

Algebra and geometry in the study of enzymatic cascades

Alicia Dickenstein¹

¹ Dto. de Matemática, FCEN, Universidad de Buenos Aires, and IMAS (UBA-CONICET),
so University of Buenos Aires and CONICET, Argentina.

In recent years, techniques from computational and real algebraic geometry have been successfully used to address mathematical challenges in systems biology. The algebraic theory of chemical reaction systems aims to understand their dynamic behavior by taking advantage of the inherent algebraic structure in the kinetic equations, and does not need a priori determination of the parameters, which can be theoretically or practically impossible.

I will give a gentle introduction to general results based on the network structure. In particular, I will describe a general framework for biological systems, called MESSI systems, that describe Modifications of type Enzyme-Substrate or Swap with Intermediates, and include many post-translational modification networks. I will also outline recent methods to address the important question of multi-stationarity, in particular in the study of enzymatic cascades, and will point out some of the mathematical challenges that arise from this application.