ABSTRACT

Mathematical biology is the most interesting contemporary application of mathematics that is fast growing and well recognized in the field of medical and chemical sciences. As biology becomes more quantitative, growing use of mathematics in biology is inevitable. Several biological phenomena can be formulated as a mathematical model by using systems of ordinary or partial differential equations. Due to insufficient information about the behaviour of the system and occurrence of calculation errors, in the biological models, the ordinary and partial differential equations representing the model faces deviation in the final solution. To overcome this practical issue and to fine-tune the solutions, Fuzzy Differential Equations (FDEs) have been used as a powerful tool to model the biological systems. Moreover, the FDEs are widely applied in modelling population as well as problems in mathematical biology and human diseases.

The other type of system used in modelling the biological phenomena is Intuitionistic Fuzzy Differential Equations (IFDEs). Further, while considering the solutions of certain biological models, FDEs and IFDEs provide better solutions when compared with Ordinary Differential Equations (ODEs). Therefore, the main aim of this work is to represent the biological models in the form of FDEs and IFDEs and also obtain the semi analytical expressions of the parameters involved in the models.

In theory, most of the biological models in the form of nonlinear differential equations do not have a precise analytical solution, so there is a need to obtain an approximate solution for these nonlinear equations. Homotopy Analysis Method (HAM) and Homotopy Perturbation Method

(HPM) are powerful methods to obtain the semi analytical solutions for the nonlinear problems. In this current work, the parameters of the biological models are considered as fuzzy and intuitionistic fuzzy numbers and the above two methods are applied to find the approximate solutions of the nonlinear problems.

The first work is on non-linear Thomas model for empirical rate equations with substrate inhibition, where the parameters of the model face imprecision. Accordingly, in the proposed model the differential equations and their initial conditions are fuzzified and analyzed in fuzzy environment. The FDEs formed are converted to a set of crisp differential equations using Hukuhara derivative. In this study, the approximate fuzzy analytical expression of concentration profiles of oxygen and uric acid are derived using the homotopy analysis method. The derived fuzzy analytical solution is tested with the numerical solution and crisp solution. It is observed that the fuzzy differential equations give better solution than ordinary differential equations.

In the second model, the depletion of plankton-oxygen dynamics system that deals with non-spatial processes is represented in the form of non-linear fuzzy differential equations. This kinetic mechanism is based on the system of non-linear reaction diffusion equations. In this model, both the plankton-oxygen dynamics and its initial conditions are fuzzified. Here again, the FDEs formed are converted to a set of crisp differential equations using Hukuhara derivative. An approximate fuzzy analytical expression of concentration profiles of oxygen, phytoplankton and zooplankton is derived using the homotopy perturbation method for all hypothetical values of the parameters. The results of the analysis are found to be in agreement with the existing results.

The third model considered for the research study is ecology model. In ecology, harvesting plays an important role to predict the yield of a respective product. Biological model of quota harvesting process for a single species population density in fuzzy environment is more appropriate to analyze the harvest nature. Therefore, in this work the mathematical modelling of quota harvesting model in fuzzy environment under non-steady state conditions is presented. Semi analytical expressions for the system parameters, the population compactness, harvesting constant rate and growth rate are derived by using homotopy perturbation method. Here, an analysis on population is done by using both (i) gH differentiable and (ii) gH differentiable. Further, the values of all the system parameters are compared with the simulation results.

The mathematical modelling of diseases control and analysis of the diseases behavior play an important role in biological problems. Of this, HIV spreading is a major global health problem. Therefore, in the fourth model, the Nowak-May mathematical model is considered to represent HIV dynamical system. In general, a HIV infection analysis involves three main parameters, namely number of uninfected cells, infected cells and free virus particles. Due to impression involved in these parameters, they are defined as intuitionistic fuzzy numbers. Using (i)-gH differentiable and (ii)-gH differentiable, the intuitionistic fuzzy HIV model is converted in to a set of ordinary nonlinear differential equations. In addition, the semi analytical expressions for uninfected cells, infected cells and free virus particles are derived by homotopy perturbation method.

In this work, four mathematical models such as chemical reaction, climate change, quota harvesting and human disease are fuzzified and the semi analytical expressions are derived with the help of homotopy analysis and

homotopy perturbation method. The derived expressions are compared with numerical results.