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Predicting the Number of Infected Cells of HIV Infection of $CD4^+$ T-Cells: Database Management and Health Policy Implication with Noise-Induced Fluctuation Effect

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Abstract

The dynamics of infected cells of HIV infection of $CD4^+$ T-cells has been studied using the technique of a mathematical modelling. However, the weekly prediction of the number of infected cells of HIV infection of $CD4^+$ T-cells that can be used as vital data to manage and mitigate this endemic disease remains to be an open problem. In order to tackle this complex problem, we have used a simulation analysis to successfully analyse this proposed problem. We have varied the maximum proliferation rate of target cells denoted by ain the intervals of [0.68, 3.40] and [7.48, 10.20] without random noise effects. The maximum proliferation rate of target cells interval of [7.48, 10.20] supports an increase in the number of infected cells of HIV infection indicating a dominant survival regime whereas the maximum proliferation rate of target cells interval of [0.68, 3.40] supports a decrease in the number of infected cells of HIV infection indicating a dominant regime in which a proportion of the predicted number of infected cells of HIV infection is destroyed. Another scenario corresponds to the interval of [0.68, 3.40] and the other scenarios when the maximum proliferation rates of target cells are 5.44 and 4.04 with a random noise intensity of 0.4. Our simulation study has indicated a decrease in the number of infected cells of HIV infection in contrast to the instances when the maximum proliferation rates of target cells are 54.4, 27.2, 13.6 and 8.16 that support the survival of the number of infected cells of HIV infection of $CD4^+$ T-cells. This present analysis has produced sufficient weekly data which can be utilized to build an effective database system for the purpose of the health planning of HIV infection. These novel contributions have not been seen elsewhere, they are presented here and discussed.

1.0 Introduction

The system of non-linear first order ordinary differential equations that defines the number of infected cells of HIV infection of $CD4^+$ T-cells as one of the time-dependent variables is a popular system of three model equations [1, 2]. Since this mathematical model was approximated and its parameters were estimated without a sound testing for the sensitivity analysis of these parameters, it is a good numerical mathematics practice to study this system with some degree of random noise. Due to the lack of a standard method of selecting the precise value of the random noise intensity, we have chosen the value of the noise intensity to be 0.4. This study has combined the techniques of deterministic and random noise or stochastic calculations in order to deduce one of the best methods of building a realistic data base system which is computationally efficient and replicable. Precise values of the maximum proliferation rates of target cells were taken to be 4.08, 5.44, 8.16, 13.6, 27.2 and 54.4 in addition to other intervals of maximum proliferation rates of target cells such as [0.68, 3.40] and [7.48, 10.20] with and without random noise characterization. This present study is distinct from the earlier study as reported in the work of [2] in which the model parameters of the model proposed in the work of [1] were tested for their sensitivity behaviour. The list of cited references to this study is limited because the idea leading into this simulation study is not a popular cited topic within the application of numerical mathematics in the management of disease-related surveyed data in a fast developing country like Nigeria. As far as we know, this present study stands as the first of its kind in the mathematical modelling and numerical simulation of HIV/AIDS infection and its subsequent health-care plan, database management, health policy and capacity

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building initiative.Other related mathematical models [3, 4, 5] which describe the dynamics of HIV/AIDS without random noise implications and without weekly predicted assumptions only provide adequate theoretical bases with rare policy formulations. Despite the stress associated with the stage of HIV infection [6], we report that the parameters which were estimated to explain the dynamics of HIV infection are beyond deterministic characteristic, hence random noise in the estimated parameters and HIV infection data [7] makes this simplifying assumption in our present study necessary.

