Modeling the Spread of HIV/AIDS

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Introduction

Since HIV was first diagnosed, the HIV epidemic has spread world-wide with about 40 million HIV/AIDS patients currently. Mathematical models employed are typically purely deterministic, which means the output of the model is fully determined by known parameter values. Very few stochastic models, those that possess some randomness, are available to complement the theory. Using existing data from the NACO in India we developed a Markov Chain that described the probabilities of the movement of an individual with AIDS through six different states of the illness. After completing data analysis we summarized survival rates depending on the state in which the individual began. Given a specific state that an individual could start in, we can determine the average number of steps before absorption which is then compared to the deterministic values.

Markov Chain

This model describes the movement and associated probabilities of an individual with AIDs through different stages of the disease.

Transition Matrix

The absorbing Markov Chain shown is represented by the transition matrix, $\mathbf{T}$; $\mathbf{T}$ is a 6x6 matrix that has a block decomposition where rows and columns are in x_1, x_2, x_3, y_1, y_2, x_4 order.
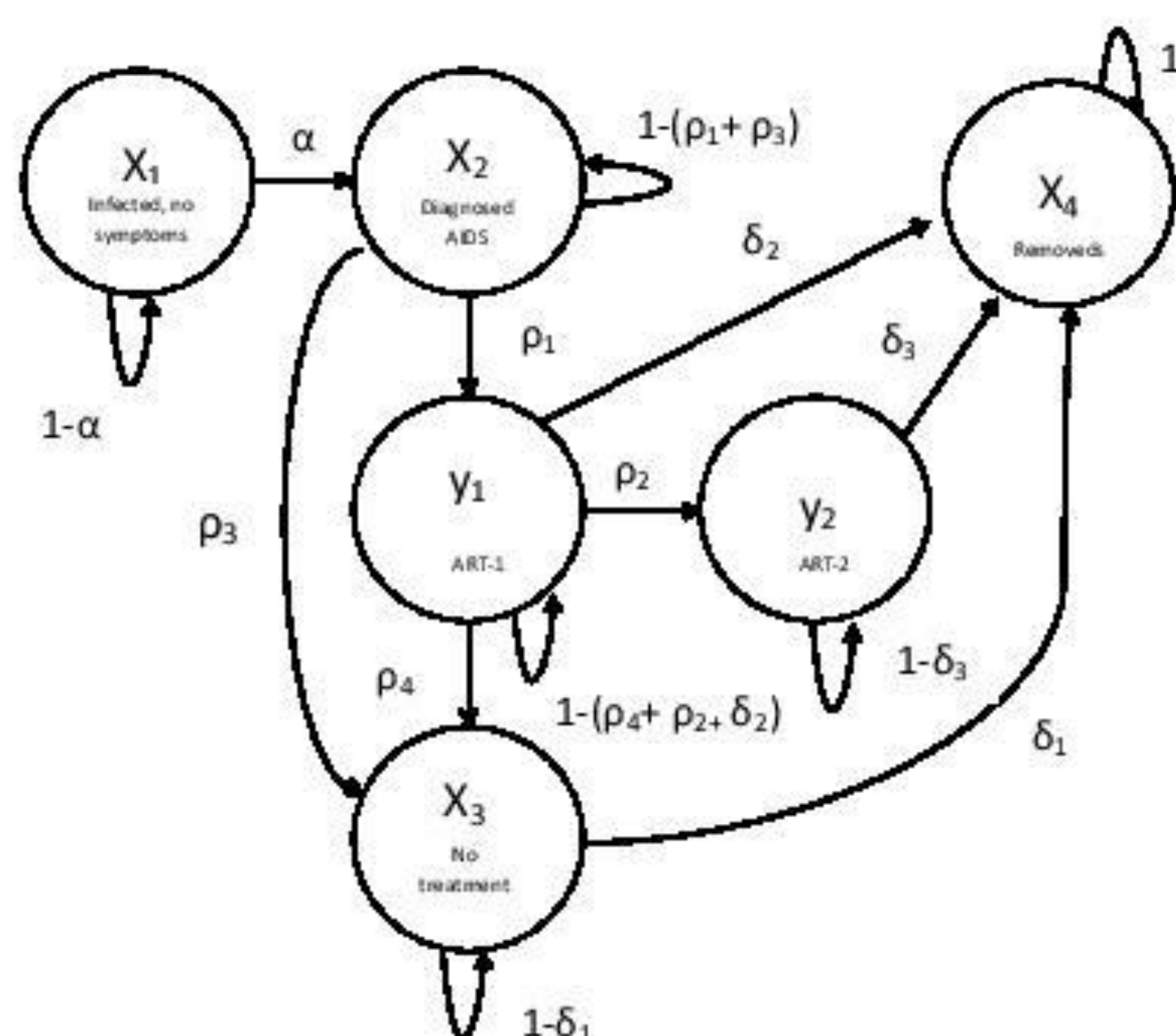
$$\mathbf{T} = \begin{bmatrix} 1-\alpha & 0 & 0 & 0 & 0 & 0 \\ \alpha & 1-(\rho_1+\rho_3) & 0 & 0 & 0 & 0 \\ 0 & \rho_3 & 1-\delta_1 & \rho_4 & 0 & 0 \\ 0 & \rho_1 & 0 & 1-(\rho_4+\rho_2+\delta_2) & 0 & 0 \\ 0 & 0 & 0 & \rho_2 & 1-\delta_3 & 0 \\ 0 & 0 & \delta_1 & \delta_2 & \delta_3 & 1 \end{bmatrix}$$

