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Identifying the core of biochemical networks: complexity reduction preserving dynamical behavior

Biochemical systems are often very complex. The complexity stems from both the number of components and the intricate interactions that may occur. When a mathematical model is used to describe such a system, its complexity may lead to a very long computing time, non-identification of parameters, and most importantly may hinder us in understanding the underlying mechanism of the biochemical system. Therefore, effective methods are required to capture the key components and interactions of the system.

We present a novel and efficient reduction method to identify the core of a biochemical system. This new method is based on the exploration of the so-called admissible region, that is the set of parameters for which the mathematical model yields the required output. For illustrational purpose, the reduction is first applied to a very small artificial network, consists of just three nodes and three parameters. Our method reveals that there are many parameter sets that give rise to similar dynamical behavior, which indicates, despite its simplicity, the system is not identifiable. Next, the reduction is applied to an epidermal growth factor receptor (EGFR) network model. It turns out only about 62% of the network components are required to yield the correct response to epidermal growth factor (EGF), whereas the rest could be considered redundant. Furthermore, although parameter sensitivity is expected to give an indication to the redundancy of a parameter, we found that a highly sensitive parameter is not always necessarily important, whereas a slightly sensitive parameter is not always removable. This implies that parameter sensitivity on its own is not a reliable tool for model reduction.