The multi-scale dynamics of signal transduction: dissecting the MAPK pathway

Abstract

Mathematical and biological questions about the MAPK/ERK pathway will be studied through both experimental and mathematical methods. The components of the cascade or their upstream regulators are activated in most human tumors. Thus, the pathway has great biomedical importance, and its components are prime therapeutic targets. Feedback loops and crosstalks with other signaling pathways generate a complex behavior which can only be analyzed with the help of mathematical models. Typically, such models are large systems of differential equations exhibiting multi-scale behavior encompassing different time (or spatial) scales of the regulatory process. The dynamic complexity of regulatory systems is reflected, however, not by the dimension of the system, but rather by the number of feedback loops which is typically much smaller, allowing systematic model reduction into much smaller systems, which exhibit qualitatively the same dynamics. In this project, model reduction and qualitative analysis will rely strongly on novel dynamical systems methods for multi-scale systems. We propose an integrated collaborative approach to study dynamic responses of the MAPK/ERK pathway based on: experiments (targeting the key components of the pathway by knockouts or overexpression), development of mathematical models, simulations, derivation and mathematical analysis of simplified models, and identification of key components and parameters of biological significance.

Scientific disciplines:
101020 - Technical mathematics (34%) | 106023 - Molecular biology (33%) | 106044 - Systems biology (33%)

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Further links about the involved persons and regarding the project you can find at
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