2.0 Mathematical Formulation

The three non-linear model equations of first order ordinary equations type that describe the dynamics of HIV infection has been formulated in the work of [1] with the following mathematical structure

$$\frac{dT}{dt} = s - dT + aT(1 - \frac{T}{T_{\max}}) - \beta TV \qquad (1)$$

$$\frac{dI}{dt} = \beta_1 TV - \delta I \qquad (2)$$

$$\frac{dV}{dt} = \rho I - cV \qquad (3)$$

with the defined initial conditions.The notation T is called the number of target cells while the notations I and V are called the number of infected cells and the viral load of the virions at time t in the unit of days. The notation s stands for the rate at which new T cells are created from sources within the body such as the thymus whereas the notation a is called the maximum proliferation rate of target cells. The notation $T_{\max}$ stands for the T population density at which proliferation shuts off whereas the notation d stands for the death rate of the T cells. The notation β_1 is represented by the exponential equation $\beta_1 = \beta e^{-m\tau}$ where β is the infection rate constant whereas the term $e^{-m\tau}$ accounts for cells that are infected τ time units later. The notation δ stands for the death rate of infective cells whereas the notation ρ is the reproductivity rate of the infected cell. The notation c represents the clearance rate constant of virions. This model formulation did not look at the data base implementation with its health policy. This omitted idea is a vital issue for the purpose of tackling this endeamic infection.

3.0 Method of Solution

The formulated model equations do not have closed-form solutions, hence a simulation method of solving this problem was proposed. First, the equations were coded with the model parameter values using a Matlab programming language as a controlled numerically integrable sub-program of interaction functions over time t from $t = 0$ to $t = 100$ in the unit of days in which all the model parameters were fixed:

$d = 0.01, \delta = 0.5, c = 10, a = 6.8, T_{\max} = 1300, s = 5, \beta = 0.0002, \rho = 1000$.

Next,the same interaction functions where coded using a Matlab programming language as another numerically integrable sub-program for the time range in which all the model parameters' values were fixed except $a = 6.8$ that was varied by the chosen percentage range.

These two sub-Matlab programs were then coded with the capability to integrate these programs using an inbuilt $ODE45$ integration scheme which is computationally more efficient than $ODE23$ integration scheme [these two computational schemes are said to be numerically robust]. Within this solution sub-program, we have used the solution trajectories of the three model equations to define and compute the number of infected cells of HIV infection for the first day of the first week denoted by $I(1)$ which was followed up with the number of infected cells of HIV infection for the first day of the second week denoted by $I(8)$. The numbers of the infected cells of HIV infection for the first day of the third week and the first day of the fourth week were computed using the notations of $I(15)$ and $I(22)$ respectively. The same numerical procedure was systematically followed to compute the number of infected cells of HIV infection for the first day of the fifth week and other scenarios of weekly data. It is these data that can be used to manage the pattern in the number of infected cells of HIV infection to investigate if there would be some sorts of destructions and survival of the number of infected cells. It is these insights that are capable to propel a realistic and applicable HIV/AIDS health policy and health-care planning.

4.0 Results and Discussion

On the basis of the above method, we present our results in the tables listed below. In Table 1, we have predicted the number of infected cells of HIV infection when the maximum proliferation rate of target cells ranges between a = 0.68 and a = 3.40.In the symbol 'count (bn: an:n) as shown in Table 1', '**n'** specifies the number of infected cells ofHIV infection when a

= 6.8, '**an'** specifies the number of infected cells that is bigger than the number of infected cells when a = 6.8, '**bn'** specifies the number of infected cells that is smaller than the number of infected cells when a = 6.8.

For this simulation study for the interval [0.68, 3.40], we observed that out of the 130 data points, only five (5) data points indicate no change from the original number of target cells while one hundred and twenty five (125) data points indicate smaller values from the original number of target cells. In these twenty six (26) examples, the number of infected cells of HIV infection will unanimously suffer huge damage. An information data base system of this sophistication does prompts for answers on the weekly behaviour of these data. The third column of Table 1 predicts the number of infected cells of HIV infection when the maximum proliferation rate of target cells is fixed for the value of 6.8. Example 1 depicts the fact that the number of infected cells of HIV infection remains the same irrespective of the changes in the maximum proliferation rate of target cells due to the scientific fact that the proliferation rate of target cells is expected to change due to the anatomy and physiology of the human body and their subsequent impacts on the flow of blood. Our numerical results mimic real life situations for patients on a weekly monitoring system. The clinician knowing the relationship between the maximum proliferate rate of target cells and the number of infected cells of HIV infection of $CD4^+$ T-cells is keen to know how the number of infected cells calculated experimentally will respond to the changes in the maximum proliferate rate of target cells one-at-a-time on a weekly basis as a probable decision mechanism for a patient. Looking at example 2, we have observed that the number of infected cells for the first day of the second week is 483 for $a = 6.8$ while the number of infected cells for the first day of the second week is 60 for $a = 0.68$. For other changes in the value of the maximum proliferation rate of target cells along that row of example 2, we have found that as proliferation rate of target cells increases, the number of infected cells of HIV infection also increase but the five new predicted numbers of infected cells of HIV infection are all smaller in value than the original number of infected cells of HIV infection when the maximum proliferation rate of target cells is fixed for the value of 6.8. This observation is systematically uniform for the 25 examples except example 1.

