
computer simulation and modeling for biological problems

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One of the most recent and interesting techniques is the Modelling and simulation of Human Biology. Infectious and cell diseases are very serious and are open fields of study. Some of these diseases are never understood yet others need more and more effort to be completely solved. Constructing mathematical and simulation models for some of these diseases are the main object of this study. Understanding and possibly controlling and predicting the nature and dynamics of these diseases are the results of such research. The hepatitis C virus (HCV) and the hepatitis B virus (HBV) are considered among the most dangerous infectious diseases in the world. Egypt has possibly the highest HCV and HBV prevalence in the world [28]. [8]. These two viruses are the common causes of cirrhosis and hepatocellular carcinoma (HCC). Hepatitis C virus infection is found in 0.5 % to 8.0 % of blood donors worldwide. Because the infection is chronic in more than 60 % of infected persons, the disease is an important public health and economic problem [14]. On the other hand, the world health organization has estimated that around 300 million persons worldwide suffer from chronic hepatitis D virus infection, 25-30 % of whom eventually will die from chronic sequel [20]. Interest in (HSV) epidemiology has increased due to the [HIV} (AIDS) epidemic, as the transmission routes and clinical features show many similarities for these two infections due to the fact that better understanding of (HBV) epidemiology could lead to new insights on the future development of the (HIV) epidemic [10]. Due to the importance of these two diseases, two mathematical models had been constructed to study the harmful behavior of these two diseases. The first is the deterministic model, while the second is the stochastic model. Moreover, a numerical simulation for these two mathematical models was also constructed. Due to the uncertainty concerning the database of these diseases in Egypt, another Monte Carlo simulation model had been built and the results obtained from this model had been compared with the other results as obtained from the numerical simulation of the mathematical models. This thesis contains five chapters. Chapter one, is considered as a review of previous work in the field of human biology, where it introduces introduction to the mathematical modelling process and some simple examples of the field of human biology, moreover, it produces a deterministic model of HBV as previous study. Finally, it produces a simple review of the Monte-Carlo simulation technique. In chapter two a stochastic model and Monte-Carlo simulation of the spread of HBV had been formulated and discussed. The numerical simulation

of the stochastic model proved the threshold level below which the disease will die out, and above it, the disease becomes endemic. Moreover, The results obtained from Monte Carlo simulation model could not confirm the other results as concluded from the other numerical simulation of the deterministic and stochastic models. Chapter three, is a deterministic model and its numerical simulation of the spread of HCV in Egypt. This public health problem had been studied both mathematically and by using computer simulations for the spread of HCV subtype (4a) and the relation between (HCV-subtype 4a) and other subtypes of HCV. The mutation factor (μ) plays a key result for this study. We derived the values of reproduction numbers (R_0 , R_0^2) which defined as the expected number of secondary cases produced by a single infected individual entering a disease free population at equilibrium (11). The conditions on these numbers were determined for the disease to be endemic or die out. Intuitively the disease die out when both (R_0 and R_0^2) are less than one in value otherwise the disease becomes endemic. The numerical simulation of deterministic model were used to predict the behavior of the dynamics of the disease and to estimate the numbers of persons in each stage. In chapter four a stochastic model and Monte-Carlo simulation of the spread of (HCV-subtype 4a) had been formulated and discussed. The results obtained from numerical simulation for stochastic model and Monte-Carlo simulation had been compared with the other results as obtained from the numerical simulation of the deterministic model. Both types of results are found in good matching and fitting well to each other. Chapter five is the conclusions of this research. Software (Mathematica 5.0), has been used to enhance the numerical simulations for the stochastic models. Furthermore, a program language (Visual-Basic under Excel) has been used to obtain the numerical simulation for the deterministic model and Monte Carlo simulation model.