Title: Gene expression *Modeling for synthetic biology*

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5) Abstract

In synthetic biology, the design of genetic circuits commonly involves selecting genetic elements such as promoters, Ribosome Binding Sites, and terminators. However, selecting an appropriate combination that ensures the circuit function as designed becomes increasingly challenging as the number of genetic parts grows. This study introduces a novel modeling approach, explaining gene expression through the incorporation of reaction equations for transcription and translation processes. Our model applies quantitative characteristics of genetic parts to these reaction equations and is constructed using a cell-free system to minimize biological uncertainties. Parameter estimation was executed using the Markov Chain Monte Carlo sampling method, followed by simulations via Ordinary Differential Equation solvers to validate the model against real data. We initially estimated unknown parameters with only transcription equations under three distinct conditions. Subsequently, the parameters in translation reactions were inferred using the three variant sets of transcription parameters. The model can be extended to the simulations involving multiple genes and living cells. We expect this modeling approach enables the prediction and evaluation of circuit designs without necessitating experiments, thereby significantly curtailing time and labor in synthetic biology research.

key word : synthetic biology, machine learning, modeling