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SÉMINAIRE

Uncovering operational interactions in genetic networks: application to an apoptosis network

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Biological networks of large dimensions, with their diagram of interactions, are often well represented by a Boolean model with a family of logical rules. An advantage of Boolean and discrete modelling is the possibility of fully characterizing all qualitative dynamical trajectories of a particular network, based simply on the structure of links and interactions between nodes. A biological network may have different qualitative behaviours in response to different conditions. For instance, in response to different inputs, the system may have a single steady state, or multiple steady states, or exhibit oscillatory behaviour. In this context, using the asynchronous transition graph of the Boolean network, we have developed a method for identifying the groups of active or operational interactions that are responsible for a given dynamic behaviour. As an example, a model of an apoptosis network will be analysed. Two core groups of elements and interactions are identified: they correspond to two different mechanisms that may be used by the cell for the decision between apoptosis or cell survival.