Table 1: Predicting the number of infected cells of HIV infection when the maximum proliferation rate of target cells ranges between a = 0.68 and a = 3.40

Example	**I_{wp} (t)**	**I_w (t) a = 6.8**	**a = 0.68**	**a = 1.36**	**a = 2.04**	**a = 2.72**	**a = 3.40**	**count(bn:an:n)**
1	I (1)	1	1	1	1	1	1	0:0:5
2	I (8)	483	60	69	79	92	115	5:0:0
3	I (15)	416	51	84	83	135	228	5:0:0
4	I (22)	369	34	86	94	169	158	5:0:0
5	I (29)	344	43	84	107	139	182	5:0:0
6	I (36)	332	46	81	114	134	178	5:0:0
7	I (43)	325	42	79	114	147	171	5:0:0
8	I (50)	322	42	77	112	145	182	5:0:0
9	I (57)	321	43	77	110	140	172	5:0:0
10	I (64)	321	43	76	109	143	179	5:0:0
11	I (71)	322	43	76	109	144	175	5:0:0
12	I (78)	323	43	76	109	143	177	5:0:0
13	I (85)	324	43	76	110	143	176	5:0:0
14	I (92)	326	43	76	110	143	176	5:0:0
15	I (99)	327	43	76	110	143	177	5:0:0
16	I (106)	329	43	76	110	143	176	5:0:0
17	I (113)	330	43	76	110	143	176	5:0:0
18	I (120)	332	43	76	110	143	176	5:0:0
19	I (127)	333	43	76	110	143	176	5:0:0
20	I (134)	334	43	76	110	143	176	5:0:0
21	I (141)	336	43	76	110	143	176	5:0:0
22	I (148)	337	43	76	110	143	176	5:0:0
23	I (155)	338	43	76	110	143	176	5:0:0
24	I (162)	339	43	76	110	143	176	5:0:0
25	I (169)	339	43	76	110	143	176	5:0:0
26	I (176)	340	43	76	110	143	176	5:0:0

Table 2: Predicting the number of infected cells of HIV infection when the maximum proliferation rate of target cells ranges between a = 7.48 and a = 10.20

Example	**I_{wp} (t)**	**I_w (t) : a = 6.8**	**a = 7.48**	**a = 8.46**	**a = 8.84**	**a = 9.52**	**a = 10.20**	**count(bn:an:n)**
1	I (1)	1	1	1	1	1	1	0:0:5
2	I (8)	483	496	496	492	488	485	0:5:0
3	I (15)	416	470	449	416	396	402	2:2:1
4	I (22)	369	449	403	367	416	602	1:4:0
5	I (29)	344	431	367	390	579	546	0:5:0
6	I (36)	332	414	350	499	504	422	0:5:0
7	I (43)	325	397	364	512	407	572	0:5:0
8	I (50)	322	381	412	439	458	549	0:5:0
9	I (57)	321	367	460	385	565	426	0:5:0
10	I (64)	321	356	461	409	464	573	0:5:0
11	I (71)	322	348	428	502	404	544	0:5:0
12	I (78)	323	345	391	490	524	426	0:5:0
13	I (85)	324	347	369	420	530	581	0:5:0
14	I (92)	326	354	375	387	426	536	0:5:0
15	I (99)	327	364	413	443	434	426	0:5:0
16	I (106)	329	377	449	507	561	590	0:5:0
17	I (113)	330	388	447	461	480	527	0:5:0
18	I (120)	332	396	418	400	407	426	0:5:0
19	I (127)	333	399	387	401	504	599	0:5:0
20	I (134)	334	397	374	483	539	519	0:5:0
21	I (141)	336	391	390	493	434	427	0:5:0
22	I (148)	337	383	426	429	425	605	0:5:0
23	I (155)	338	375	447	390	557	510	0:5:0
24	I (162)	339	368	433	436	489	429	0:5:0
25	I (169)	339	363	404	503	408	610	0:5:0
26	I (176)	340	361	381	464	491	501	

