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Eigenvalue method for the solution of multi-compartment model of HIV-AIDS transmission

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Abstract. The aim of this study is to formulate a multi-compartment mathematical model regarding the transmission and dynamics of HIV-AIDS. The model is formulated on the basis of a system of linear, ordinary differential equations and admits two locally and globally stable equilibria. Primarily, the existence and uniqueness of solution of the model are demonstrated which is then obtained analytically using the fundamental matrix method and eigenvalue approach. The obtained solution serves as the pedestal for studying the dynamics and spread of HIV-AIDS in general. Nevertheless, as an endorsement to the obtained results the simulations are also carried out with model outcomes being contrasted to the exact data of the disease in India.

AMS (MOS) Subject Classification Codes: 92B05; 92C10; 92-08
Key Words: HIV-AIDS; Compartmental modelling; Simultaneous differential equations.

1. INTRODUCTION

We frequently see persons who are afflicted with various diseases, the majority of which are treatable. However, there are some disorders for which there is currently no cure. AIDS is one of them., an acronym for Acquired Immune Deficiency Syndrome. About 3 million people died due to AIDS in 2003 [13, 14] and the disease is still spreading at a high rate. It affects the people of all castes, colour, age, creed and gender. UNAIDS (United Nations AIDS), UNICEF (United Nations International Childrens Education Fund) and WHO (World Health Organization) have risen to the occasion. Large sums of money are being

provided, and efforts are being made to stop the disease from spreading. Despite these attempts, the disease spreads due to a lack of knowledge about it, its virus (HIV), the modes of transmission of the virus and a careless lifestyle [13, 14]. AIDS is caused by the HIV (Human Immunodeficiency Virus) virus. Its name comes from factors such as its ability to infect only people, the fact that it causes a weakness in the immune system, and the fact that it is a virus that reproduces by hijacking the machinery of the human cell. HIV is an RNA (Ribo-Nucleic Acid) virus that weakens the human immune system, eventually leading to AIDS. It belongs to the Lentivirus subgroup of the Retroviridae family and is a RNA (Ribo-Nucleic Acid) virus responsible for weakening the human immune system, gradually leading to AIDS. It is a last stage of infection with HIV. The development of AIDS can take more then 8-10 years post the infection.

HIV infection has expanded from a few instances in the United States to all around the world in just 22 years. In December 2003, it was estimated that 37 million adults and 2.5 million children under the age of 15 were living with HIV-AIDS over the world [14, 15], with 3 million deaths. Approximately 5 million adults and children contracted HIV in 2003 alone. Presently, South Africa is the country with the greatest number of HIV infected people in the world, followed by Nigeria and India respectively. In India the first HIV infected person was detected in April 1986 and the first AIDS patient in May 1986 in Chenai. Official Indian estimates of people living with HIV-AIDS range from 2-3 million as of 2020 [14, 15]. According to the recently released Indias HIV Estimation 2019 report, the evaluated adult (15-49 years) HIV prevalence has shown a decline in India since its peak in the year 2003 and is stabilizing from the past recent years [14, 16].

As a matter of concern, it is imperative to study the transmission and dynamics of the disease to restrict its spread for the well-being of human life. To this regard, mathematical modelling plays a vital role and helps in understanding the transmission, behaviour and spread of such diseases between different population groups, by means of developing mathematical models followed by experimental investigations [12]. Many researchers have studied the behaviour, spread and transmission of the HIV-AIDS among various population classes by means of mathematical modelling, in order to help biologists and the related medical researchers to restrict and diminish the spread of the disease. A novel HIV/AIDS epidemic model was developed by Huo et al., [4] to study the spread of the disease. They conducted numerical simulations to support their model. The spread of AIDS epidemic with immigration of HIV infectives was mathematically analysed by Naresh et al., [10] in a population of varying size. Huang et al., [3] also developed an HIV infection mathematical model and theoretically analysed the model simulations to defend their results. To confirm the endemicity of the disease, an SIR epidemic model was developed by Mbah et al., [8]. A sex-structured mathematical model was also stud- ied by Mukandavire et al., [9] to investigate the transmission and spread of HIV-AIDS, based on a system of discrete delay differential equations. Junjie et al., [6] studied the dynamic mathematical modelling of the HIV-AIDS transmission and control. Abueldahab and Mutombo [1] also developed an SIR epiedmic model to study the spread of HIV-AIDS in a particular region (Khartoum) and considered the relevance of their modelling approach to the HIV in Khartoum.

