

Dynamical behaviors of complex biological systems determined from structure of networks

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One of the largest problems in modern biology is the huge amount of information of the interaction between biomolecules. It is believed that the dynamics of molecular activities based on such networks are the origin of biological functions. However, the dynamics resulting from, and encoded in, such complex network systems are not understood sufficiently. One of the difficulties is the observation of dynamic processes.

The second problem is the reliability of the network information. The third and largest problem is that the information on the network alone is not sufficient to determine the resulting dynamics. To overcome these problems, we have developed two "structural theories", by which important aspects of the dynamical properties of the system are determined from information on the network structure, only, without assuming other quantitative details. The first theory, named Linkage Logic, determines a subset of molecules in regulatory networks, by which any long-term dynamical behavior of the whole system can be identified/controlled. The second theory, named Structural Sensitivity Analysis, determines the sensitivity responses of the steady state of chemical reaction networks to perturbations of the reaction rate. These achievements provided fundamental theorems, which are not only mathematically important but also practically useful to analyze real biological systems.

Further Reading

1. Mochizuki A. et al. (2013) Dynamics and control at feedback vertex sets. *J. Theor. Biol.* 335, 130-146.
2. Okada T. and Mochizuki A. (2016) Law of Localization in Chemical Reaction Networks. *Phys. Rev. Lett.* 117, 048101.

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