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On a Model of Hepatitis of Type B

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ABSTRACT

In this paper we present a numerical solution for an epidemic model ofhepatitis of type B. In this model essential factors for this epidemy are appeared. The factors are: susceptible rate, expositive rate, vaccination rate, infection rate and recovery rate. We use of the classical Rung-Kuttamethod of order four to find the numerical solutions by Matlab software. We also draw some plots in different cases and discuss on the case which the model implies to an epidemic.
KEYWORDS: Hepatitis, Epidemic, HBV, Mathematical model.

INTRODUCTION

Mathematical models in biology are essential means for scientific and economical programming [1, 2, 4, 5, 6].Epidemiologists are interested in know when an epidemic will happen in population. Also how could they control an epidemic by changing the initial conditions and the disease factors?
Our aim is investigate several conditions that cause an epidemic in population. So at first we introduce a model for HBV, then we are going to find a numerical solution for differential system corresponding to the HBV model. At the end, by drawing some diagrams in different conditions we could easily determine when an epidemic will happen in population.

In the next section of this paper we present a mathematical model for hepatitis of type B (HBV) in an open society when the unit time is arbitrary. Then in section 3 we use of Rung-Kutta method to determine its solutions.

In the last section by using of Matlab software we are going to discuss about the epidemic situation in a population by drawing some graphs with different parameters.

First let us explain Rung-Kutta method [3]of higher-order initial-value problems. The techniques discussed are limited to thosethat transform a higher-order equation into a system of first-order differential equations.Before discussing the transformation procedure, some remarksare needed concerning systems that involvefirst-order differential equations.
An m order system offirst-order initial-value problems has the form

$$\frac{du_1}{dt} = f_1(t, u_1, u_2, \dots, u_m),$$
$$\frac{du_2}{dt} = f_2(t, u_1, u_2, \dots, u_m), \qquad (1.1)$$
$$\frac{du_m}{dt} = f_m(t, u_1, u_2, \dots, u_m),$$

for$a \le t \le b$,with the initial conditions$u_1(a) = \alpha_1, u_2(a) = \alpha_2, \dots, u_m(a) = \alpha_m$.
The object is to find$m$functions $u_1, u_2, \dots, u_m$that satisfy each of the differential equations together with all the initial conditions.

Let an integer $N > 0$ be chosen and set$h = \frac{b-a}{N}$. Partition the interval $[a, b]$into N subintervals with the mesh points$t_j = a + j$ for each$j = 0, 1, \dots, N$.

We use of the notation w_{ij}, for $j = 0, 1, \dots, N$and$i = 0, 1, \dots, m$to denotean approximation to $u_i(t_j)$. That is, w_{ij} approximates the ith solution $u_i(t)$of (1.1) at the jth mesh pointt_j. For the initial conditions, set
$w_{1,0} = \alpha_1, w_{2,0} = \alpha_2, \dots, w_{m,0} = \alpha_m$.
Suppose that the values$w_{1,j}, w_{2,j}, \dots, w_{m,j}$ have been computed. We obtain$w_{1,j+1}, w_{2,j+1}, \dots, w_{m,j+1}$
Byfirst calculating$k_{1,j} = hf_i(t_j, w_{1,j}, w_{2,j}, \dots, w_{m,j})$, (1.2)for$i \in \{1, 2, \dots, m\}$.
$k_{2,i} = hf_i\left(t_j + \frac{h}{2}, w_{1,j} + \frac{k_{1,1}}{2}, w_{2,j} + \frac{k_{1,2}}{2}, \dots, w_{m.j} + \frac{k_{1,m}}{2}\right)$,for$i \in \{1, 2, \dots, m\}$.

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$k_{3,i} = hf_i\left(t_j + \frac{h}{2}, w_{1,j} + \frac{k_{2,1}}{2}, w_{2,j} + \frac{k_{2,2}}{2}, \dots, w_{m.j} + \frac{k_{2,m}}{2}\right)$,for$i \in \{1, 2, \dots, m\}$.

$k_{4,i} = hf_i\left(t_j + \frac{h}{2}, w_{1,j} + k_{3,1}, w_{2,j} + k_{3,2}, \dots, w_{m.j} + k_{3,m}\right)$,for$i \in \{1, 2, \dots, m\}$.

And then$w_{i,j+1} = w_{i,j} + \frac{1}{6(k_{1,i}+2k_{2,i}+2k_{3,i}+k_{4,i})}$, for $i \in \{1, 2, \dots, m\}$.

