MATHEMATICAL BIOLOGY I

Place and time: In M100 on Thursday, Jan 4, at 10:30–12:00
Organizers: Mats Gyllenberg (University of Helsinki)
Eva Kisdi (University of Helsinki)
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Planar S-Systems

Josef Hofbauer *(University of Vienna)*, `josef.hofbauer@univie.ac.at`

Abstract. S-systems are simple examples of power-law dynamical systems (polynomial systems with real exponents). They arise in biochemical systems theory. For planar S-systems, we present results on the global stability of the unique positive equilibrium, construct examples with two limit cycles, and solve the center problem.

This talk is based on the paper: http://arxiv.org/abs/1707.02104

Joint work with B. Boros, S. Müller and G. Regensburger.

A universal classification for discrete-time competitive systems via the carrying simplex

Mats Gyllenberg *(University of Helsinki)*, `mats.gyllenberg@helsinki.fi`

Abstract. We study the permanence and impermanence for discrete-time Kolmogorov systems admitting a carrying simplex. Sufficient conditions to guarantee permanence and impermanence are provided based on the existence of a carrying simplex. Particularly, for low-dimensional systems, permanence and impermanence can be determined by boundary fixed points. For a class of competitive systems whose fixed points are determined by linear equations, there always exists a carrying simplex. We provide a universal classification via the equivalence relation relative to local dynamics of boundary fixed points for the three-dimensional systems by the index formula on the carrying simplex.

The theoretical results are applied to concrete models such as the Leslie-Gower, Atkinson-Allen and Ricker models.

Joint work with J. Jiang, L. Niu, P. Yan.

Numerical bifurcation analysis of nonlinear delay equations for biology

Francesca Scarabel *(University of Helsinki)*,
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Abstract. In mathematical models for biological systems, delays often enter the model as integrals over the past time. 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. No software is capable of studying numerically the bifurcation properties of this kind of nonlinear systems. To address this gap, we propose the pseudospectral discretization technique as a way to approximate a general nonlinear delay equation with a low-dimensional system of ordinary differential equations, whose properties can be studied with existing software. The technique can be applied to systems coupling both renewal and delay differential equations, and involving bounded or unbounded delays [1,2]. Using some numerical examples, we explore the effectiveness and flexibility of the method.

[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.

Joint work with D. Breda, O. Diekmann, M. Gyllenberg and R. Vermiglio.