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Population Dynamics of Genetic Regulatory Networks

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Unlike common objects in physics, a biological cell processes information. The cell interprets its genome and transforms the genomic information content, through the action of genetic regulatory networks, into proteins which in turn dictate its metabolism, functionality and morphology. Understanding the dynamics of a population of biological cells presents a unique challenge. It requires to link the intracellular dynamics of gene regulation, through the mechanism of cell division, to the level of the population. We present experiments studying adaptive dynamics of populations of genetically homogeneous microorganisms (yeast), grown for long durations under steady conditions. We focus on population dynamics that do not involve random genetic mutations. Our experiments follow the long-term dynamics of the population distributions and allow to quantify the correlations among generations. We focus on three interconnected issues: adaptation of genetically homogeneous populations following environmental changes, selection processes on the population and population variability and expression distributions. We show that while the population exhibits specific short-term responses to environmental inputs, it eventually adapts to a robust steady-state, largely independent of external conditions. Cycles of medium-switch show that the adapted state is imprinted in the population and that this memory is maintained for many generations. To further study population adaptation, we utilize the process of gene recruitment whereby a gene naturally regulated by a specific promoter is placed under a different regulatory system. This naturally occurring process has been recognized as a major driving force in evolution. We have recruited an essential gene to a foreign regulatory network and followed the population long-term dynamics. Rewiring of the regulatory network allows us to expose their complex dynamics and phase space structure.