Scilab solution to genetic network problem

Abstract

Genetic networks can be represented by a system of ordinary differential equations. These representations give the opportunity for researchers to simulate the behaviour of its gene numerically. In this paper, we apply two fourth order methods, namely Adam-Bashforth-Moultan (an implicit method which produce a very high accuracy solution) and fourth order Runge-Kutta (an explicit method which also produce a very high accuracy solution) using a free open source software named Scilab. We use both methods to simulate problem in toggle switch and biological clock of Neurospora Crassa. Finding shows that both methods perform well in simulating toggle switch and biological clock problem. Simplistic approach but outstanding solution (output) gathered via Scilab was the main attractive characteristic for using the software. Choosing Scilab was very relevant and beneficial for solving problem numerically. Usage of the software will reduce organization budget in teaching and learning