Motivated by the aforementioned works, our aim is to formulate a mathematical model to study and predict the behaviour, spread and dynamics of HIV-AIDS in India, by taking into account the different control measures. The model is formulated using the compartmental analysis and is based on a system of five linear ordinary differential equations. The proposed work is supposed to aid researchers and biologists in the medical field to restrict the spread of the epidemic.

2. Model Formulation

In this section, we shall formally develop a novel epidemic model to study the transmission and dynamics of HIV-AIDS and simulate the model using the data of HIV-AIDS from India. The formulation of the model is based on some classical models such as SIR, SIRD and SEIR models (see [12], [7]) and other existing models (see [4]-[1]). To facilitate the narrative, we divide the section into a few sub-sections as shown in Figure (1) below.

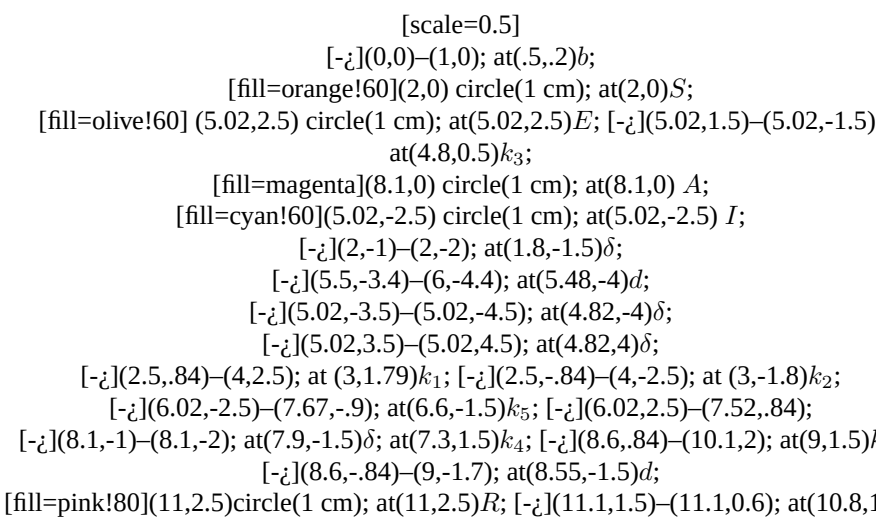

FIGURE 1. Schematic representation of the formulated HIV-AIDS model. The arrows indicate the transition of one population-class to another, represented by means of different compartments.

2.1. **Nomenclature and Symbols.**

The following parameters and symbols are used in the formulated model;

t= time variable,
$N(t)$= total population at any time,
$E(t)$= Susceptible class of population,
$E(t)$= Exposed class of population,
$I(t)$= Infected class of population,
$A(t)$= Population class presently having AIDS,

$R(t)$= Recovered class.

Moreover, b denotes the recruitment rate; δ denotes the death rate caused by reasons other than HIV-AIDS and d represents the death rate due to HIV-AIDS. The model is schematically represented by a multi-compartment diagram as shown in Figure (1). The parameters k_i ($i = 1,\ 2,\ ...,\ 6$) represent the transmission-rates between the corresponding compartments population classes, shown in Figure (1).

