P005 Metabolic Flux Quantification and Evaluation for Metabolic Network Analysis

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Metabolic fluxes have been regarded as an important quantity as they reveal cause-effect relationships between genetic modifications and resulting changes in metabolic activity. The use of 13C labelling experiments has proven to be useful for metabolic flux analysis which provides the quantitative framework for determining fluxes through the biochemical pathways of a whole network. Combining the use of labelled substrates with metabolite balancing, we present computational intelligence and classical optimisation approaches to the estimation of metabolic fluxes. In particular, the effect of measurement noise to estimation equality of the methods is compared via simulation of the cyclic pentose phosphate pathway under different noise environments and identifiability conditions.