

Classification of physiologic/pathologic phenotypes in cell signaling networks: A mathematical approach

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It is the complex network of interactions between molecules such as proteins in the cell that ultimately leads to the biocomplexity that we observe. Under different parametric conditions, the same cellular network may operate quite differently and gives rise to disparate phenotypes. Given a network, one can construct a mathematical model to explore the dynamical properties constrained by the network, through sampling the parameter space of the model. The classification of qualitatively different dynamics may lead to the mathematical characterization of physiologic/pathologic phenotypes. In this talk, I introduce a different approach. Instead of the brute-force searching for patterns themselves, I focus on the critical conditions of two patterns (i.e., the “boundary” between two different dynamics). Such a critical condition is more degenerate than a regular condition, and is thus mathematically more tractable. This approach has been applied to the AKT signaling pathway, a highly conserved pathway integrating nutrient and mitogenic signals. The phenotypes constrained by the pathway were identified and mapped onto the parameter space, which include cancer and certain metabolic diseases. The analysis illuminates the parameter space and reveals system-level mechanisms in regulating biological functions (cell growth, survival, proliferation and metabolism) and how their deregulation may lead to the development of diseases. The analytical expressions summarize the synergistic interactions among many molecules, which provides valuable insights into therapeutic interventions.

Biography

Guanyu Wang has completed his Ph.Ds from Zhejiang University in 1998 and from University of Cologne in 2005. He completed his postdoctoral studies from University of Texas Health Science Center at Houston, Rice University. He is now an assistant professor of Physics at George Washington University. He has published more than 30 papers in reputed journals and serving as an editorial board member of Journal of Biochemistry and Analytic Biochemistry.