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Title of the Thesis: Study of Discrete Biological Models with Nonstandard Finite Difference Method

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Nonlinear systems of differential equations play a very important role in studying different physical, chemical, and biological phenomena. However, in general, nonlinear differential equations cannot be solved analytically and therefore discretization is inevitable for good approximation of the solutions. Another reason for constructing discrete models, at least in the case of the population model, is that it permits arbitrary time-step units. Unfortunately, conventional discretization schemes, such as the Euler method, Runge-Kutta method, etc. show dynamic inconsistency. It produces spurious solutions that are not observed in its parent model and its dynamics depend on the step-size. It is therefore of immense importance to construct a discrete model which will preserve the properties of its constituent continuous models. In the recent past, considerable effort has been given to the construction of a discrete-time model to preserve the dynamic consistency of the corresponding continuous-time model without any limitation on the step-size.

In the case of the systems of ordinary differential equations, there are two fundamental issues regarding the construction of nonstandard finite difference (NSFD) models. First, how to construct the denominator function of the discrete first-order derivative? Second, how to discretize the nonlinear terms of a given differential equation with nonlocal terms? In this study, we define a uniform technique for nonlocal discretization and construction of the denominator function for NSFD models. We have demonstrated it using a couple of highly nonlinear continuous-time population. We have given analytical proof in each case to show that the proposed NSFD model has identical dynamic properties to the continuous-time model. It is also shown that each NSFD system is positively invariant, and its dynamics do not depend on the step-size. Numerical experiments have also been performed in favour of such claims. In addition, we have discretized a predator-prey model and an epidemiological model with both horizontal and vertical disease transmissions by the NSFD method and the Euler forward method, and then compare their dynamic properties with their corresponding continuous-time models. We show that NSFD systems preserve the positivity of the solutions and are completely consistent with the dynamics of the corresponding continuous-time model. On the other hand, the discrete models formulated by the forward Euler method do not show dynamic consistency with their continuous counterparts. Rather they show scheme-dependent instability when step-size restriction is violated.

In the case of the systems of PDEs, discretization using the NSFD scheme becomes harder and the major obstacles are how to discretize the second-order derivative terms and how to give the nonlocal transformations to both linear and nonlinear terms so that the positivity of the NSFD discrete system does not depend on the step-sizes and also the proposed NSFD scheme should

guarantee accuracy and consistency concerning both time and space step-sizes, maintaining stability. The recently developed NSFD techniques for partial differential equations do not provide consistency or first-order accuracy in time, or else they fail to retain positivity in the absence of step-size requirements. In this study, we propose an NSFD scheme for both two-dimensional and three-dimensional continuous systems, which ensures consistency of the suggested NSFD scheme as well as first-order accuracy in time and second-order accuracy in space while maintaining the positivity of solutions undiminished. Additionally, we show the Von Neumann stability of the proposed scheme. To illustrate the effectiveness of the proposed NSFD scheme, we compared the dynamics of the solutions of the discrete systems following our suggested NSFD scheme with the solutions of the other two systems discretized by the previously defined NSFD scheme and the Crank-Nicolson scheme.

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