

Analysis of large-scale biological networks with constraint based approaches

Carito Guziolowski

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To this date many approaches exist that model regulatory networks in order to elucidate the dynamics of the system. Most of them focus mainly on small-scale regulatory models. I will present Bioquali, which is a discrete modeling approach to model qualitative large-scale regulatory networks. We test the coherency between the network topology and gene expression data, by using a general interaction logical causal rule. The outputs of our approach are to measure the consistency of our data, diagnose inconsistent regions of the network with respect to the experimental data, and infer the qualitative variation of new network molecules. Our method reasons over the whole network of interactions using efficient algorithms based either on dependency graphs or answer set programming. We proposed programs and bioinformatic tools that, based on these efficient implementations, automatize this reasoning. We validated this approach using the transcriptional networks of *E. coli* and *S. cerevisiae*, and the signaling network of the EWS-FLI1 human oncogene. Currently we want to use it to analyze the Hepatocyte Growth Factor (HGF) signaling events that have an effect over differentially expressed genes upon HGF stimulation.