Note that all the values $k_{1,1}, k_{1,2}, \dots, k_{1,m}$ must becomputed before any of the terms of the form $k_{2,i}$can be determined. Ingeneral, each $k_{l,1}, k_{l,2}, \dots, k_{l,m}$must be computed before any of$k_{l+1,i}$.

In our epidemic model which will be considered in the next section, we know the initial conditions for differential system, soby using of Rung-kutta method and Matlab software we will determine a suitable approximation for the solutions of the model. Then in each case of given parameters we could obtain a lot of information about the population and theepidemic.

THE MODEL WITH CONTINUOUS TIME

In this section we are going to introduce a model for HBV in an open societywhen the unit time is arbitrary.

We suppose that per capita transmission rate, birth rate and mortality rateare constant and we denote them by β, λ andμ. Also we assume that$m$ andα denote per unit time of susceptible people and people inthe exposed period who are selected for vaccination. All parameters areconstant in this model.

In the HBV model [7] we supposed that we have five compartments, susceptible, exposed, infected, vaccinated and recovered.We have denoted them by $S, E, I, V$and Rrespectively. How did we write the differential system?

We supposed that an average member of the population makes contact sufficient to transmit infection at time t with$\beta N(t)$ others per unit time, where$N(t)$ represents total population size. Since the probability that a randomcontact by an infective with a susceptible is$\frac{S(t)}{N(t)}$, the number of new infections in unit time is $N(t)\frac{S(t)}{N(t)}$, giving a rate of new infections that theyare in exposed class$\beta N(t)\frac{S(t)}{N(t)}I(t) = \beta S(t)I(t)$.So$\beta S(t)I(t)$ is the rate ofleaving class $S(t)$at time t. Also we assumed all newborns are susceptible. So the rate of new susceptible is $\lambda N(t)$ at time t. $mS(t)$isthe rate of those who leave class $S(t)$and enter to the vaccination class. And$\mu S(t)$ is the rate of those wholeavingthepopulation by death.So

$$\frac{dS}{dt} = -\beta S(t)I(t) + \lambda N(t) - mS(t).$$

We suppose a rate$\alpha E(t)$ of exposed individuals vaccinated so they enter tothe class$V(t)$ at time t, and a rate$(1-\alpha)kE(t)$ of exposed individuals are infected and they enter to the class $I(t)$at time t. So

$\frac{dE}{dt} = \beta S(t)I(t) - (\mu + \alpha + (1-\alpha)k)E(t)$.

We know the vaccination is not perfect, so a small fraction σ of vaccinated people are going to the infected class. So the probability of a random effect contact byan infective with a vaccinated person is$\frac{V(t)}{N(t)}$, the number of new infectionsin unit time per infective is$(\beta\sigma N(t))\frac{V(t)}{N(t)}$, giving a rate of new infections$\left(\beta\sigma N(t)\right)\frac{V(t)}{N(t)}$ $\mathrm{I(t)} = \beta\sigma\mathrm{V(t)I(t)}$.

Also a rate$\gamma I(t)$ of infected people are recovered and they enter to the class$R$ at time$t$ and a rate$\mu I(t)$ is the rate of those who leaving the population because of death. So

$\frac{dI}{dt} = \beta\sigma\mathrm{V(t)I(t)} + (1-\alpha)\mathrm{kE(t)} - (\mu+\gamma)\mathrm{I(t)}$.

We assume a rate$\eta V(t)$of vaccinated people recover at time t. So

$\frac{dV}{dt} = \beta\sigma\mathrm{V(t)I(t)} + \alpha\mathrm{E(t)} + \mathrm{mS(t)} - \eta\mathrm{V(t)}$.

A rate$\gamma f I(t)$ of infective people and a rate$\eta f_v V(t)$ of vaccinated individuals are recover at time t. So

$\frac{\mathrm{dR}}{\mathrm{dt}} = \gamma f I(t) + \eta f_v V(t) - \mu R(t)$.

The rates$(1-f)\gamma I(t)$ and$(1-f_v)\eta V(t)$ left the population by death. So

$\frac{\mathrm{dN}}{\mathrm{dt}} = -(1-f)\gamma I(t) - (1-f_v)\eta V(t) + \lambda N(t) - \mu N(t)$.

