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| Modeling large-scale metabolic networks | |
| <p>A major goal of systems biology is to relate genome sequence to cellular behaviour. It has recently become possible to reconstruct cell-scale metabolic networks of microbes using available genomic, biochemical and physiological data. These reconstructions are not only databases of the metabolism of a certain organism, but they can also be used to predict quantitative phenotypic effects, e.g. those of gene knockouts and gene additions. One way to do this is to convert the metabolic network reconstruction into a model which contains all known reactions of an organism in a mathematically computable fashion. We present a basic overview of the computational tools to simulate large-scale metabolic networks along with some applications in basic and applied research.</p> | |