

STATISTICAL TIME SERIES ANALYSIS FOR DYNAMICS OF HIV

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Abstract

HIV has become global disease. These days a lot of people are suffering. Mostly *HIV*-positive people are not aware that they have been infected. Therefore, a strict check on donor blood and blood products have to be followed. Hence, it becomes important to interpret the chemical mechanism of *HIV* infection and its spread. It infects a diverse range of immunity cells. It gets carried into the macrophages and $CD^{4+}T$ cells because of the communication among virion wrap glycoproteins with the CD^4 molecule on the target cells. These virions then infect a large amount of cellular targets and diffuse into every part of human body. Mathematical modeling for the mechanics of *HIV* infection has been done to reduce its propagation, find cures for discourse. The model discussed in this paper consists of these states: T , number of cells not infected, I , number of cells infected, V , number of blood virus particles. The non-linear behavior for *HIV* modelling is studied using time series analysis. Further, statistical tools like Regression, Correlation, Fractal dimension, Hurst Exponent, Predictability Index, Box plot etc. helps to understand the virion behavior in a better way. It is observed that as the state variables changed then the viral dynamics changes behavior from regular to chaotic.

Keywords and phrases: Time series, Statistical Analysis, Regular motion, Chaotic motion, *HIV* dynamics.

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1 Introduction

Human Immunodeficiency Virus (*HIV*) represents the kind of virus that straightaway weakens the immunity of the body and leads to a life threatening infection called Acquired Immunodeficiency Syndrome (*AIDS*). It is a state where immune system gradually stops responding and allows the infection to grow rapidly. *HIV* is a lentivirus that belongs to the family of retroviridae which causes chronic and lethal diseases. Lentiviruses are (+) positive-sense single-stranded *RNA* (+*ssRNA*) viruses. They invade in the target cell to convert *RNA* virus into *DNA*. This process of conversion from single-stranded *RNA* to double stranded *DNA* is called reverse transcriptase. The resulting *DNA* virus then replicates inside the cell nucleus. Alternatively, the virus may reproduce new *RNA* virus to restart the replication process. *HIV* infection reduces the level of $CD^{4+}T$ cells. Patients are identified as *AIDS* patients if the level of $CD^{4+}T$ cells reduces to a critical level of 200 cells per mm^3 or lower. Medicines forbid *HIV* from increasing in the host tissues. This helps in reduction in the infection of *HIV*. Reverse Transcriptase Inhibitor (*RTI*) drugs are used for treatment

of *HIV* infection. They block the process of reverse transcriptase which prevents the host cell from getting infected. Alternatively, Protease Inhibitor (*PI*) drugs are used to forbid the production of mature viruses at the end stage of the replication cycle.

Barunik J. *et al* [1] estimated hurst exponent for heavily tailed distributions. Beard J. *et al* [2] discussed economic level for life results of therapy for *HIV/AIDS*. Bhardwaj *et al* [3-5] studied various statistical characteristics of various real life phenomena of meditating body, to forecast weather, rainfall, environment data. Boshoff C. *et al* [6] discussed *AIDS*-related malignancies. Box G.E.P. *et al* [7] forecasted and controlled time series. Carbone A. *et al* [8] researched noise in various systems. Chu and Selwyn [9] discussed the complications of *HIV* infection. Fuller W.A. [10] gave description of statistical time series. Grech D. *et al* [11] suggested techniques in detrended time series. Hurst H. *et al* [12] published a transaction on the rescaled analysis. Malta *et al* [13] described antiretroviral therapy for human immuno deficiency virus among drug users. Nicholas *et al* [14] studied managing symptoms, self-care for peripheral neuropathy in *HIV/AIDS*. Perelson and Nelson [15] discussed mathematical analysis of *HIV-1* dynamics. Post and Holt [16] reviewed recent developments in *HIV* and the kidney. Rangarajan and Ding [17] gave amalgamated access to the assessment of correlation in time series data. Samanta [18] discussed permanency and termination of a non-autonomous *HIV/AIDS* epidemic model incorporated delay time. Walker [19] studied selected control of *HIV* infection, its applications for vaccines. Wanga B.D. *et al* [20] suggested how vaccines and treatment can play a role in controlling *HIV*. Yarchoan R. *et al* [21] explained the influence of antiviral therapy on pathogenesis.

None of the authors have studied the time series, fractal and Hurst exponent analysis of *HIV* model. This paper, studies impact of time on amount of uninfected cells; virus particles in the blood cells and infected cells. Also, time series, fractal dimension, Hurst exponent, predictability index and behaviour of these cells is observed.