2.2. **Assumptions.** To construct the model for investigating the transmission and dynamics of HIV-AIDS, the following assumptions are made (see [15], [7]):

(i) The resultant population of the proposed system at any time is the sum of populations of different classes.
(ii) The population in each class (compartment) is a continuous non-negative function of time.
(iii) Deaths due to HIV-AIDS occur only in the $I(t)$ and $A(t)$ classes.
(iv) All the transmission rates between particular population classes and the death rates are constant for a particular period of time, such that all rates are non-negative.
(v) The recovered class is immune to HIV-AIDS.
(vi) Total population remains conserved at any instant of time .

2.3. **Governing Equations.** The formulated HIV-AIDS model shown diagrammatically in Figure (1) is based on compartment modelling and is governed by the system of five linear ODE's [2] which are arrived at, using the conservation laws as the individuals either die due to HIV-AIDS/other reason or are simply transferred to a different compartment. Due to this reason, these equations are sometimes known as transfer equations and are given by;

$$\begin{aligned}
\frac{dS}{dt} &= b - (k_1 + k_2 + \delta)S, \\
\frac{dE}{dt} &= k_1 S - (k_3 + k_4 + \delta)E, \\
\frac{dI}{dt} &= k_2 S + k_3 E - (k_5 + \delta + d)I, \\
\frac{dA}{dt} &= k_4 E + k_5 I - (k_6 + \delta + d)A, \\
\frac{dR}{dt} &= k_6 A - \delta R,
\end{aligned} \tag{2. 1}$$

with initial conditions given as;

$$\begin{aligned}
&I(0) = I_0 > 0, \\
&E(0) = E_0 \geq 0, \\
&A(0) = A_0 \geq 0, \\
&R(0) = R_0 = 0, \\
&N(0) = N_0 \approx S(0) = S_0.
\end{aligned} \tag{2. 2}$$

The initial conditions are suitably chosen as in every population class, the number of individuals is greater or equal to zero. However for the disease to spread in the population

there must be some infectious people and initially whole of the population except the Infective class $(I(t))$ is considered susceptible to the disease.

The system (2. 1) represents a time dependent model that depicts the number of individuals in each class $S(t)$, $E(t)$, $I(t)$, $A(t)$ and $R(t)$ at different times. As the disease progresses within the population, the dynamics of the spread of HIV-AIDS is clearly explainable using these equations.

3. Model Analysis and Properties

In this section, the model analysis and its qualitative properties, including region invariance (boundedness), existence and uniqueness of the solution, equilibria and their stability, are discussed.

3.1. **Region-Invariance.** Using assumptions (i) and (vi), we obtain;

$$N(t) = S(t) + E(t) + I(t) + A(t) + R(t). \tag{3. 3}$$

Hence, we have

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dA}{dt} + \frac{dR}{dt}. \tag{3. 4}$$

Now, using Equation (2. 1) in Equation (3. 4), it is obtained that;

$$\frac{dN}{dt} = b - \delta N - d(I + A).$$

Since it is assumed that deaths due to HIV-AIDS occur only in the $I(t)$ and $A(t)$ classes, therefore the death rate due to AIDS in class $I(t)$ and $A(t)$ is $d \geq 0$, using $d(I + A) \geq 0$ in above equation, we get;

$$\frac{dN}{dt} \leq b - \delta N. \tag{3. 5}$$

Rearranging inequation (3. 5), we get,

$$\frac{dN}{dt} + \delta N \leq b.$$

which is linear with integrating factor I.F = $e^{\int \delta dt} = e^{\delta t}$.

