Congreso Bienal de la Real Sociedad Matemática Española
Santander, 4 - 8 febrero 2019

Algebraic methods for the study of biochemical reaction networks

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In recent years, techniques from computational and real algebraic geometry have been successfully used to address mathematical challenges in systems biology. (Bio)chemical reaction networks define systems of ordinary differential equations with (in general, unknown) parameters. Under mass-action kinetics, these equations depend polynomially on the concentrations of the chemical species. 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 describe general results based on the network structure. In particular, I will explain 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 multistationarity.