In this pioneering challenging simulation study, a variation of the maximum proliferation rate of target cells**a**has indicated two scenarios of interpretation namely: for the maximum proliferation rate interval [0.68, 3.40], the predicted weekly data show that the number of infected cells of HIV infection will suffer some damage whereas for the maximum proliferation rate interval [7.48, 10.20], the predicted weekly data indicate that the number of infected cells of HIV infection will enhance a growing pattern. This observation can provide a vital insight for the purpose of HIV intervention policy.

Since the model parameters and the model modelling formulation were estimated and approximated, it is a good practice in a scientific report of this sophistication to investigate the impact of random noise on the weekly predicted data for the two selected proliferation rate intervals. Our first insight of analysis is purely deterministic while this later inclusion of induced random noise is more stochastic which renders the predicted weekly data to have some fuzzy dimension in the interpretation of the outcomes of this analysis in the context of closeness to reality. This approach is expected to both minimize error and bridge the inevitable selection bias between the deterministic and stochastic scenarios. To tackle this issue succinctly, we have proposed exploring low random noise intensity and high random noise intensity regimes.

5.0 Illustrating Example

In this example, we have considered when the random noise intensity value is 0.4. The application of the random noise characterization on the maximum proliferation rate of target cells of HIV infection can be attributed to the expected trauma and social stigmatization which is yet to be legally controlled within the Nigerian health policy culture. We will consider a brief analysis of this complex phenomenon in this study pending when we will present a comprehensive analysis in the near future research contribution.

Table 3: Predicting the number of infected cells of HIV infection when the maximum proliferation rate of target cells ranges between a = 0.68 and a = 3.40 due to a random noise intensity of 0.4 on the proliferation rate.

Example	I_{wp} (t)	I_w (t) : a = 6.8	a = 0.68	a = 1.36	a = 2.04	a = 2.72	a = 3.40	count(bn:an:n)
1	I (1)	1	1	1	1	1	1	0:0:5
2	I (8)	483	62	71	82	97	124	5:0:0
3	I (15)	416	74	81	91	168	241	5:0:0
4	I (22)	369	50	86	115	170	156	5:0:0
5	I (29)	344	49	89	129	139	213	5:0:0
6	I (36)	332	52	89	126	156	172	5:0:0
7	I (43)	325	52	86	116	157	199	5:0:0
8	I (50)	322	54	87	118	146	177	5:0:0
9	I (57)	321	54	87	118	160	191	5:0:0
10	I (64)	321	52	85	121	154	182	5:0:0
11	I (71)	322	52	82	121	148	191	5:0:0
12	I (78)	323	52	86	120	157	185	5:0:0
13	I (85)	324	53	82	122	151	191	5:0:0
14	I (92)	326	53	84	119	152	187	5:0:0
15	I (99)	327	54	80	119	152	186	5:0:0
16	I (106)	329	54	82	116	153	183	5:0:0
17	I (113)	330	52	85	115	153	185	5:0:0
18	I (120)	332	51	86	119	152	191	5:0:0
19	I (127)	333	55	85	122	151	185	5:0:0
20	I (134)	334	53	84	117	153	188	5:0:0
21	I (141)	336	50	84	121	149	180	5:0:0
22	I (148)	337	51	88	122	153	194	5:0:0
23	I (155)	338	54	85	118	157	182	5:0:0
24	I (162)	339	51	83	117	148	193	5:0:0
25	I (169)	339	51	83	116	154	182	5:0:0
26	I (176)	340	53	86	120	154	187	5:0:0

In Table 3, our analysis shows that a huge damage of the number of infected cells of HIV infection is expected when the induced-random noise intensity is 0.4. What if the random noise affects a single variation of the maximum proliferation rate of target cells of HIV infection over a few repeated simulations such as a = 4.08, a = 5.44 and a = 8.16? What can be considered as a realistic health policy implication? For example, we have carefully considered when this parameter is varied by 60 percent under the induced noise intensity value of 0.4 under the simplifying assumption of 130 (that is each new value of model parameter **a**will correspond to 26 repeated simulations of which a total of five similar variations will produce 130 simulations) repeated simulations. The output of this level of analysis is displayed in Table 4.