The general solution of (3. 5) is obtained as;

$$N(t).(I.F) \leq \int b.(I.F)dt + c.$$

Equivalently,

$$N(t).e^{\delta t} \leq \int b.e^{\delta t}dt + c.$$

Further simplifying and using $N(t = 0) = N_0$ we have;

$$N(t) \leq \frac{b}{\delta} + \big(N_0 - \frac{b}{\delta}\big)e^{-\delta t}.$$

Hence, the general solution of inequality (3. 5) an be expressed as;

$$N(t) \leq \frac{b}{\delta} + \eta e^{-\delta t}. \tag{3. 6}$$

where $\eta = \left(N_0 - \frac{b}{\delta}\right)$ and $N_0 = N(t=0)$. From inequality (3. 6), it follows that,

$$\lim_{t\to\infty} N(t) = \frac{b}{\delta}.$$

Thus, $\forall\ t \geq 0$, the region given by;

$$\Re = \{(S(t), E(t), I(t), A(t), R(t)) \,\epsilon\, \mathbb{R}^5_{\geq 0} :\ N(t) \leq\ \frac{b}{\delta}\}$$

represents the feasible region of the model, where the total population is non-negative, and remains bounded.

3.2. **Existence and Uniqueness of the Solution.** To study dynamics of transmission HIV-AIDS among various population classes using the proposed model, it is imperative to prove the existance, uniqueness and authenticity of solution of the framework. We have the following results.

[11] If $\mathscr{F}$ denotes the region $|t-t_0| \leq a,\ ||x(t)-x_0|| \leq c$ where $x = (x_1(t), x_2(t),\ ..., x_n(t))$, and $x_0 = x(t=0)$ and assume that $f(t,x)$ satisfies the Lipchitz condition;

$$||f(t,x) - f(t,y)|| \leq K||x-y||\ \forall\ (t,x),\ (t,y)\ \epsilon\ \mathscr{F}$$

where a, c and K are positive constants. Then there exists a non negative constant β such that there is a unique solution vector $x(t)\ \epsilon\ \mathscr{F}$ satisfying $x_0 = x(t=0)$.

It is pertinent to mention that the requirement for the result to hold good is that all the partial derivatives $\partial f_i/\partial x_j$, $i,j = 1,\ 2,\ ...,n$ are continuous and bounded in $\mathscr{F}$. The solution of the initial value problem (IVP) represented by the system of equations (2. 1) and initial conditions (2. 2), exists uniquely in $\mathbb{R}^5_{\geq 0}\ \forall\ t \geq\ 0$.

Suppose that;

$$\begin{aligned}
b - (k_1 + k_2 + \delta)S &= f_1.\\
k_1 S - (k_3 + k_4 + \delta)E &= f_2.\\
k_2 S + k_3 E - (k_5 + \delta + d)E &= f_3.\\
k_4 E - k_5 I - (k_6 + \delta + d)A &= f_4.\\
k_6 A - \delta R &= f_5.
\end{aligned}$$

Moreover, taking $x_1 = S$, $x_2 = E$, $x_3 = I$, $x_4 = A$ and $x_5 = R$, it clearly follows that $\partial f_i/\partial x_j$, $i,j = 1,\ 2,\ ...,5$ are continuous and bounded. Hence, *Result 1* guarantees that the system of equations (2. 1) has a unique solution.

3.3. **Nature and Stability Analysis of Equilibria.** Here, we shall find the equilibrium points of the system of equations (2. 1), by equating the right hand side of the system to zero and simultaneously solving the system. The system is found to have two equilibrium points: Disease free equilibrium (P_0) and the epidemic equilibrium (P_1), where;

$$P_0 = (S^*, 0, 0, 0, 0) \text{ with } S^* = \frac{b}{k_1 + k_2 + \delta}, \text{ and in this case } k_1 = k_2 = 0,$$

and,

$$P_1 = (S^*, E^*, I^*, A^*, R^*)$$

such that;

$$E^* = \frac{k_1 S^*}{(k_3 + k_4 + \delta)}, I^* = \frac{k_2 S^* + k_3 E^*}{k_5 + \delta + d}, A^* = \frac{k_4 E^* + k_5 I^*}{k_6 + \delta + d}, R^* = \frac{k_6 A^*}{\delta}.$$

