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Estimation and control of cell populations

Abstract

Feedback mechanisms are at the heart of many cell functions, including genetic regulation. Engineering such mechanisms in living cells synthetically has proved to be a challenging task, however. This is partly due to the difficulties associated with making the process robust against cell-to-cell variability. We discuss how stochastic analysis and control methods can be used to shed light into the uncertainty affecting these systems. We first investigate how modeling and analysis methods can be extended to account for stochasticity not only at the level of individual cells, but also at the level of cell to cell variability. We then use the resulting models for system identification, optimal experiment design for strain characterization, and ultimately regulation of gene expression. We demonstrate the methodological contributions by experimental results on a yeast strain, using a light-sensitive transcription factor as the input and flow cytometry measurements of the resulting fluorescent protein as the output.