Metabolic flux analysis for antibiotics production in Streptomyces and its application to DNA microarray

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Flux analysis, determination of intracellular fluxes from the measurement of extracellular rates, has been used successfully on several biological systems. Prediction of complex metabolic fluxes through solving stoichiometric matrix using the mathematica 5.5 program was successfully accomplished. Here, inverse flux analysis for increased antibiotic production which allows the prediction of the flux distribution as a function of internal fluxes is presented. Mainly the regulation of central metabolic pathway and CoA metabolism is concerned in this kinetic simulation because acetyl CoA, malonyl CoA, and propionyl CoA are known to be very important precursors for the antibiotics production. The result of this inverse flux analysis was applied to comparing the DNA microarray result.