Numerical values are entered for probabilities α, ρ_1, ρ_2, ρ_3, ρ_4, δ_1, δ_2 and δ_3 so the fundamental matrix, $\mathbf{F}$, can be formed. To obtain $\mathbf{F}$, first raise $\mathbf{T}$ to a large power. Taking the upper right 5x5 matrix of this, a new matrix $\mathbf{A}$ is formed. Finally, $\mathbf{F}=(\mathbf{I}-\mathbf{A})^{-1}$, where $\mathbf{I}$ is a 5x5 identity matrix. Summing the ith column of the fundamental matrix, $\mathbf{F}$, gives the average number of steps before absorption for an individual beginning in the stage that correlates to column i, as shown in the table below.

Stage	x_1	x_2	x_3	y_1	y_2
Average number of steps until absorption	16.73	7.53	4.5	5.98	5.20

Results and Comparison to Deterministic

For final results, we wish to compare the deterministic and stochastic models where appropriate. Thus, taking the sum of the x_2 and x_3 average number of steps we see infectives have an average of approximately 12 years before being removed from the system. We compare this to the numerical approximation of the same system described by differential equations and numerically approximated solution. Thus, from the plot of infective class behavior below, we can see the population remains steady between 10 and 15 years. Hence, the deterministic and stochastic averages are comparable.
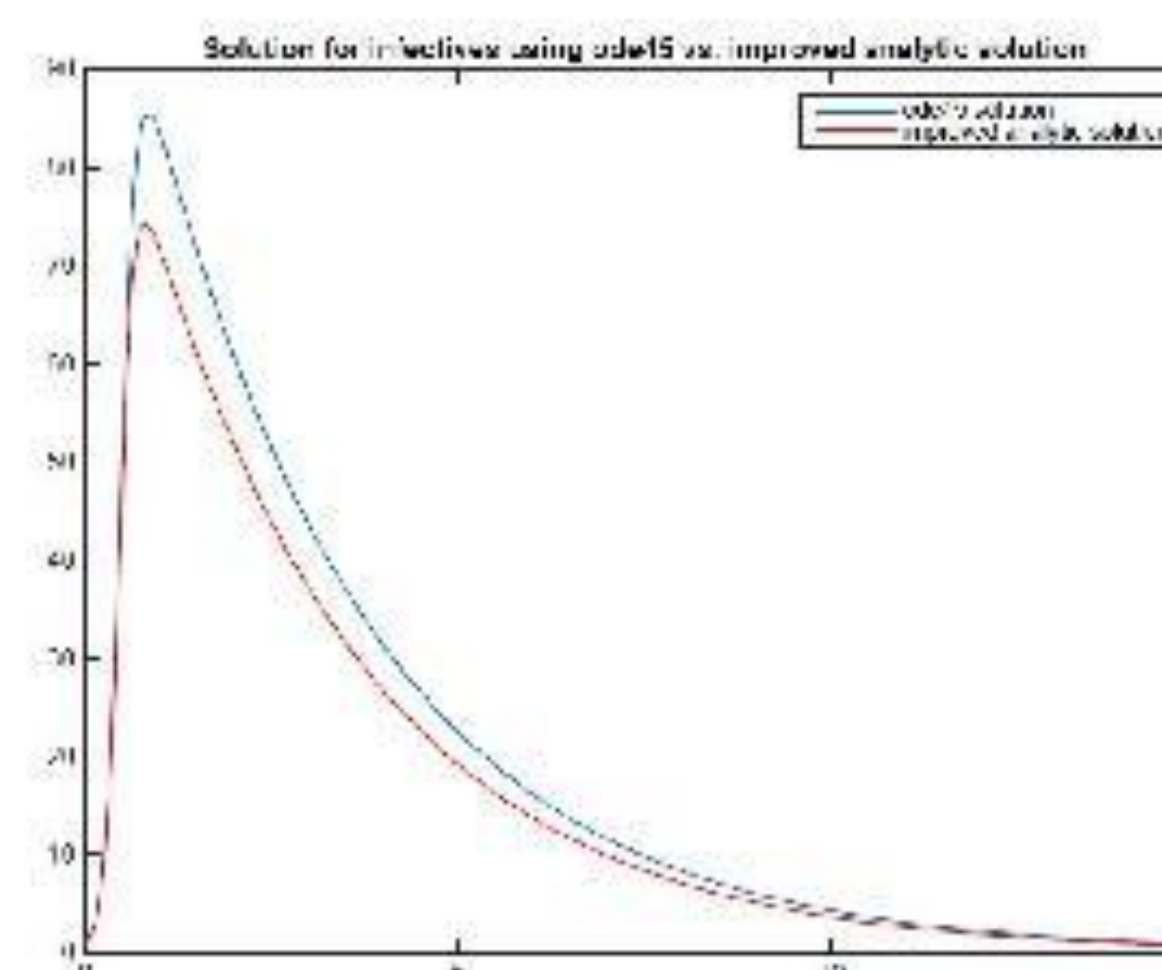
References

Rao et al. Improvement in survival of people living with HIV/AIDs and requirement for 1st- and 2nd-line ART in India: A mathematical model. Notices AMS. 59 (2012), no. 4, 560562.