The Babesiosis Disease in Bovine and Tick Populations Model and its Global Analysis

Hossein Pourbashash¹, Hossein Kheiri²

¹ Department of Mathematics, University of Garmsar, Garmsar-Iran h.pourbashash@ugsr.ir

² Department of Applied Mathematics, Faculty of Mathematical Sciences, University of Tabriz, Tabriz-Iran h-kheiri@tabrizu.ac.ir

Keywords: Babesiosis disease; local stability; global stability; second compound matrices; Sinc method.

Tick-borne diseases (TBDs) affect 80 of the world's cattle population, hampering livestock production throughout the world. In this article we will consider the Babesiosis disease in bovine and tick populations model [1] . We conduct the local and global stability analysis of the model [2]. We present a dynamic behavior of this model using an efficient computational algorithm, namely the multistage modified sinc method(MMSM). The MMSM is used here as an algorithm for approximating the solutions of proposed system in a sequence of time intervals. In order to show the efficiency of the method, the obtained numerical results are compared with the fourth-order Runge-Kutta method (RKM). It is shown that the MMSM has the advantage of giving an analytical form of the solution within each time interval which is not possible in purely numerical techniques like RKM.

References

- J. Mosqueda, A. Olvera-Ramrez, G. Aguilar-Tipacam and G.J. Cant, *Current Advances in Detection and Treatment of Babesiosis*, Curr Med Chem., **19(10)** (2012) 15041518.
- [2] Wang, L., Li, M.Y., Mathematical analysis of the global dynamics of a model for HIV infection of CD4⁺ T cells, Math. Biosci., 200: 44-57 (2006).