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Generalized system of trial equation methods and their applications to biological systems

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ABSTRACT

It is shown that many systems of nonlinear differential equations of interest in various fields are naturally embedded in a new family of differential equations. In this paper, we improve new and effective methods for nonautonomous systems and they produce new exact solutions to some important biological systems. The exact solution of predator and prey population for different particular cases has been derived. The numerical examples show that new exact solutions can be obtained for many biological systems such as SIR model, Lotka–Volterra model. The methods perform extremely well in terms of efficiency and simplicity to solve this historical biological models.

The Lotka–Volterra nonlinear differential equations for two competing species, namely X and Y, contain six independent parameters. Their general analytic solutions, valid for arbitrary values of the parameters, are at present unknown. However, when two or more of these parameters are interrelated, it is possible to obtain the exact solutions in the X, Y phase plane, and six cases of solvability are given in this paper. The dependence of the solutions on the parameters and the initial conditions can thus be readily investigated.

1. Introduction

The considerable interest to nonlinear differential equations arises from broad applications. Nonlinear ordinary differential equations are important especially in applied and pure mathematics with applications in engineering, applied mechanics, quantum physics, analytical chemistry, astronomy, and biology. Over the years, most of the researchers searched for a solution to nonlinear differential equations both numerically and analytically. The disadvantage of the numerical methods is that the results are not exact. This underlines the importance to be aware of all past and present methods producing a solution to both linear and nonlinear type nonlinear ordinary differential equations.

Many research papers with methods of finding exact solutions of nonlinear differential equations were published in the recent years. For these studies, we refer the papers [3–5,13]. Usually, nonlinear differential equations have three main characteristics characteristic to produce an exact solution, partial solution and without an exact solution. The researchers usually attempt to solve nonlinear differential equations producing an exact or partial solution. This paper, focus on problems with a nonlinear differential equation that normally do not produce an exact solution. The exact solutions help to understand the mechanism of complicated physical phenomena and the model for the dynamical process. Furthermore, it helps to

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analyze the stability of these solutions. The new method based on generalized trial equation method applied to Lotka–Volterra equations and to the equations relating ebola disease.

1.1. Lotka–Volterra system

The Lotka–Volterra equation presents present a common ecological system dynamics model based on the relationship between predator and prey species. The Lotka–Volterra equations represent one of the keys to a particular kind of interdisciplinary: a concept that can be applied across many disciplines because of the nature of what is a generic problem – modeling the competition for resources'. In a particular instance of a research challenge, the trick is to be aware that the problem may be generic and that there are elements of a toolkit embedded in another discipline. The Lotka–Volterra equations, at some point, the predator population reduces to a minimum level that the rate of reproduction in the prey species is higher than the rate of prey consumption by the predators and the prey species begins to rebound. Because the predator species population takes longer to rebound, the prey species experiences growth that is, for the moment, virtually unchecked by predation. Eventually, the predator population begins to rebound due to the abundance of prey until the system returns to the original predator and prey populations and the entire cycle then repeats itself at infinity.

The most interesting fact about this system is that it returns again and again to the same initial conditions (not to count for numerical error). This is even more remarkable given the fact that the Lotka–Volterra system of equations is actually non-linear.

The Lotka–Volterra model of interspecific competition is a simple mathematical model that can be used to understand how different factors affect the outcomes of competitive interactions. Competitive interactions between organisms can have a great deal of influence on species evolution, the structuring of communities (which species coexist, which do not, relative abundance, etc.), and the distributions of species (where they occur). Modeling these interactions provides a useful framework for predicting outcomes. The important point to discover is to identify the coexisting circumstances for two species. This identifies the circumstances of one species to outcompete another. The solution to such problem modeled with the addition of a term involving the competition coefficient in the logistic equation. The competition coefficient represents the effect that one species has on the other. The Lotka–Volterra model of interspecific competition has been a useful starting point for biologists thinking about the outcomes of competitive interactions between species. The assumptions of the model may not be very realistic, but are necessary simplifications. A variety of factors not included in the model can affect the outcome of competitive interactions by affecting the dynamics of one or both populations. Environmental change, disease, and chance are just a few of these factors.

1.2. SIR and Ebola models

The Ebola virus disease was first discovered in 1976 in the present Democratic Republic of Congo. Therefore, by combining our interest in mathematics which lies in the solution to nonlinear differential equation along with curiosity for the repetition of the disease, we decided to determine the exact solution to such important application. Ebola Epidemics spread using an SIR model. An SIR model is an epidemiological model which measures the number of people infected with a particular disease over a period of time using three fundamental equations. The SIR model illustrates the transfer of the epidemic through the interaction of the following three different variables:

S="number of people that are susceptible to Ebola"
I="number of people infected with Ebola"
R="number of people recovered from Ebola with total immunity"

It is logical to assume that a fixed population of N people, whereby there are no births and deaths by natural cause, consists of the number of people susceptible plus the number of people infected plus a number of people resistant:

$$N = S + I + R.$$

This is because the population is fixed and therefore, there are only three compartments in which the population may fit into. Thus, the total of the number of people susceptible infected and recovered in equivalent to the total population.

The model includes two parameters which can be used to calibrate it, β and γ where $\beta, \gamma > 0$. Given these parameters, the model uses three differential equations. These will be different numbers for any given disease and situation and will depend on things like method of transmission, and the contact rate.

1.3. Trial equation methods

Trial equation method was introduced by LIU Cheng-Shi for the solution of nonlinear differential equations in the paper [8]. This method depends on a representation of the solution which satisfies a first order constant coefficient differential equation. In [12], the simple trial method is defined as

$$u' = F(u) = \sum_{i=0}^{m} a_i u^i \tag{1}$$