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Mass-action equilibrium and non-specific interactions in protein binding networks[1]

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Large-scale protein binding networks serve as a paradigm of complex properties of living cells. These networks are naturally weighted with edges characterized by binding strength and protein-nodes – by their concentrations. However, the state-of-the-art high-throughput experimental techniques generate just a binary (yes or no) information about individual interactions. As a result, most of the previous research concentrated just on topology of these networks. In a series of recent publications [1-4] my collaborators and I went beyond purely topological studies and calculated the mass-action equilibrium of a genome-wide binding network using experimentally determined protein concentrations, localizations, and reliable binding interactions in baker's yeast. We then studied how this equilibrium responds to large perturbations [1-2] and noise [3] in concentrations of proteins. We demonstrated that the change in the equilibrium concentration of a protein exponentially decays (and sign-alternates) with its network distance away from the perturbed node. This explains why, despite a globally connected topology, individual functional modules in such networks are able to operate fairly independently. In a separate study [4] we quantified the interplay between specific and non-specific binding interactions under crowded conditions inside living cells. We show how the need to limit the waste of resources constrains the number of types and concentrations of proteins that are present at the same time and at the same place in yeast cells.

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[4] J. Zhang, S. Maslov, and E. I. Shakhnovich, Mol Syst Biol 4, 210 (2008).

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