From Table 4, we similarly observed a dominant pattern in which the number of infected cells of HIV infection is predicted to suffer a huge damage when the induced-random noise intensity is 0.4. This result corresponds to a scenario when the maximum proliferation rate of target cells is 4.08.

Table 4: Predicting the number of infected cells of HIV infection when the maximum proliferation rate of target cells is 4.08 due to a random noise intensity of 0.4 on the proliferation rate.

Example	I_{wp} (t)	I_w (t) : a = 6.8	a = 4.08	a = 4.08	a = 4.08	a = 4.08	a = 4.08	count(bn:an:n)
1	I (1)	1	1	1	1	1	1	0:0:5
2	I (8)	483	176	176	175	176	174	5:0:0
3	I (15)	416	226	222	223	224	222	5:0:0
4	I (22)	369	232	226	234	229	237	5:0:0
5	I (29)	344	202	202	206	201	203	5:0:0
6	I (36)	332	237	239	242	236	237	5:0:0
7	I (43)	325	207	205	201	209	213	5:0:0
8	I (50)	322	226	224	230	225	221	5:0:0
9	I (57)	321	218	219	213	222	224	5:0:0
10	I (64)	321	219	219	217	214	212	5:0:0
11	I (71)	322	223	225	225	226	221	5:0:0
12	I (78)	323	217	213	215	214	218	5:0:0
13	I (85)	324	223	229	220	217	222	5:0:0
14	I (92)	326	216	213	223	224	220	5:0:0
15	I (99)	327	221	226	214	218	215	5:0:0
16	I (106)	329	222	221	220	221	222	5:0:0
17	I (113)	330	217	214	225	220	215	5:0:0
18	I (120)	332	221	233	213	219	228	5:0:0
19	I (127)	333	225	212	223	219	215	5:0:0
20	I (134)	334	211	219	219	216	223	5:0:0
21	I (141)	336	225	220	219	222	220	5:0:0
22	I (148)	337	213	218	220	220	217	5:0:0
23	I (155)	338	226	223	219	217	222	5:0:0
24	I (162)	339	220	212	214	220	219	5:0:0
25	I (169)	339	218	221	225	220	227	5:0:0
26	I (176)	340	217	222	215	218	212	5:0:0

Table 5: Predicting the number of infected cells of HIV infection when the maximum proliferation rate of target cells is 5.44 due to a random noise intensity of 0.4 on the proliferation rate.

Example	**I_{wp} (t)**	**I_w (t) : a = 6.8**	**a = 5.44**	**a = 5.44**	**a = 5.44**	**a = 5.44**	**a = 5.44**	**count(bn:an:n)**
1	I (1)	1	1	1	1	1	1	0:0:5
2	I (8)	483	374	375	378	374	371	5:0:0
3	I (15)	416	226	228	227	227	226	5:0:0
4	I (22)	369	257	258	256	260	258	5:0:0
5	I (29)	344	303	307	304	302	309	5:0:0
6	I (36)	332	314	316	317	326	326	5:0:0
7	I (43)	325	295	290	285	295	291	5:0:0
8	I (50)	322	268	274	261	269	268	5:0:0
9	I (57)	321	269	275	274	272	281	5:0:0
10	I (64)	321	285	287	292	284	291	5:0:0
11	I (71)	322	295	308	299	295	291	5:0:0
12	I (78)	323	294	298	289	292	287	5:0:0
13	I (85)	324	287	278	279	291	286	5:0:0
14	I (92)	326	272	268	284	282	287	5:0:0
15	I (99)	327	269	286	292	277	284	5:0:0
16	I (106)	329	289	297	280	279	282	5:0:0
17	I (113)	330	292	292	289	294	290	5:0:0
18	I (120)	332	290	272	292	300	292	5:0:0
19	I (127)	333	287	275	286	284	281	5:0:0
20	I (134)	334	294	290	284	276	280	5:0:0
21	I (141)	336	291	298	282	284	287	5:0:0
22	I (148)	337	288	296	281	290	295	5:0:0
23	I (155)	338	285	285	288	295	293	5:0:0
24	I (162)	339	286	278	285	289	290	5:0:0
25	I (169)	339	285	280	284	282	276	5:0:0
26	I (176)	340	282	288	286	285	274	5:0:0

