

- ▶ JÖRG ACKERMANN, INA KOCH, *Network Decomposition in Biology - Computational Challenges*.

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Nature forms complex and huge biochemical systems which can be considered at different levels of abstraction. The abstraction level depends on the experimental methods and on the context of scientific interest. Until now, however, only small biochemical networks or medium-sized networks can be handled computationally. Hence, model reduction by model decomposition becomes more and more important in bioinformatics and systems biology. In this paper, we discuss the task to analyze large systems and describe existing approaches for steady-state network decomposition based on bipartite graphs. Since there exists several methods implemented by biologists as well as by computer scientists, we give an overview about the most important methods and compare several implementations of this NP-hard problem. The results show that we cannot predict which algorithm is best one for a network. We conclude and refer shortly to additional reduction techniques as MCT-sets and t-clusters.