



UNDERSTANDING THE LIMITS OF INFORMATION PROCESSING IN SIGNALING PATHWAYS THROUGH COMBINATION OF MODELING AND EXPERIMENTATION

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Signal transduction in single cells relies on activity of dedicated sets of biochemical reactions, occurring in small and 'noisy' intracellular compartments. Nevertheless, living cells can, under most circumstances, both survive and perform complex decision, through the merger of dynamic signaling information and the more static information contained in their genomes. In this talk, introducing diverse notions and techniques from both computational and experimental analysis domains, I will illustrate how we can, in a systematic and comprehensive fashion, achieve considerable quantitative understanding of the molecular organization, dynamical activation and information processing in signaling networks. Using examples from the signaling involved in the innate immune response and cell survival pathways, we will explore how the use of microfluidic devices, genetic and molecular biology analyses, dynamical systems modeling and information theory, can together improve our understanding of such properties as the importance of feedback interactions, signaling cross-talk and coping with and using noise in signaling processes.