For testing the stability of the equilibrium points, we take the Jacobian matrix associated with the system of equations (2. 1) as:

$$J = \begin{bmatrix} \lambda_1 & 0 & 0 & 0 & 0 \\ k_1 & \lambda_2 & 0 & 0 & 0 \\ k_2 & k_3 & \lambda_3 & 0 & 0 \\ 0 & k_4 & k_5 & \lambda_4 & 0 \\ 0 & 0 & 0 & k_6 & \lambda_5 \end{bmatrix} \tag{3. 7}$$

,
where $\lambda_1 = -(k_1+k_2+\delta)$, $\lambda_2 = -(k_3+k_4+\delta)$, $\lambda_3 = -(k_5+\delta+d)$, $\lambda_4 = -(k_6+\delta+d)$, $\lambda_5 = -\delta$.

Clearly, the matrix J is a lower triangular matrix [11] and hence its eigenvalues are λ_1, λ_2, λ_3, λ_4 and λ_5 which are all negative (at all equilibrium points P_0, P_1). Therefore, all equilibria are asymptotically stable, both locally as well as globally [11].

4. Solution of the Model

Rearranging the system of equations (2. 1) into the matrix form we have:

$$\frac{dX}{dt} = JX + B \tag{4. 8}$$

where $X = [S\ E\ I\ A\ R]'$ such that $[.]'$ denotes the matrix transpose and $B = [b\ 0\ 0\ 0\ 0]'$.

Suppose that $F(t)$ denotes the fundamental matrix (see [11], [5]) corresponding to the homogeneous part of Equation (4. 8), then the unique solution [5] of the system is obtained

as:

$$X(t) = F(t)F^{-1}(0)X(0) + F(t)\int_0^t F^{-1}(s)B(s)ds \tag{4. 9}$$

Equation (4. 9) gives the transmission dynamics and the nature of each population class at any instant of time.

5. Numerical Simulations

In this section, we shall execute some numerical simulations to depict the transmission and dynamics of HIV-AIDS by using the proposed model and the solution obtained in Equation (4. 9). The numerical values of the various parameters used in the simulatory process are given in Table (1).

TABLE 1. Numerical/practical (average) values of various parameters per day in India involved in the formulated model [13, 14, 15] .

Parameter	Value	Parameter	Value
b	77756	k_2	190
k_1	77000	k_3	185
k_4	196	k_5	195
δ	28230	k_6	10
d	800		

Using the values from Table (1), we calculate the eigenvalues of J as $\lambda_1 = -(k_1 + k_2 + \delta) = -105420$, $\lambda_2 = -(k_3 + k_4 + \delta) = -28611$, $\lambda_3 = -(k_5 + \delta + d) = -29225$, $\lambda_4 = -(k_6 + \delta + d) = -29040$, $\lambda_5 = -\delta = -28230$.

The Fundamental matrix $F(t)$, appearing in Equation (4. 9) is given by [ref. **Appendix**];

$$F(t) = \begin{bmatrix} v_1 e^{\lambda_1 t} & v_2 e^{\lambda_2 t} & v_3 e^{\lambda_3 t} & v_4 e^{\lambda_4 t} & v_5 e^{\lambda_5 t} \end{bmatrix} \tag{5. 10}$$

where v_i ; $i = 1, 2, 3, 4, 5.$, is the eigenvector corresponding to eigenvalue λ_i of the Jacobian matrix J.

$$F(t) = \begin{bmatrix} v_1 e^{-105420t} & v_2 e^{-28611t} & v_3 e^{-28611t} & v_4 e^{-29040t} & v_5 e^{-28230t} \end{bmatrix} \tag{5. 11}$$

The eigenvectors v_i ; $i = 1, 2, 3, 4, 5.$, are obtained using Wolfram MATHEMATICA sftware and then used in equation (4. 9) to get its unique solution depicting the transmission dynamics of HIV-AIDS within the population.

