Systematic complexity reduction of signaling models and application to a CD95 signaling model for apoptosis

Abstract:
A major problem when designing mathematical models of biochemical processes to analyze and explain experimental data is choosing the correct degree of model complexity. A common approach to solve this problem is top-down: Initially, complete models including all possible reactions are generated; they are then iteratively reduced to a more manageable size. The reactions to be simplified at each step are often chosen manually since exploration of the full search space seems unfeasible. While such a strategy is sufficient to identify a single, clearly structured reduction of the model, it discards additional information such as whether some model features are essential. In this chapter, we introduce alternate set-based strategies to model reduction that can be employed to exhaustively analyze the complete reduction space of a biochemical model instead of only identifying a single valid reduction.