Phase transitions in the evolution of gene regulatory networks
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— The role of gene regulatory networks is to respond to environmental conditions and optimize growth of the cell. A typical example is found in bacteria, where metabolic genes are activated in response to nutrient availability, and are subsequently turned off to conserve energy when their specific substrates are depleted. However, in fluctuating environmental conditions, regulatory networks could experience strong evolutionary pressures not only to turn the right genes on and off, but also to respond optimally under a wide spectrum of fluctuation timescales. The outcome of evolution is predicted by the long-term growth rate, which differentiates between optimal strategies. Here we present an analytic computation of the long-term growth rate in randomly fluctuating environments, by using mean-field and higher order expansion in the environmental history. We find that optimal strategies correspond to distinct regions in the phase space of fluctuations, separated by first and second order phase transitions. The statistics of environmental randomness are shown to dictate the possible evolutionary modes, which either change the structure of the regulatory network abruptly, or gradually modify and tune the interactions between its components.

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