In this scenario as presented in Table 5, we have also observed that a new value of **a** equals to 5.44 indicates a dominant damage of the number of infected cells of HIV infection is expected when the induced-random noise intensity is 0.4.

Table 6: Predicting the number of infected cells of HIV infection when the maximum proliferation rate of target cells is 8.16 due to a random noise intensity of 0.4 on the proliferation rate.

Example	**I_{wp} (t)**	**I_w (t) : a = 6.8**	**a = 8.16**	**a = 8.16**	**a = 8.16**	**a = 8.16**	**a = 8.16**	**count(bn:an:n)**
1	I (1)	1	1	1	1	1	1	0:0:5
2	I (8)	483	492	493	493	495	496	0:5:0
3	I (15)	416	440	442	439	438	433	0:5:0
4	I (22)	369	389	390	394	385	387	0:5:0
5	I (29)	344	354	356	362	355	362	0:5:0
6	I (36)	332	352	365	353	365	364	0:5:0
7	I (43)	325	403	426	396	431	411	0:5:0
8	I (50)	322	479	482	465	486	483	0:5:0
9	I (57)	321	489	471	480	472	480	0:5:0
10	I (64)	321	444	421	431	417	433	0:5:0
11	I (71)	322	400	381	389	371	389	0:5:0
12	I (78)	323	369	373	370	361	372	0:5:0
13	I (85)	324	381	418	409	409	397	0:5:0
14	I (92)	326	432	477	458	470	456	0:5:0
15	I (99)	327	476	457	452	471	477	0:5:0
16	I (106)	329	447	414	422	426	442	0:5:0
17	I (113)	330	402	380	392	386	397	0:5:0
18	I (120)	332	376	387	383	381	374	0:5:0
19	I (127)	333	384	435	422	417	400	0:5:0
20	I (134)	334	424	457	465	464	452	0:5:0
21	I (141)	336	463	439	454	460	466	0:5:0
22	I (148)	337	455	397	407	423	433	0:5:0
23	I (155)	338	422	381	376	389	401	0:5:0
24	I (162)	339	389	415	385	382	392	0:5:0
25	I (169)	339	392	457	442	417	415	0:5:0
26	I (176)	340	431	450	455	463	444	0:5:0

In contrast, Table 6 shows that a new value of **a** equals to 8.16 predicts a dominant survival of the number of infected cells of HIV infection when the induced-random noise intensity is 0.4.

Table 7: Predicting the number of infected cells of HIV infection when the maximum proliferation rate of target cells is 13.6 due to a random noise intensity of 0.4 on the proliferation rate.

