World Academy of Science, Engineering and Technology
International Journal of Biotechnology and Bioengineering
Vol:8, No:11, 2014

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

Authors : Mona Heydari, Ehsan Motamedian, Seyed Abbas Shojaosadati

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
Conference Title : ICSBB 2014 : International Conference on Systems Biology and Bioengineering
Conference Location : Istanbul, Türkiye
Conference Dates : November 28-29, 2014