Abstract:
During the last 10 years, systems biology has matured from a fuzzy concept combining omics, mathematical modeling and computers into a scientific field on its own right. In spite of its incredible potential, the multilevel complexity of its objects of study makes it very difficult to establish a reliable connection between data and models. The great number of degrees of freedom often results in situations, where many different models can explain/fit all available datasets. This has resulted in a shift of paradigm from the initially dominant, maybe naive, idea of inferring the system out of a number of datasets to the application of different techniques that reduce the degrees of freedom before any data set is analyzed. There is a wide variety of techniques available, each of them can contribute a piece of the puzzle and include different kinds of experimental information. But the challenge that remains is their meaningful integration. Here we show some theoretical results that enable some of the main modeling approaches to be applied sequentially in a complementary manner, and how this workflow can benefit from evolutionary reasoning to keep the complexity of the problem in check. As a proof of concept, we show how the synergies between these modeling techniques can provide insight into
some well studied problems: Ammonia assimilation in bacteria and an unbranched linear pathway with end-product inhibition.

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