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Solving Nonlinear Systems of First Order Ordinary Differential Equations Using a Galerkin Finite Element Method

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ABSTRACT A new numerical technique to solve nonlinear systems of initial value problems for nonlinear first-order differential equations (ODEs) that model genetic networks in systems biology is developed. This technique is based on finding local Galerkin approximations on each sub-interval at a given time grid of points using piecewise hat functions. Comparing the numerical solution of the new method for a single nonlinear ODE with an exact solution shows that this method gives accurate solutions with relative error 1.8×10^{-17} for a time step 1×10^{-5} . This new method is compared with the adaptive Runge-Kutta (ARK) method for solving systems of ODEs, and the results are compared for a time step 2×10^{-6} . It is shown that the relative error of the Galerkin method decreases approximately linearly with the log of the number of hat functions used. Unlike the ARK method, this new method has the potential to be parallelizable and to be useful for solving biological problems involving large genetic networks. An NSF commissioned video illustrating how systems biology helps us understand that a fundamental process in cells is included.

INDEX TERMS Biological clock, Galerkin method, finite element method, hat function, Newton-Raphson method, ordinary differential equations, toggle switch, systems biology.

1. INTRODUCTION

In the new cross-disciplinary field of systems biology merging genetics, bioinformatics and engineering the focus is on using networks of genes and their products to predict fundamental processes in the cell [1]. The field began in the 1990s with the assembly of biochemical pathways to describe the functioning of some cells [2-4]. The field was transformed with the development of new genomic technologies [1], [5], [6] to measure how many genes and proteins behave simultaneously in cells. We are now poised to describe the cellular dynamics of an entire cellular network [7], [8]. The challenge is to be able to simulate such large networks. The dynamics of these cellular networks are often described by very large systems of ordinary differential equations [9]. One of the major problems in systems biology is solving large systems of ordinary differential equations describing how genetic networks behave [10], a challenge arising in

other areas of science and engineering as well [11]. The Galerkin method has been employed for solving different kinds of ordinary differential equations [12-19]. Here we show how Galerkin's method can be used in conjunction with Finite Element Method (FEM) piecewise hat functions to solve systems of nonlinear first-order ordinary differential equations (ODEs). Here our method is applied to systems of ODEs describing several genetic networks [20], [21]. The importance of these networks over many study lines is summarized in an NSF commissioned video attached [22]. The idea behind the method is to find local Galerkin approximations to the solutions of the ODEs on each sub-interval of a given mesh using a collection of hat functions. In addition to the fact that this method is a new method for solving any nonlinear system of ODEs with high accuracy and stability that is comparable with the ARK method, it has the potential to be parallelizable and to be useful for solving biological problems that depend

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