
Dynamic Models in Biology, Computer Lab:

Noisy transcription

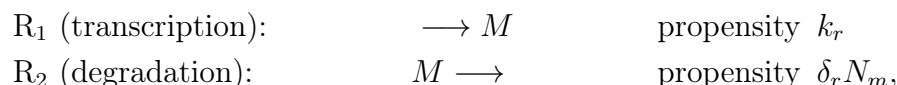
Gene regulatory networks typically involve relatively small numbers of reacting and interacting molecules. Therefore, fluctuations in the number of molecules can become a significant aspect of the dynamics. In this lab, you'll investigate a model of stochastic transcription and degradation of mRNA.

Model

The model simulates the processes of unregulated mRNA (M) transcription and mRNA degradation as



where k_r is the production rate and δ_r the degradation rate constant. The Matlab program `stochastic_transcription.m` uses Gillespie's algorithm to implement a stochastic version of these processes, keeping track of the number of mRNA molecules. The reaction network is:



where N_m is the number of mRNA molecules.

Baseline run

Run `stochastic_transcription.m`. Examine model outputs and compute the mean value of the number of mRNA molecules (disregarding any transients).

Deterministic model comparison

Compare the mean value of mRNA abundance to the mRNA concentration fixed point in the corresponding deterministic system.

Rate variations

Vary the transcription rate parameter k_r . For each value tested, plot the resulting distribution of mRNA abundance and compute its mean value and coefficient of variation. How do these measures vary with changes in k_r ?

How do the same measures vary with changes in δ_r ?

Bursty transcription

Experimental observations have revealed that transcription is sometimes a “bursty” process in which each transcription event leads to the production of multiple copies of mRNA. Modify the model so that it simulates bursty transcription in which each transcription reaction leads to the production of five, not one, mRNA molecules. To allow direct comparison with the original model, reduce the propensity k_r of this bursty transcription reaction by a factor of 5, so that the time-averaged mRNA production rate is unchanged.

How does bursting change the mRNA fluctuations?