THE NUMERICAL SOLUTIONS OF THE MODEL

Now in this section we use of Rung-Kutta method that is mentioned inthe introduction to solve the differential system. We define

$f_1\left(t, S(t), E(t), I(t), V(t), N(t)\right) = -\beta S(t)I(t) + \lambda N(t) - mS(t)$.

$f_2\left(t, S(t), E(t), I(t), V(t), N(t)\right) = \beta S(t)I(t) - (\mu + \alpha + (1-\alpha)k)E(t)$.

$f_3\left(t, S(t), E(t), I(t), V(t), N(t)\right) = \beta\sigma\mathrm{V(t)I(t)} + (1-\alpha)\mathrm{kE(t)} - (\mu+\gamma)\mathrm{I(t)}$.

$f_4\left(t, S(t), E(t), I(t), V(t), N(t)\right) = \beta\sigma\mathrm{V(t)I(t)} + \alpha\mathrm{E(t)} + \mathrm{mS(t)} - \eta\mathrm{V(t)}$.

$f_5\big(t, S(t), E(t), I(t), V(t), N(t)\big) = -(1-f)\gamma I(t) - (1-f_v)\eta V(t) + \lambda N(t) - \mu N(t)$.
and we suppose that $w_{1,0} = S_0, w_{2,0} = E_0, w_{3,0} = I_0, w_{4,0} = V_0$ and $w_{5,0} = N_0$,where S_0, E_0, I_0, V_0 and N_0 are the initial conditions in population. By using of these assumptions and Matlab programmingthe solutions are sketched in the next section for different parameters.

DISCUSSION

We suppose that$M = 100, S_0 = 50, E_0 = 20, I_0 = 10, V_0 = 10$and $N_0 = 100$.Also a, b, c and d in the diagrams are the graphs of $S(t), E(t), I(t)$ and $V(t)$ respectively.
In the first case we assume thatthe parameters in the model are $f = 0.7, \gamma = 0.6, \alpha = 0.4, \beta = 0.3, k = 0.7, \lambda = 0.2, \eta = 0.7, f_v = 0.8, m = 0.4, \mu = 0.1$ and $\sigma = 0.01$.
By these assumptions we sketched the solutions in the following diagram(Diagram 1).