6. Results and Analysis of HIV Model in India

In this section, solutions S(t), E(t), I(t), A(t) and R(t) of Equation (4. 9) are plotted graphically using the numerical/ practical values for various transfer coefficients (given in Table (1)) involved in the model and the initial conditions (2. 2) with the help of Wolfram MATHEMATICA software. The graphical simulations obtained from the developed model are shown in Figures (2)-(4).

Figure (2) shows the behaviour of the Susceptible ($S(t)$) and Exposed ($E(t)$) population classes according to the model Equation (4. 9), where it is clear that both the classes follow the Verhulst's logistic growth pattern, which is also predicted by several existing models in the literature (see [4]-[1]).

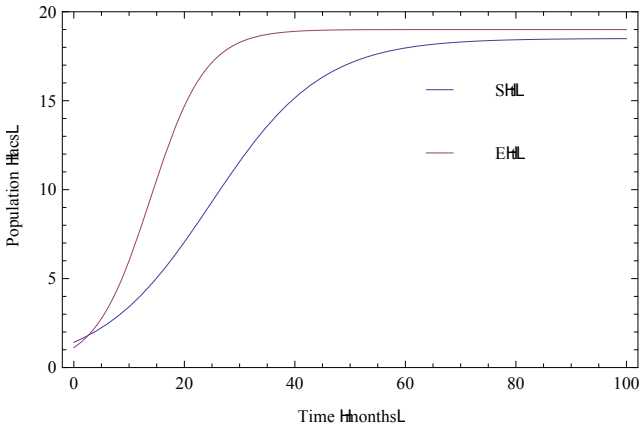

FIGURE 2. Population (solution) curves for the population classes: Susceptibles (S) and Exposed (E) classes according to Equation (4. 9), where the initial conditions (2. 2) are taken from [14, 15, 16].

Moreover, Figure (3) shows the dynamics of the population classes; $I(t)$, $A(t)$ and $R(t)$ as per Equation (4. 9).

The transmission and dynamics of the classes $I(t)$ and $A(t)$ almost follows a practical trend (see [14], [15], [16]), which show a monotonic increasing behaviour up to a certain stage and onward a decrease thereby. It is also quite visible from the figure, that the classes lie above the time-axis asymptotically (as predicted from the nature of the equilibria) at a certain intercept. The trend shows the prevalence of HIV-AIDS in India (confirming the practical situation of the disease in the region) due to the non-availability of any proper drug/ vaccine to cure the disease. Moreover, the same dynamics shown by the population class $R(t)$ is due to the theoretical positive value of the transfer rate k_6.

Finally, a comparison for the Infective ($I(t)$) class is obtained, graphically shown in Figure (4), between the model simulations and practical data (taken from [14, 15, 16]) of HIV-AIDS in India. It is quite evident from Figure (4) that the model simulations converge almost exactly with the practical data, which thereby guarantees the validity of the formulated model.

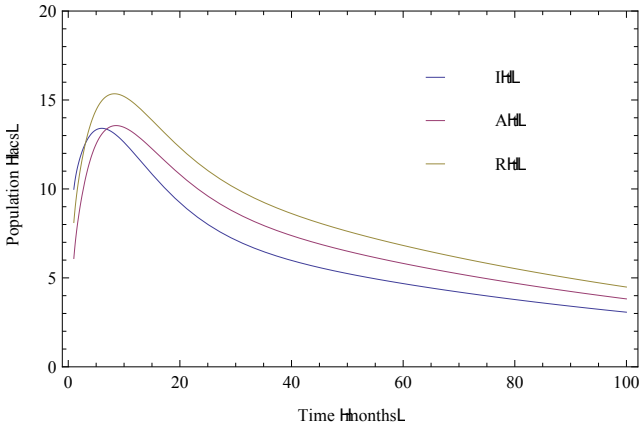

FIGURE 3. Population (solution) curves for the population classes (from 2002 onward) in India: Infectives (I), Post-Aids (A) and Recovered (R) classes according to Equation (4. 9), where the initial conditions (2. 2) are taken from [14, 15, 16].