2 Development of Mathematical Model

The mathematical model for the following three important components have been developed:

1. T , amount of uninfected cells,
2. V , amount of virus particles in the blood cells,
3. I , amount of infected cells.

The model helps to study the impact of *HIV* epidemic on these factors simultaneously with time and also to study how the change in one component influences the changes in other with respect to time. Some assumptions that are required to transform the biological condition into a mathematical model are as follows:

1. Contact rate is being considered as a time varying function.
2. Reverse Transcriptase Inhibitor effect is being considered as a time varying parameter, $0 < \gamma < 1$.
3. Protease Inhibitor effect is being considered as a time varying parameter, $0 < \eta < 1$.
4. transmission system coefficient is considered a time varying parameter, β .

All parameters considered to be positive constants. Mathematical model can be generated considering the dynamics of *HIV* infection

$$dT = (S - bT - (1 - \gamma)\beta TV)dt, \quad (2.1)$$

$$dV = ((1 - \eta)NaI - cV)dt, \quad (2.2)$$

$$dI = ((1 - \gamma)\beta TV - aI)dt, \quad (2.3)$$

with initial assumption: $T(0) = T_0$, $V(0) = V_0$, $I(0) = I_0$, where

T : measure of cells uninfected

dT : changing rate of uninfected cells

S : constant source rate producing T cells

b : clearing rate of uninfected T cells

Infection rate reduces from βTV to $(1 - \gamma)\beta TV$.

V : measure of blood virus particles

dV : changing rate of each cell infected producing the virus

N : average amount of virions produced by the cell infected over its life span

a : clearing rate of infected cells

$(1 - \eta)NaI$: virions under affected by PI drugs

c : rate at which virus are cleared

I : measure of infected cells

dI : changing rate in infected cells.

3 Methodology

3.1 Time Series Analysis

Time Series $\{x_t : t \in T\}$ is a collection of random variables usually parameterized by

- the real line $T = R = (-\infty, \infty)$,
- the non-negative real line $T = R^+ = [0, \infty)$,
- the integers $T = Z = \{\dots, -2, -1, 0, 1, 2, \dots\}$,
- the positive integers $T = Z^+ = \{0, 1, 2, \dots\}$.

Univariate time-series analysis is the investigation of a unary order of data whereas *multivariate* time-series analysis consists of various sets of data for the similar order of time intervals. Here, we have a multivariate time series for the analysis. The probability measure of a time series is defined by specifying the joint distribution (in a consistent manner) of all finite subsets of $\{x_t : t \in T\}$. There are two categories of statistics that describe data. First, explains the central position involving the mode, median, and mean. Second, measures of spread which consists of summing a group of data to describe the spread of the scores.

3.2 Rescaled Range Analysis

H.E.Hurst developed this scaling process. With time it was refined by Mandelbrot and Wallis. In this simulation, take the input of the time sequence measuring T . Divide these in N equivalent time intervals measuring μ , i.e. $N\mu = T$. Taking every time interval separately, calculate the average measure and construct new-sprung sequence of congregated deviations of mean. Then, range and standarddeviation of actual time sequence for every time interval, is measured. Standardise every range through related standarddeviation to form the rescaled range. Hence, the averagerescaledrange for the considered time intervals of length $(R/S)_\mu$ is deliberated. The rescaledrange approxes to: $(R/S)_\mu \approx c\mu^H$, in which c - invariable not dependent on μ . Next, bring out the law of scaling using usual regression least squares on logs on both L.H.S. and R.H.S is applied to $\log(R/S)_\mu \approx \log c + H \log \mu$, in which HE - Hurst exponent. Regression line slope in $(R/S)vs.t$ in log-log axes calculates

Hurst exponent. If $HE > 0.5$, the procedure involves positive inappropriate for summing auto-covariance coefficients at all delays and is referred as continual. Whereas if $HE < 0.5$, the procedure involves negative and can be summed auto-covariances at all delays and is referred non-continual.

Consider $D = 2 - H$ where $1 \leq D \leq 2$ and is referred as the *Fractal Dimension*. The fractal dimension of a take statistical distribution denotes its self-similarity. It has been observed that the localized abnormality of series depends upon fractal dimensions. A value of 1.5 indicates Brownian motion.

Index of Prediction explains the activeness of time series i.e. $PI = 2|D - 1.5|$. If it is computed near zero, then the process approximates towards the chaotic orbit which is regarded as unpredictable. If it is computed around one, which categorizes the process as being predictable.

4 Results and Discussions

Using Equations (1-3), time series plot of each variable and statistical characteristics i.e. Slope, Mean, Standard Deviation, Kurtosis, Skewness, Hurst exponent, Fractal Dimension, Predictability Index are calculated. Also, log-log axes for (R/S) vs time(t) were plotted to find the Hurst exponent. Fig.1,2 and 3 depict how each variable individually vary with time for variable T, V, I respectively. Fig. 4, 5 and 6 shows log-log representation for $\log(R/S)$ vs $\log(time)$ for T, V, I respectively. Table 1 and 2 gives the behaviour of statistical parameters with Hurst exponent, fractal dimension of all variables.

