Discrete Models for the Simulation and Control of Gene Regulatory Networks

David Murrugarra

University of Kentucky

Abstract: Understanding how the physiology of organisms arises through the dynamic interaction of the molecular constituents of life is an important goal of molecular systems biology, for which mathematical modeling can be very helpful. Different modeling strategies have been used for this purpose. Dynamic mathematical models can be broadly divided into two classes: continuous, such as systems of differential equations and their stochastic variants and discrete, such as Boolean networks and their generalizations. This talk will focus on the discrete modeling approach, which employs techniques from discrete mathematics, combinatorics, graph theory, and computational algebra. Discrete models play an important role in modeling processes that can be viewed as evolving in discrete time, in which state variables have only finitely many possible states.
This talk will present an approach for stochastic simulations of discrete models. This stochastic setting will be used to study optimal control problems to identify a control policy to navigate the system so that the probability of reaching a desirable state is maximized. Our algorithms assume a set of intervention targets represented by control nodes and edges in the wiring diagram and use techniques from Markov decision processes for the identification of a control policy that dictates how to move from one state to another.