61 in the age group 40-49, $\lambda$ =0.89 in the age group 20-24, $\lambda$ =0.61 in the age group less than 14, $\lambda$ =0.44 in the age group $50^{+}$, $\lambda$ =0.12 in the age group 15-19 and lowest $\lambda$ =0.01 for others. The corresponding estimated number of individuals is shown in Table 2 accordingly.

**Age group (not specified)**

Due to the uncertainly of determining accurate age and having lowest infection rate, approx.10 individuals would have got infected in this group within the time of 10 years, while the rate of infection ($\lambda$ =0.01) remains constant. Table-3 shows the rates of infection according to different modes of transmission.

| Mode of transmission | Homo-sexual | Hetro-sexual | Blood & Blood pro | IDU | Parent to child | others | not speci-fied | Male | Female |
|---|---|---|---|---|---|---|---|---|---|
| rate of infection(λ) | 0.05 | 8.86 | 0.23 | 0.11 | 0.55 | 0.06 | 0.16 | 12.4 | 10.3 |

**Table 3: Rate of infection for different modes of transmissions**

## According to the mode of transmission

For Uttar Pradesh with the highest infection rate ($\lambda$ = 8.86) in the category of heterosexual route of transmission of disease also, it is assumed that approximately 7044 persons will get infected within a year only, while the second highest rate of infection is found for parent to child mode ($\lambda$ = 0.55), and the lowest rate of transmission of disease is found for homosexuals ($\lambda$ = 0.05) when the population and rate of infection remain constant in each category.

## According to the sex discrimination

On this basis, the rate of infection is higher ($\lambda$ = 12.4) in males than females ($\lambda$ = 10.4), which shows that the growth will be higher in males, but it is also true that in country like India, females are generally not allowed to get even tested.

## Conclusion

Conclusively it is found that disease load in different groups rose year after year with respect of time. As different types of control program and strategies are running currently from different governmental and non governmental agencies so this growth may be de-accelerated. Hence with the help of these models, we may be aware of deficits in our preventing measures and can prepare and develop our resources before the problem become irreversible.

## References


1. Bookmaker R and Jiangang Liao (1990). Statistical modeling of the AIDS epidemic for forecasting health care needs, Biometrics,Vol.46 (4), p. 1151-1163.
2. Brookmayer R and Gail M H (1986), Minimum Size of the acquired Immunod-efficiency Syndrome (AIDS) epidemic in the United States, The Lancet, ii, p. 1320-1322.
3. Brookmeyer R and Gail M H. (1994). AIDS Epidemiology-A Quantitative Approach,. Oxford University Press.
4. Crawford, Catherine M. (1990). A model for future HIV/AIDS incidence in New York City.
5. Joel, W. Hey and Frank, A. Wolak (1990). Bootstrapping HIV/AIDS projection models: Back calculation with liner inequality-constrained regression, Hoover Institution, Stanford University, Economics Working Paper No. E-90-5.
6. Lee, Ronald D. and Carter, Lawrence R. (1992). Modeling and Forecasting of U S mortality, JASA, Vol.87 (419), p. 659-672.
7. NACO.www.naco.nic.in, 2007-2009
8. Solomon P. J. and Wilsonm, S.R. (1990). Accommodating change due to treatment in the method of back projection for estimating HIV infection incidence, Biometrics, Vol.46, p. 1165-1170.
9. Waema, R (2002). HIV epidemic- Mother To Child Transmission (MTCT) model. University of Nairobi, Kenya, p. 1-97.
10. Waema, R and Olowofeso, O. E. (2005). Mathematical modeling for human immunodeficiency virus (HIV) using generating function approach. Kragujevae J. Sci, 27, p. 115-130.
11. Wu, Hulin and Zhang, Jin-Ting (2002). The study of long term HIV dynamics using semi-parametric non linear mixed effect models, Statistics in Medicine, Vol. 21, p. 3655-3675.