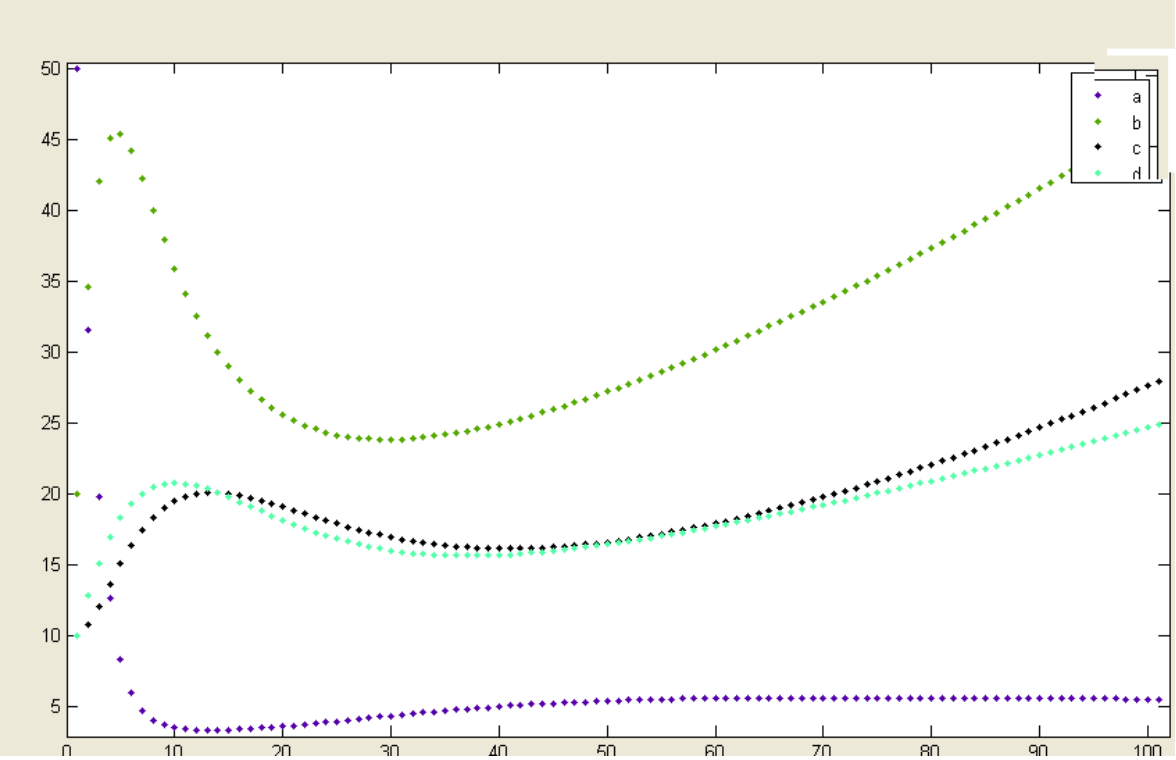

Diagram1. $f = 0.7, \gamma = 0.6, \alpha = 0.4, \beta = 0.3, k = 0.7, \lambda = 0.2, \eta = 0.7, f_v = 0.8, m = 0.4, \mu = 0.1, \sigma = 0.01$

By these results we observe that at first the number of susceptible are reduced very fast, and the number of people in exposed, infectious and vaccination groups are going to increase. So there is an epidemic in population. This situation continued until around 10 unit times, after that susceptible people are fewer than which could epidemic happened. So the number of the other groups are going to reduce. After 50 unit times because of $\lambda > \mu$ the population grow up so the susceptible population is going to increase. Hence epidemic will happen again but the epidemic is light. If we increase the vaccination parameter m in population then the second epidemic will not happened and disease will control.

In the second case we assume that$\beta = 0.1$ so in this case the transmission rate is lower than the first case and the other parameters are similar the pervious case. In this situation the number of infected people are fewer than thefirst case and there is no big epidemic in population. The next diagram (Diagram 2) determines this situation.

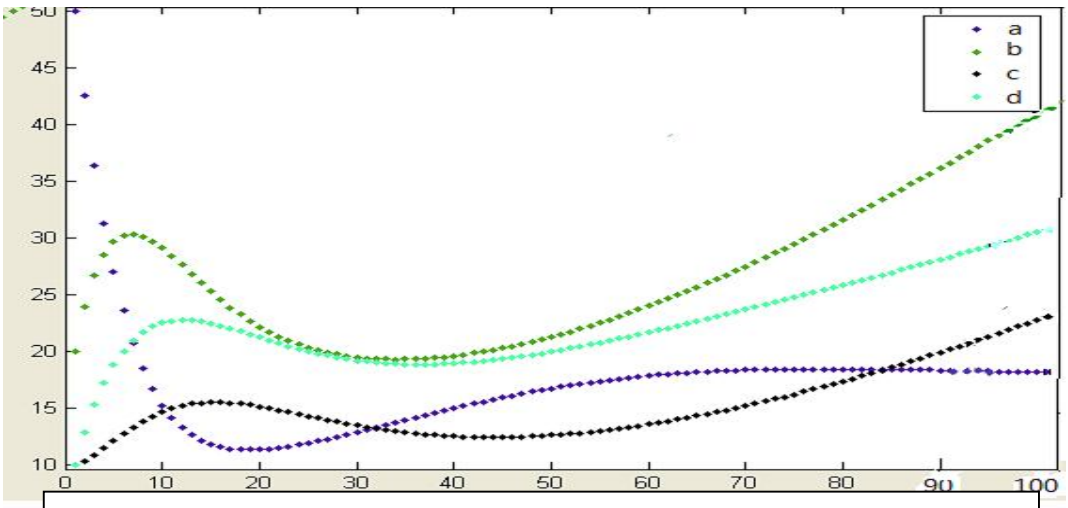

Diagram2. $f = 0.7, \gamma = 0.6, \alpha = 0.4, \beta = 0.1, k = 0.7, \lambda = 0.2, \eta = 0.7, f_v = 0.8, m = 0.4, \mu = 0.1, \sigma = 0.01$

In the third case we assume that the mortality rate and birth rate are equal$\lambda = \mu = 0.2$ and the transmission rate is as same as the second case. So we have the following diagram (Diagram 3).

