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MOLECULAR SYSTEMS BIOLOGY AND MANAGEMENT OF COMPLEX DATA SETS

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Theoretically, high throughput technologies that have become available in molecular biology and are continuously refined to generate even more reliable datasets permit more and more insights into ongoing dynamic events that may result in improvements of biological systems or the development of diseases. The more comprehensive datasets are the more they reflect the status of a molecular system. If they are obtained at various time points, they encompass its development. In practice, however, their biological interpretation remains a challenge. Presently, we do not have the tools required to decode the full biological message encrypted in e.g. expression profiling, genome-wide DNA-methylation patterns or in the so-called "histone code". Consequently, strategies are aimed at picking molecular subnetworks that we are familiar with from previous work. Alternatively, unbiased approaches use as many data as possible for insertion into mathematical programs to perform time-dependent computer simulations of increasingly larger networks. Although this strategy appears to be straightforward and very attractive, its mandatory extension to large molecular networks presently reveals a lack of efficient mathematical tools and computational power. Advantages and shortcomings of available algorithms will be discussed.