

Predicting bistable gene expression through input-output transfer functions

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In this work we explored the idea of using measurements of gene expression input-output relations to predict steady-state properties, especially bistability, of the galactose uptake network in *S. cerevisiae*. This genetic system is composed by a handful of components and traditional approaches that attempted to understand its steady-state properties have focused on microscopic models that describe the underlying reactions with a certain amount of detail. An alternative approach, based on the theory of monotone systems, consists in considering a related system in which one of the interactions is severed reducing the dynamical complexity of the underlying system but allowing the measurement of a steady-state transfer function between two of its components. In some cases this information is enough to predict the steady-state properties of the original system. As a proof of principle we have explored this idea by engineering open-loop variants of the galactose network in *S. cerevisiae*, measuring the resulting input-output relations and confronting the results with the properties of the corresponding closed-loop system.