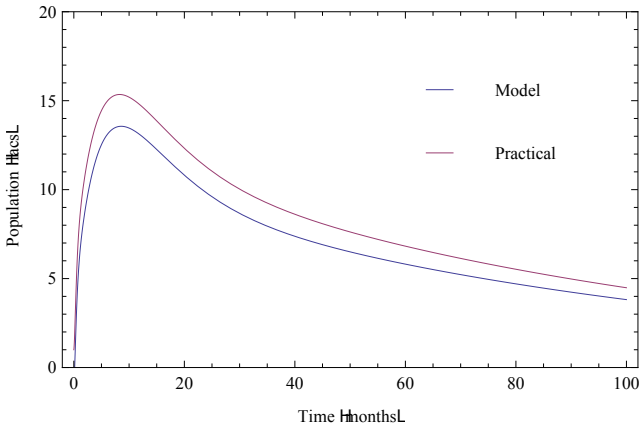

FIGURE 4. Comparison of the Population (solution) curves for the Infective (I) population class between the model simulations and the practical data (mentioned in [14]) in India (from 2002 onward), according to Equation (4. 9), where the initial conditions (2. 2) are taken from [14, 15, 16].

7. DISCUSSION AND CONCLUSION

In the present study, we formulated a multi-compartment mathematical model, based on a linear-system ODE's, regarding the transmission-dynamics of the infectious disease (HIV-AIDS) in India. The total population is divided into different compartments (population classes). It is demonstrated that model admits a unique solution and the same is obtained analytically using the fundamental matrix method and eigenvalue approach. Besides, the existence and nature of the equilibria of the model have also been investigated in detail. The outcomes of the proposed model have been simulated graphically, using the

numerical/ practical values of various parameters involved in the model, with the aid of Wolfram MATHEMATICA software. The graphical representation of the model outcomes has been presented in Figures (2)-(4), which depict the dynamics of different population classes and comparison of the infectious class with the practical data.

From the numerical outcomes it is quite evident that the formulated model predicts a quite closer dynamics with the practical data in India. Moreover, the proposed model generalizes many existing models (see [8]-[6]) in the following two fashions:
(i) The proposed model describes the transmission and dynamics of the various population classes (five compartments; S, E, I, A, R). However, the above cited have used just 3-4 compartments to analyse and predict the spread of HIV-AIDS.
(ii) The model is solved analytically, and is hence more accurate and general than those existing in the recent literature.

Furthermore, the formulated model predicts that there has not been any suitable decrease in the infectious cases, which is quite justifiable and endorses the validity of the proposed model, as till date there has not been an availability of a proper medicine to vanish the virus/ disease. Thus, the proposed model and its outcomes may be of substantial importance for studying the transmission dynamics of HIV-AIDS in India as well as across the globe. Moreover, the model is expected to help the biologists and researchers of different countries to asses their strategies and preparedness to control and diminish the spread of this epidemic.

APPENDIX

Consider the following system of n non homogeneous linear differential equations in the matrix form

$$\frac{d}{dt}X(t) = AX(t) + B(t)$$

such that $X(t)$ is an $n \times 1$ column matrix (to be determined), $B(t)$ is also an $n \times 1$ column matrix and A is the coefficient square matrix of order n. If λ_1, λ_2, ...,λ_n denote the eigenvalues of A and v_1, v_2, ...,v_n represent the respective corresponding eigenvectors, then the square matrix $F(t)$ of order n, given as

$$F(t) = \left[v_1 e^{\lambda_1 t}\ v_2 e^{\lambda_2 t} \ldots v_n e^{\lambda_n t}\right]$$

is called the **fundamental matrix** corresponding to the homogeneous part $\frac{d}{dt}X(t) = AX(t)$. Clearly, the matrix $F(t)$ is invertible for all values of t [11].

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