Title:	EXPLORING ALTERNATE METABOLIC PATHWAYS IN SINGLE GENE DELETION STRAIN OF ESCHERICHIA COLI USING FLUX BALANCE ANALYSIS
Authors:	Mridul (/jspui/browse?type=author&value=Mridul)
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Abstract:	Microorganisms exhibit diverse metabolic capability and show physiological adaptation to genotype/environment perturbations. Metabolic robustness is attributed mostly to complex interplay and dynamic interactions among metabolic network components. In the event of disruption of metabolic gene function, it has been shown that fluxes are routed through alternate pathways to maintain constant flow of metabolites in order to sustain cellular growth. To understand resilient nature of Escherichia coli metabolic networks, the study of flux rerouting in single gene deletion strains can be studied using constraint based methods such as Flux Balance Analysis (FBA), which facilitates computation of in silico fluxes. Due to limitation of experimental growth rate in continuous culture condition for every single gene deletion strain, in the present study, we explore the possibility of using experimental large-scale single gene deletion in E. coli (fitness score data of generated from growth on solid media) to understand metabolic flux distribution in genetic perturbation. In the present study, we have used fitness scores of single deletion strains only on fermentable carbon sources viz. glucose, maltose, glucosamine, and N-acetyl glucosamine and used FBA with biomass function optimization to analyze flow of fluxes in alternate pathways.
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