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Comparing optimal central carbon metabolic pathway of *S. cerevisiae* with and without feedback inhibition through a constraint based modeling approach

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Abstract

Metabolic pathways are efficient in a way that they produce maximal amount of biomass to maintain a homeostasis. To regulate the production of a substrate, the metabolic pathway incorporates feedback inhibition of the enzymes. Recently, we have modeled product feedback inhibition of the enzymes under flux balance analysis and found out the optimal pathways under with and without feedback inhibition conditions [De et al., 2012]. Here, we have hypothesized that the concentration of the product inhibited enzymes would be lower when they are not required by the cell system. We have constructed the central carbon metabolic pathway of *S. cerevisiae* to demonstrate the effectiveness of the proposed methodology. After implementation of the method, we have found the lower concentration of the regulatory enzymes as hypothesized. We have validated some of the results through available experimental evidences. My oral presentation will be based on this model and the results. We now describe the method and the results in brief.