Inference of genomic dynamics

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Abstract

Gene-regulatory systems, signaling pathways and metabolic fluxes are examples in the life-sciences where non-linear dynamics plays an important role. Ignoring single-cell fluctuations, these systems can be described by non-linear systems of differential equations. These models have been very popular in many branches of science due to their flexibility and their ability to describe dynamical systems. Despite the importance of such models in many branches of science they have not been the focus of systematic statistical analysis until recently.

In this talk we describe a variety of ways we can deal with such systems statistically. For large systems, we propose a class of dynamic graphical models, whereas for smaller systems we propose a general approach to estimate the parameters of systems of differential equations measured with noise. Our methodology is based on the maximization of a penalized likelihood where the differential system of equations is used as a penalty. To do so, we use a Reproducing Kernel Hilbert space that allows us to formulate the estimation problem as an unconstrained, easy-to-solve numeric maximization problem. Both methods is tested in real and simulated examples showing its utility in a wide range of scenarios.

Ospite: Clelia Di Serio