

Boolean modeling of gene networks

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Abstract: Due to the lack of kinetic information of biochemical interactions, it is difficult to study and analyze continuous models of gene networks. The nonlinearity of these interactions makes the problem even less tractable. The Boolean framework (where gene activity is assumed to be either 0=OFF or 1=ON) provides a complementary approach that focuses on qualitative analysis. In this talk, I will show how the Boolean framework is used in modeling biological systems, and how tools from graph theory and combinatorics are well-suited for the analysis of these Boolean models.

This talk will have the format of a tutorial/lecture.