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Analysis of Feedback in GAL Signalling Cascade

The GAL network cascade in yeast (*Saccharomyces cerevisiae*) contains dynamic molecular interactions. The complex interplay of galactose, Gal3p, Gal80p and Gal4p regulate the transcriptional activity of enzymes in galactose utilization. Mathematical models have been proposed to understand such biological signalling processes. Further studies suggested that the models exhibit bistability/multistability due to the systems' positive feedback loop, ultrasensitivity, etc. In this study, an ODE model in which the feedback possesses a sigmoidal characteristic is used. We are interested to investigate how robustly positive feedback loop gives rise to bistability depending on whether it is mediated by stoichiometric complexes of signalling proteins, enzymes, or transporter molecules. In particular, we will examine how feedback in GAL signalling pathway can be used to apprehend the enhancement of cellular memory.

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