Example	**I_{wp} (t)**	**I_w (t) : a = 6.8**	**a = 13.6**	**a = 13.6**	**a = 13.6**	**a = 13.6**	**a = 13.6**	**count(bn:an:n)**
1	I (1)	1	1	1	1	1	1	0:0:5
2	I (8)	483	523	521	524	524	524	0:5:0
3	I (15)	416	775	791	780	770	781	0:5:0
4	I (22)	369	668	620	645	662	656	0:5:0
5	I (29)	344	619	635	632	616	629	0:5:0
6	I (36)	332	878	873	862	875	880	0:5:0
7	I (43)	325	544	545	547	541	547	0:5:0
8	I (50)	322	746	754	729	748	765	0:5:0
9	I (57)	321	717	708	746	718	689	0:5:0
10	I (64)	321	605	605	587	608	614	0:5:0
11	I (71)	322	860	863	862	872	862	0:5:0
12	I (78)	323	560	558	559	551	565	0:5:0
13	I (85)	324	696	696	702	720	691	0:5:0
14	I (92)	326	824	800	798	761	821	0:5:0
15	I (99)	327	561	568	574	584	563	0:5:0
16	I (106)	329	841	829	831	859	804	0:5:0
17	I (113)	330	578	598	579	558	619	0:5:0
18	I (120)	332	676	664	676	704	640	0:5:0
19	I (127)	333	846	857	844	805	876	0:5:0
20	I (134)	334	557	552	560	573	544	0:5:0
21	I (141)	336	806	795	815	826	776	0:5:0
22	I (148)	337	602	621	625	588	677	0:5:0
23	I (155)	338	657	648	633	664	607	0:5:0
24	I (162)	339	859	860	883	868	878	0:5:0
25	I (169)	339	552	549	549	552	551	0:5:0
26	I (176)	340	769	768	765	801	722	0:5:0

The same observation has been made for the scenarios when the maximum proliferation rate of target cells are 13.6, 27.2 and 54.4 [Table 7, Table 8, Table 9] due to a random noise intensity of 0.4 on the proliferation rate.

Table 8: Predicting the number of infected cells of HIV infection when the maximum proliferation rate of target cells is 27.2 due to a random noise intensity of 0.4 on the proliferation rate.

Example	**I_{wp} (t)**	**I_w (t) : a = 6.8**	**a = 27.2**	**a = 27.2**	**a = 27.2**	**a = 27.2**	**a = 27.2**	**count(bn:an:n)**
1	I (1)	1	1	1	1	1	1	0:0:5
2	I (8)	483	1310	1299	1305	1303	1311	0:5:0
3	I (15)	416	1118	1157	1128	1135	1122	0:5:0
4	I (22)	369	1694	1636	1670	1667	1674	0:5:0
5	I (29)	344	1204	1167	1193	1182	1189	0:5:0
6	I (36)	332	1317	1550	1398	1446	1451	0:5:0
7	I (43)	325	1550	1451	1516	1473	1498	0:5:0
8	I (50)	322	1114	1078	1102	1081	1094	0:5:0
9	I (57)	321	1704	1759	1715	1772	1750	0:5:0
10	I (64)	321	1378	1316	1389	1294	1349	0:5:0
11	I (71)	322	1084	1113	1079	1191	1099	0:5:0
12	I (78)	323	1720	1680	1738	1608	1685	0:5:0
13	I (85)	324	1223	1190	1250	1148	1196	0:5:0
14	I (92)	326	1329	1458	1232	1584	1435	0:5:0
15	I (99)	327	1555	1491	1601	1433	1511	0:5:0
16	I (106)	329	1119	1091	1148	1078	1095	0:5:0
17	I (113)	330	1670	1753	1545	1757	1747	0:5:0
18	I (120)	332	1403	1361	1451	1279	1337	0:5:0
19	I (127)	333	1077	1083	1078	1167	1093	0:5:0
20	I (134)	334	1747	1742	1759	1632	1709	0:5:0
21	I (141)	336	1261	1251	1296	1156	1232	0:5:0
22	I (148)	337	1179	1245	1140	1543	1237	0:5:0
23	I (155)	338	1633	1600	1652	1482	1589	0:5:0
24	I (162)	339	1159	1139	1180	1088	1134	0:5:0
25	I (169)	339	1511	1640	1455	1750	1651	0:5:0
26	I (176)	340	1447	1431	1502	1319	1407	0:5:0

Table 9: Predicting the number of infected cells of HIV infection when the maximum proliferation rate of target cells is 54.4 due to a random noise intensity of 0.4 on the proliferation rate.

