

Comparative study of numerical analyses for validating cell signaling network model

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Systems biology targets biological systems of diverse scales, from molecular scale potentially to a whole body. In order to understand the system comprehensively with quantitative information, computational analysis of mechanistic model is essential. However it is not straightforward because of non-linearity of reactions and uncertainty in parameters such as rate constants, initial conditions, and topology. In addition, experimentally measured data contains errors from various origins. Therefore sophisticated computational tools are required that can handle these features. Here a series of biological questions to be asked about the network are raised and numerical tools are suggested to help answer these questions for the case of TRAIL-induced cell apoptosis. Various parametric sensitivity analyses were applied for the identification of network components and rate constants most critical to the cellular behavior. And the grid search or the random search methods were investigated to get identifiable global optimum solution and to reduce computation time in great extent.