

## “Shifting equilibrium in mass-action reaction networks: Example of protein-protein binding”

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We study how the mass action dynamic equilibrium of the reversible model binding networks and the protein-protein-binding network in yeast *Saccharomyces cerevisiae* responds to large changes in abundances of individual proteins. The magnitude of shifts between free and bound concentrations of their immediate and more distant neighbors in the network is influenced by such factors as the network topology, the distribution of protein concentrations among its nodes, and the average binding strength. Our primary conclusion is that, on average, the effects of a perturbation are strongly localized and exponentially decay with the network distance away from the perturbed node, which explains why, despite globally connected topology, individual functional modules in such networks are able to operate fairly independently. We also found that under specific favorable conditions, realized in a significant number of paths in the yeast network, concentration perturbations can selectively propagate over considerable network distances (up to four steps). Such “action-at-a-distance” requires high concentrations of heterodimers along the path as well as low free (unbound) concentration of intermediate proteins.

**MARTES 29 MARZO, 13:00 HORAS**



Sala de Conferencias, Tercer Piso, Departamento de Física  
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