

NUMERICAL BIFURCATION ANALYSIS OF INFINITE-DELAY EQUATIONS IN BIOLOGY

Francesca Scarabel^{1*}, Mats Gyllenberg¹ and Rossana Vermiglio²

¹University of Helsinki, Finland

²University of Udine, Italy

francesca.scarabel@helsinki.fi (*corresponding author)

In mathematical models for biological systems, delays often enter the model as integrals over the past history. Populations with age or size structure, for instance, can be described with a renewal equation for the population birth rate, possibly coupled with a delay differential equation for the environmental variable. In some cases it is impossible to bound a priori the maximal delay and the mathematical equations contain infinite-delay terms.

The pseudospectral discretization technique can be used to approximate a nonlinear delay equation with a low-dimensional system of ordinary differential equations, whose properties can be studied with existing software [1, 2]. We show how to adapt the technique to treat infinite delays and we explore the effectiveness and flexibility of the method using some numerical examples.

References

- [1] Breda D., Diekmann O., Gyllenberg M., Scarabel F., and Vermiglio R. (2016). *Pseudospectral discretization of nonlinear delay equations: new prospects for numerical bifurcation analysis*, SIAM Journal on applied dynamical systems, 15(1), 1–23.
- [2] Gyllenberg M., Scarabel F., Vermiglio R. *Equations with infinite delay: numerical bifurcation analysis via pseudospectral discretization*, submitted.