Dynamically consistent numerical methods for solving dynamical systems in Biology

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Numerical algorithms are more and more used to solve continuous dynamical systems in various domains in Biology, like in Epidemiology [3], in Ecology, in Agronomy [1]. Researchers use softwares, like Matlab, in which standard/classical algorithms have been implemented, to run numerical simulations in order to illustrate their research papers. Unfortunately, sometimes, these standard methods failed or do not preserve the qualitative properties of the continuous system [2]. How is it possible to propose an alternative?

The aim of this talk is twofold. First, we present standard deterministic models in Epidemiology, in Ecology, ... for which standard numerical schemes failed. Second, we give some simple and straigtforward advices to construct a so-called dynamically consistent numerical method, that preserves most of the qualititative properties of the related continuous system [2]. We illustrate our approach with various examples.

References

[1] A. Bonneu, Y. Dumont, H. Rey, C. Jourdan, and T. Fourcaud, *Splitting advection, diffusion and reaction processes in a continuous model of root growth*, Proceedings FSPM 2010, UC Davis.

[2] R. Anguelov, Y. Dumont, J.M-S. Lubuma and M. Shillor, *Comparison of some standard and nonstandard numerical methods for the MSEIR epidemiological model*, ICNAAM Conference, AIP 1168, Volume 2 (2009), pp. 1209–1212.

[3] Y. Dumont and F. Chiroleu, Vector Control for the Chikungunya Disease, Mathematical Bioscience and Engineering 7(2) (2010), 315-348.