A kinetic model of thiamine biosynthesis in Escherichia coli

Thiamine can only be synthesized by prokaryotes and some eukaryotes, humans for example get it through their diet. Yet, it is key for the correct functioning of the carbohydrate and amino acid metabolism, and thiamine deficiency in humans can cause beriberi, which can result in muscle weakness or cardiovascular problems, among other symptoms. Nowadays it is common to add thiamine to commercial foods. Thus, it is important to produce it in a sustainable and efficient way. One approach to produce thiamine in a sustainable way is to use cell factories, and modeling of the metabolic network can be used to develop strategies for improved process efficiency. Constraint-based modeling methods have been successfully used to increase cell factory productivity. However, these approaches assume that the system is in a steady state, i.e., metabolite concentrations and reaction fluxes are constant along time. Therefore, kinetic models are needed to understand the dynamics of metabolite concentrations and reaction fluxes. We have built a kinetic model for the thiamine biosynthesis pathway in Escherichia coli. So far we have used convenience kinetics rate laws to describe the flux rates, but once more data has been collected, we will build enzyme modules where each elementary reaction step is explicitly modeled. This model will be used to understand the pathway dynamics and ultimately suggest genetic manipulation strategies to optimize thiamine production in *E. coli*.

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