Generating the Logicome of a Biological Network

Charmi Panchal[1,2,3], Sepinoud Azimi[1,2,3], and Ion Petre[1,2,3]
{*cpanchal*, *sazimi*, *ipetre*}@abo.fi

[1] Computational Biomodeling Laboratory
[2] Turku Centre for Computer Science
[3] Department of Information Technologies, Åbo Akademi University
Agora, Domkyrkotorget 3, FIN-20500 Åbo

Abstract. There has been much progress in recent years towards building larger and larger computational models for biochemical networks, driven by advances both in high throughput data techniques, and in computational modeling and simulation. Such models are often given as unstructured lists of species and interactions between them, making it very difficult to understand the *logicome* of the network, i.e. the logical connections describing the activation of its key nodes. The problem we are addressing here is to predict whether these key nodes will get activated at any point during a fixed time interval (even transiently), depending on their initial activation status. We solve the problem in terms of a Boolean network over the key nodes, that we call the logicome of the biochemical network. The main advantage of the logicome is that it allows the modeler to focus on a well-chosen small set of key nodes, while abstracting away from the rest of the model, seen as biochemical implementation details of the model. We validate our results by showing that the interpretation of the obtained logicome is in line with literature-based knowledge of the EGFR signalling pathway.

Keywords: Biomodeling, Boolean network, Logicome, EGFR pathway, ODE models