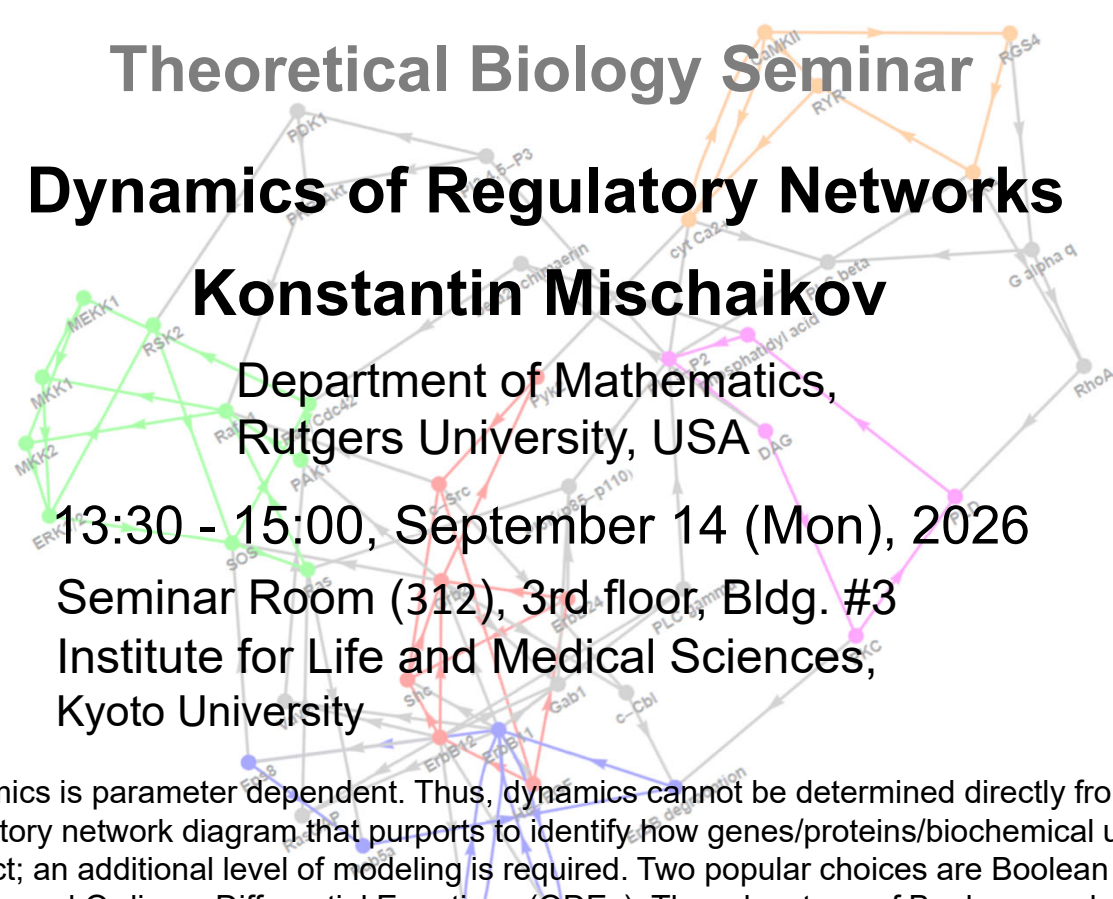




Theoretical Biology Seminar

Dynamics of Regulatory Networks

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13:30 - 15:00, September 14 (Mon), 2026

Seminar Room (312), 3rd floor, Bldg. #3
Institute for Life and Medical Sciences,
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Dynamics is parameter dependent. Thus, dynamics cannot be determined directly from a regulatory network diagram that purports to identify how genes/proteins/biochemical units interact; an additional level of modeling is required. Two popular choices are Boolean models and Ordinary Differential Equations (ODEs). The advantage of Boolean models is that they are easy to compute and reduce the need for parameter identification. The disadvantage is that the resulting dynamics is highly simplified, potentially misleading, and difficult to associate with parameters. The advantage of ODEs is that they provide precision, but at high experimental cost (nonlinearities and parameters need to be identified) and at high computational cost (solving the ODE over multiple initial conditions).

In this talk I will discuss a third approach: Dynamic Signatures Generated by Regulatory Networks (DSGRN). It is based on characterizing dynamics via order theory and algebraic topology. The major points I wish to convey about this novel approach to dynamics are the following:

1. The regulatory network defines a finite combinatorial parameterization of the DSGRN dynamics.
2. DSGRN dynamics is efficiently computable and can be used to readily detect not only dynamics, but also global bifurcations of biological interest.
3. DSGRN dynamics can be identified with dynamics of Ordinary Differential Equations.
4. Boolean dynamics is a subset of DSGRN dynamics and this DSGRN dynamics provides a natural parameterization for the analysis of Boolean networks.
5. DSGRN dynamics can be readily compared against data.

I will provide biological examples.

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