Example	**I_{wp} (t)**	**I_w (t) : a = 6.8**	**a = 27.2**	**a = 54.4**	**a = 54.4**	**a = 54.4**	**a = 54.4**	**count(bn:an:n)**
1	I (1)	1	1	1	1	1	1	0:0:5
2	I (8)	483	2833	2844	2845	2840	2830	0:5:0
3	I (15)	416	2216	2221	2218	2218	2215	0:5:0
4	I (22)	369	3365	3370	3375	3364	3375	0:5:0
5	I (29)	344	2582	2582	2609	2569	2581	0:5:0
6	I (36)	332	2396	2373	2379	2416	2441	0:5:0
7	I (43)	325	3120	3127	3109	3123	3098	0:5:0
8	I (50)	322	2358	2347	2347	2369	2341	0:5:0
9	I (57)	321	3200	3181	3232	3179	3245	0:5:0
10	I (64)	321	2807	2822	2805	2831	2789	0:5:0
11	I (71)	322	2214	2215	2210	2213	2212	0:5:0
12	I (78)	323	3336	3355	3330	3350	3324	0:5:0
13	I (85)	324	2531	2548	2543	2560	2529	0:5:0
14	I (92)	326	2562	2462	2487	2470	2519	0:5:0
15	I (99)	327	3036	3069	3085	3095	3067	0:5:0
16	I (106)	329	2306	2330	2331	2347	2323	0:5:0
17	I (113)	330	3300	3250	3256	3188	3306	0:5:0
18	I (120)	332	2778	2792	2789	2819	2759	0:5:0
19	I (127)	333	2213	2217	2212	2215	2219	0:5:0
20	I (134)	334	3311	3319	3340	3354	3278	0:5:0
21	I (141)	336	2522	2511	2543	2551	2465	0:5:0
22	I (148)	337	2524	2599	2468	2465	2700	0:5:0
23	I (155)	338	3073	3031	3064	3066	2983	0:5:0
24	I (162)	339	2338	2300	2315	2317	2272	0:5:0
25	I (169)	339	3247	3317	3269	3305	3366	0:5:0
26	I (176)	340	2804	2747	2764	2768	2711	0:5:0

6.0 Conclusion

The process of a numerical simulation has been successfully used to predict the number of infected cells of HIV infection of $CD4^+$ T-cells with data base management and health policy implications when the random-noise effect was analysed. The choice of the maximum proliferation rate of target cells has been shown to predict both weaker and severe impacts of the number of infected cells of HIV infection due to the random-noise intensity value of 0.4.

We would expect these series of numerically simulated data to provide better insight on the benefit of the weekly data of the number of infected cells of HIV infection for the purpose of mitigating and managing the spread of HIV infection. Other challenging aspects of this study can be extended in our future studies that would relate expected vital information when another model parameter combines with the maximum proliferation rate of target cells.

References

[1] X. Song, S. Chen (2005), A delay-differential equation model of HIV infection of $CD4^+$ T- cells. J. Korean Math. Soc, 42, pp. 1071-1086.

[2] E.N. Ekaka-a, B.C. Didia, E.C. Nwachukwu (2014), Parametric sensitivity analysis of a mathematical model of HIV infection of $CD4^+$ T-cells. Port Harcourt Medical Journal, Volume 8, pp. 61-66.

[3] V. Herz, S. Bonhoffer, R. Anderson, R. May, and M. Nowak (1996), Viral dynamicsin vivo: limitations on estimations on intracellular delay and virus decay, Proc.Natl. Acad. Sci. USA 93, pp. 7247-7251.

[4] Z. Grossman, M. Polis, M. Feinberg, I. Levi, S. Jankelevich, R. Yarchoan, J.Boon, F. de Wolf, J. Lange, J. Goudsmit, D. Dimitrov, and W. Paul (1999), OngoingHIV dissemination during HAART, Nat. Med. 5, 1099.

[5] J. Tam, Delay effect in a model for virus replication (1999), IMA J. Math. Appl. Med.Biol. 16, 29.

[6] M.H. Antoni (2003), Stress Management Effects on Psychological, Endocrinological, and Immune Functioning in Men with HIV Infection:Empirical Support for a Psychoneuroimmunological Model, Stress, Vol. 6 (3), pp. 173–188.

[7] A. J. Elliott, J. Russo, P. P. Roy-Byrne (2002), The effect of changes in depression on health related quality of life (HRQoL) in HIV infection, General Hospital Psychiatry, Volume 24 Issue 1, pp. 43-47