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USING SIMPLIFIED MODELS IN THE STUDY OF INTERACTIONS BETWEEN SIGNALING PATHWAYS

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ABSTRACT

Our knowledge about biological processes is continuously expending as a result of the development of new experimental techniques. However, the cost of biological experiments is very high. This is why dynamic computational models play an increasingly important role in systems biology. Such models are powerful tools that allows to develop and test several hypotheses about complex biological systems *in silico*, which leads to costs reduction of experiments. In the literature there is a growing number of a high dimensional models with a large number of parameters. Such models allow to map complex biological systems more precisely, however, requires more computational effort and are hard to parametrize due to limited methods for measuring biochemical parameters. Very often so accurate models are not necessary, especially when the ultimate goal of the study focuses on one variable and not on the whole model. In this case simplified models, which contain only components responsible for the key dynamical features of the system, may be useful.

We present an example of using a simplified model to create a model combining two signaling pathways: HSF and NFκB. The ultimate goal of the study is to develop a model reflecting the transcription factor NFκB reduction through heat shock pre-treatment. Since both models are very complex and the precise mechanism of the NFκB suppression has not been discovered yet, combining these two models and re-fitting all parameters is a huge challenge. Here we show that this is not necessary, because by using much simpler model we are able to obtain comparable results. Although the model does not explain the interaction between these two signaling pathways, it indicates the points where these interactions can occur, which is the basis for the further development of the model.

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