

Integration of Microarray Data into a Genome-Scale Metabolic Model to Study Flux Distribution after Gene Knockout

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Abstract : Prediction of perturbations after genetic manipulation (especially gene knockout) is one of the important challenges in systems biology. In this paper, a new algorithm is introduced that integrates microarray data into the metabolic model. The algorithm was used to study the change in the cell phenotype after knockout of Gss gene in Escherichia coli BW25113. Algorithm implementation indicated that gene deletion resulted in more activation of the metabolic network. Growth yield was more and less regulating gene were identified for mutant in comparison with the wild-type strain.

Keywords : metabolic network, gene knockout, flux balance analysis, microarray data, integration

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