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Algebraic parametrizations in biochemical reaction networks

It is widespread in biology to model the time evolution of species concentrations in reaction networks with systems of ordinary differential equations. Current models in systems biology employ polynomial dynamical systems and, as a consequence, the steady states of the model are the zeros of a system of polynomial equations. These systems depend often on unknown parameters and, further, only positive solutions have a physical meaning. Therefore, it is of interest to study the positive zeros of a family of polynomials with unknown coefficients. Recent work has highlighted the use of algebraic parameterisations to infer properties on the number of steady states, their stability and how the steady states depend on the unknown parameters.

In the talk I will briefly present the framework of the theory of reaction networks and give an overview of questions that are relevant for systems biology. I will then focus on my recent work on algebraic parameterisations: how to find them and what they can be used for.

The presented results are in collaboration with Carsten Conradi, Janne Kool, Maya Mincheva, Meritxell Sáez, Angélica Torres and Carsten Wiuf.