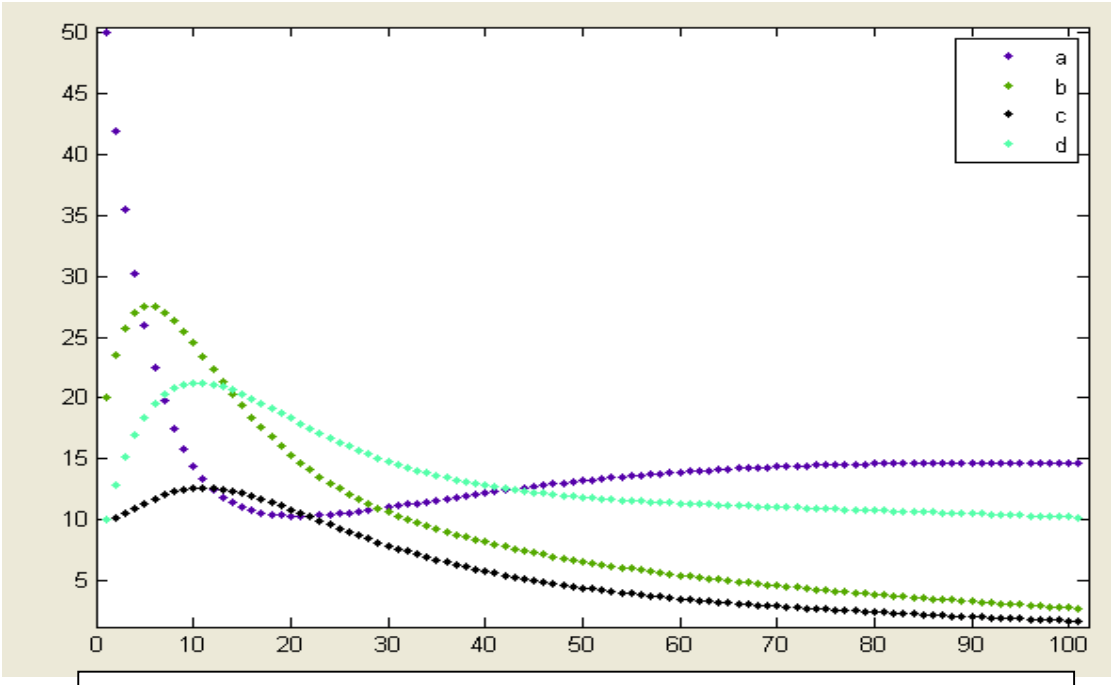

Diagram3. $f = 0.7, \gamma = 0.6, \alpha = 0.4, \beta = 0.1, k = 0.7, \lambda = 0.2 = \mu, \eta = 0.7, f_v = 0.8, m = 0.4, \sigma = 0.01$

We could observe that there is an epidemic in initial time and after some unit times the number of susceptible is going to be constant and the number of exposed and infected people are going to decrease. So there is no disease in population.

In the fourth case, we suppose the assumptions of the third case and also we assume that the vaccination parameter be larger than the previous cases$m = 0.6$. In this case the number of people who receives the vaccine is more than the previous cases. Hence there is no epidemic in population and most of people are susceptible or they are vaccinated. That diagram in this case is

