

Evolutionary models have been made for protein interaction networks and for metabolic pathways. Such models have the advantage that a homologous set of networks can then be analyzed, which is a typical situation as information are often gathered in multiple species. Since metabolism and genes interact, it is fruitful to model these in together and such models have recently been published (Shlomi et al., 2007; Yeang and Vingron, 2006). In a single organism this allows the analysis of data including both metabolic flux and expression levels, such as knockout experiements. Making evolutionary models for integrated networks would have the advantages that analysis from multiple species can now be performed and if information was obtained in one organism, such models would provide a natural framework for how to transfer this knowledge to a target specie.