

Simplification of a complex signal transduction model by the application of invariants and flow equivalent server

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Abstract: The use of qualitative and quantitative analysis is necessary to check the consistency and correctness of a biological models. Indeed, a possible methodology to analyze a large biological models can be summarized in four steps: i) readability, ii) executability, iii) validation techniques and iv) analysis techniques. In our opinion, between the exploration of executability of the model and the validation of the model's integrity it is necessary to apply a simplification step.

Here, we report our experience on modeling signal transduction pathways for the angiogenic phenomena where we devised a complexity reduction methodology applied to the detailed representation of the dynamics of the system. We model this phenomena using Petri Nets (PNs).

The quantitative validation is performed by translating the PN models into the corresponding sets of first order Ordinary Differential Equations (ODE). Obviously, the specifications of the reduced model depends on the characteristics of the original one. To perform this transformation, we apply the concept of flow equivalent server, investigating the conditions which ensure that the behavior of the simplified net is similar to that of the detailed one.

Our work must be considered as a preliminary step in the study of the model's reliability with respect to a parameter space. Our reduction methodology is a promising approach in the direction of attacking a problem that is crucial in systems biology.

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