Diagrammatic representation of steady-state distributions and static responses in evolving populations

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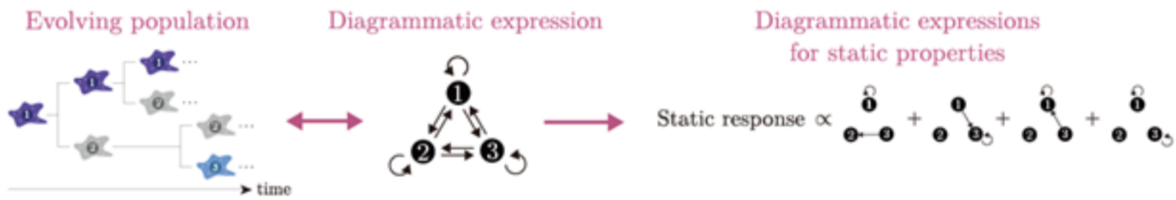
In population dynamics, the adaptability of a population to the environment is a fundamental property. The adaptability of the entire population can be quantified by the mean fitness, while the adaptability of each trait is captured by the steady-state distribution. One of the simplest models for analyzing these quantities is the parallel mutation–reproduction model [1]. This model incorporates the reproduction of each trait and mutations between traits. However, even in this simple setting, it has been difficult to express the mean fitness, the steady-state distribution, and their responses in terms of measurable quantities.

Some techniques in stochastic thermodynamics help overcome this difficulty. In this field, Markov jump processes (MJPs) have been extensively studied as models of systems coupled to heat baths. An MJP is more mathematically tractable than the parallel mutation–reproduction model because it can be viewed as a special case of the latter. Indeed, in stochastic thermodynamics, the static properties of nonequilibrium systems have been analyzed using the Markov chain tree theorem. According to this theorem, the steady-state distribution of an MJP can be expressed in terms of diagrams called spanning trees, each of which corresponds to transitions between states [2]. Thanks to this theorem, the static properties of nonequilibrium systems, such as static responses [3] and the mutual linearity between stationary currents [4], have been clarified.

In this talk, by generalizing the Markov chain tree theorem, we derive explicit representations for the steady-state distribution and the responses of the mean fitness [5]. These quantities are represented by a new class of diagrams named 0/1 loop forests, which are a natural generalization of spanning trees. Each 0/1 loop forest corresponds to the effects of reproduction and mutations, and it is assigned a real value determined by the measurable quantities: mutation rates and reproductive rates. As in stochastic thermodynamics, this diagrammatic representation provides a graph-theoretical approach to population dynamics. For example, it offers a systematic way to approximate static quantities in certain limiting regimes based on the graph structure of the population. Moreover, it enables the design of multi-drug control strategies for harmful populations by exploiting the underlying network structure.



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