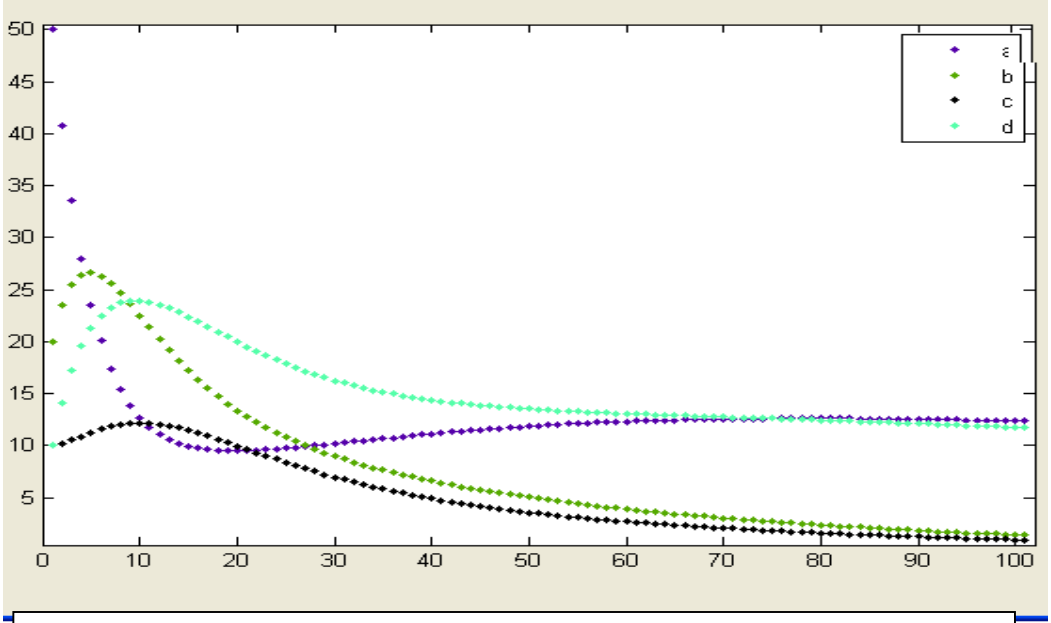

Diagram4. $f = 0.7, \gamma = 0.6, \alpha = 0.4, \beta = 0.1, k = 0.7, \lambda = 0.2, \eta = 0.7, f_v = 0.8, m = 0.6, \mu = 0.1, \sigma = 0.01$

In the next case there is not enough vaccine in the population. So at first there is a big epidemic in the population thus susceptible people are going to decrease but after some time susceptible people will increase. Then a light epidemic will happen in population (Diagram 5).

Also in the last case we consider the case which there is not enough vaccine in population $\alpha = m = 0.1$ but people to comply with health issues so the rate of transition disease is smaller than the previous cases$\beta = 0.05$. Wesee that, there is an epidemic in the population but the epidemic is so light (Diagram 6).

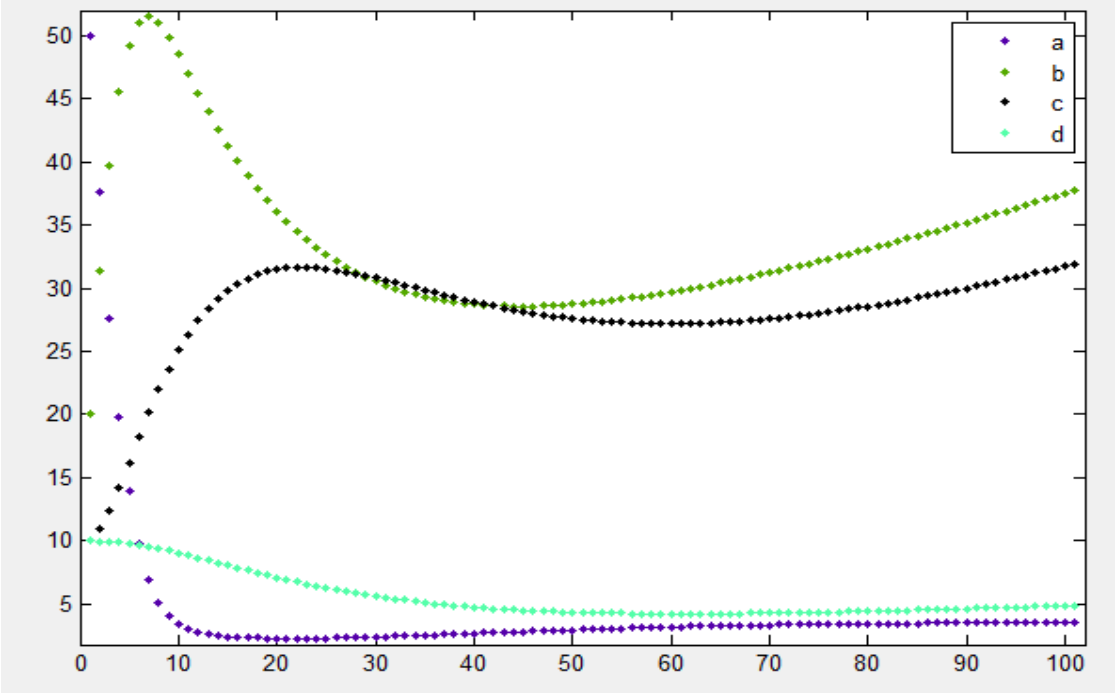

Diagram5. $f = 0.7, \gamma = 0.6, \alpha = 0.1 = m, \beta = 0.1, k = 0.7, \lambda = 0.2, \eta = 0.7, f_v = 0.8, \mu = 0.1, \sigma = 0.01$

