Extending the horizon of chemical physics to cell biology

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Conventionally chemical physics is a field that mainly investigates physical/chemical phenomena at atomic and molecular levels. Noticing the analogy between molecular (especially macromolecular) dynamics and cellular dynamics, in the past few years my lab has focused on introducing and generalizing the techniques and concepts of chemical physics into cell biology studies. Specifically in this talk I will present two projects. Recent breakthroughs of cell phenotype reprogramming not only open a new direction for quantitative understanding of phenotypic transition dynamics, but also impose theoretical challenge on unravelling the complexity of large circuits maintaining cell phenotypes coupled at many different epigenetic and gene regulation levels. A popular picture proposed by Waddington views cell differentiation as a ball sliding down a landscape with valleys corresponding to different cell types separated by ridges. Based on theories of dynamical systems and protein physics we establish a novel "epigenetic state network" framework that captures the global architecture of cell phenotypes, which allows us to translate the metaphorical low dimensional Waddington's epigenetic landscape concept into a simple-yet-predictive rigorous mathematical framework of cell phenotypic transitions. We then apply the approach to the reprogramming process of fibroblasts to induced pluripotent stem cells (iPSC) and cardiomyocytes, reproduced existing experimental observations and made testable predictions. The complex nature of a biological system often imposes challenges seldom encountered in traditional physical science studies: incomplete information, high dimensions, and multiple time scales. Based on an exact mapping

between a nonequilibrium system and a special Hamiltonian system, I derive a Zwanzig-Mori projection formula for systems without detailed balance, which provides a theoretical basis for describing the dynamics of a complex system in reduced dimension. Numerical tests on biological network systems show remarkable agreement between the results obtained with full model simulations and using the generalized Langevin equation for the reduced model system.

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