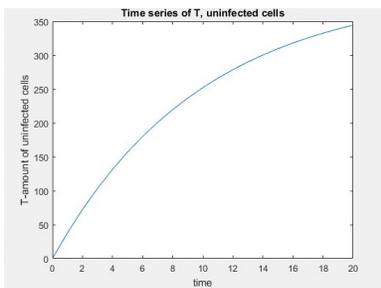


Figure 1: Time Series for Uninfected Cells, T

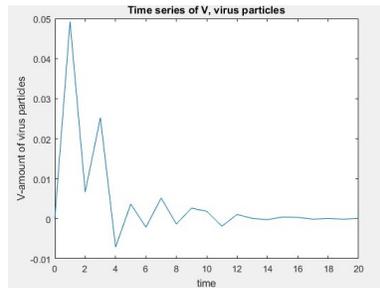


Figure 2: Time Series for Virus particles, V

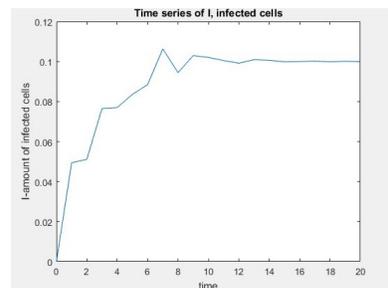


Figure 3: Time Series for Infected Cells, I

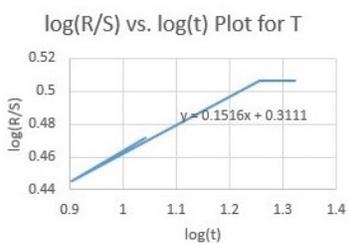


Figure 4: $\log(R/S)$ vs $\log(time)$ of T

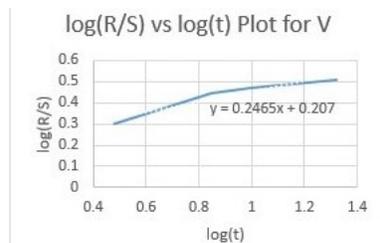


Figure 5: $\log(R/S)$ vs $\log(time)$ of V

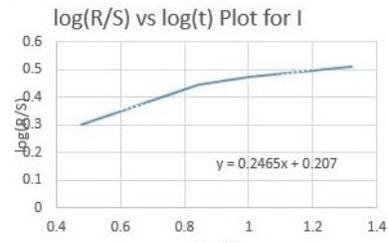


Figure 6: $\log(R/S)$ vs $\log(time)$ of I

It is observed that the parameters T, V and I show anti-persistent behaviour. This implies that there will be a situation of chaos arising as the *HIV* virion progresses inside the body cells.

Table 1: Statistical properties of the deterministic model variables

Statistical Properties	$T(x_1)$	$V(x_2)$	$I(x_3)$
Slope	15.35733	-0.00085	0.002947
Mean	223.6784	0.00399	0.087276
Standard deviation	104.774	0.011998	0.025613
Skewness	-0.7601	3.181973	-2.412
Kurtosis	-0.50799	10.83628	6.273677

Table 2: Statistical properties of the deterministic model variables

Statistical Properties	$T-t (x_1-t)$	$V-t (x_2-t)$	$I-t (x_3-t)$
Hurst Exponent	0.15161	0.246452	0.246466
Fractal Dimension	1.84839	1.753548	1.753534
Predictability Index	0.69678	0.507096	0.507068
Behaviour	Anti-persistence	Anti-persistence	Anti-persistence

Conclusion

It is observed from time series of V , virus particles in the blood grow exponentially in absence of any external factors whether environmental or treatment related. Simultaneously, I , amount of infected cells grows in the body causing a total failure of the immunity of the body system and T , amount of uninfected cells will decrease with time. Range of V , virus particles is very high as compared to T , uninfected and I , infected cells with time. T and I stabilize at a non-zero value after a period of time, there is an exponential increase in number of virus particles. The Hurst exponent, fractal dimension and index of prediction show anti-persistence behaviour of the variables with time. This implies that there will be a situation of chaos arising as the *HIV* virion progresses inside the body cells. Thus, it has been observed that *HIV* do not follow strictly deterministic model, it oscillates randomly which leads to deterministic equilibrium being not in fixed state at any instantenous time. Therefore, this Human Immunodeficiency Virion system with ergodic disturbances help to alter the behaviour of dynamical system .

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