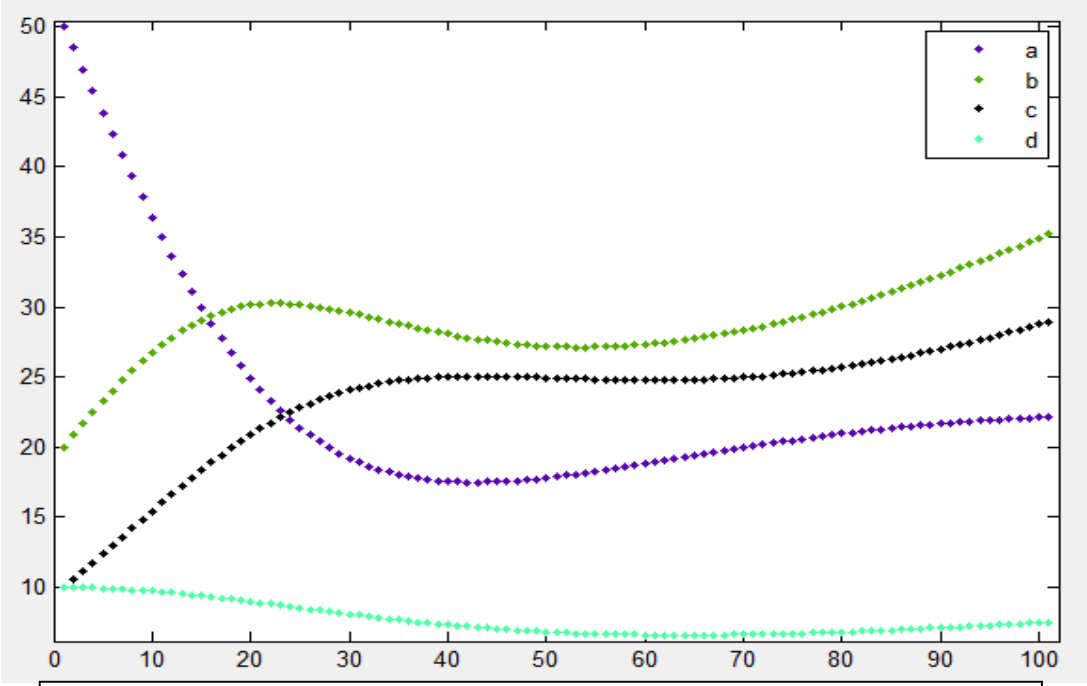

Diagram6. $f = 0.7$, $\gamma = 0.6, \alpha = 0.1 = m, \beta = 0.05, k = 0.7, \lambda = 0.2, \eta = 0.7, f_v = 0.8, \mu = 0.1, \sigma = 0.01$

CONCLUSION

In this paper we find a numerical solution for a HBV model. And by considering initial conditions and different parameters we draw some diagrams in some several cases which by these diagrams we could explain when an epidemic will happen in a population.

The limitations of this research are:

1. All the parameters are constant.
2. In real case the parameters are regional dependent.

The above two limitations can be a topic for further research. More precisely considering the HBV model when parameters are time dependent can be a topic for research from mathematical and statistical point of views when we restrict our self to a specific country or a region.

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REFERENCES

[1] Dordea, M., N. Coman, 2006. Aspects of the Evolutionary Process in small Population, StudiaUniversitati Babes-Bolyai, Biologia, LI., 2, 35-51.

[2] Farkas M., 2001. Dynamical models in biology. Academic Press.

[3]Hairer, E.,G Wanner, 1996. Solving ordinary differential equationsII: Stiff and differential-algebraic problems. Berlin, New York: Springer-Verlag.

[4] HoseiniAnvari M.R., M.R. Molaei, 2006.On the Observational Model of Genomics, StudiaUniversitatis Babes-Bolyai, Biologia, LI., 2, 53-72.

[5] KarimiMadahi S.S. , P. Salah, 2012. A Neural Network Based Method for Cost Estimation 63/20kV and 132/20kV Transformers, J. Basic Appl. Sci. Res., 2(1), 939-945.

[6]MolaeiM.R., 2010. A Mathematical Model for an Epidemic in an Open Society,StudiaUniversitatis Babes-Bolyai, Biologia, LV., 1, 61-65.

[7] Molaei M.R., T. Weazizadeh,2012. A mathematical model for HBV, To appear in J. Basic Appl. Sci. Res. .