



Sandomierz, 5th–9th September 2016

ON A NONSTANDARD FINITE DIFFERENCE SCHEME FOR THE NOWAK-BANGHAM MODEL OF CELLULAR IMMUNE RESPONSE TO VIRAL INFECTION

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ABSTRACT

The main problem in numerical simulation of the mathematical models of biomedical phenomena is to preserve the non-negativity of the solution. Other examples of qualitative simulation errors include spurious equilibria, oscillations, and even blow-ups of the solution. These problems can be avoided by imposing a limit on the step-size of the simulation. Therefore, conventional simulation methods (*e.g.* the 4-th order Runge-Kutta method) are usually combined with an adaptive algorithm that guarantees the step-size to be small enough.

Another approach to dealing with the qualitative errors of simulation are the nonstandard finite difference (NSFD) schemes [2, 3]. These methods assume that the continuous model should be discretized in a way that the obtained difference equations preserve the qualitative properties of the original model independently of the chosen step-size.

We have constructed a nonstandard finite difference scheme for the Nowak-Bangham model of cellular immune response to viral infection [4]. This mathematical model is often used as a basis for more complicated description of virus - immune system dynamics (see *e.g.* [5]). Our numerical approach [1] preserves the essential qualitative features of the original continuous model: (i) the non-negativity and (ii) boundedness of the solution, (iii) equilibria and (iv) their stability conditions. All of these properties are preserved independently of the chosen step-size.

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