Dynamic Models in Biology
Lab 10
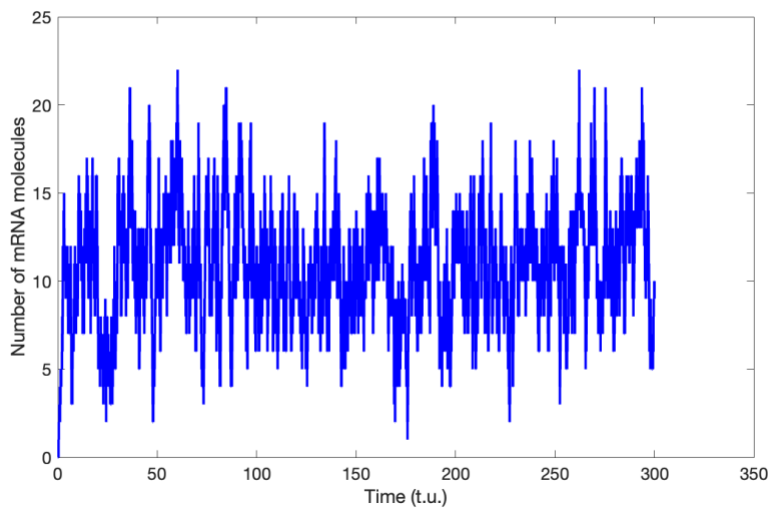Jonathan Levine
Fall 2023
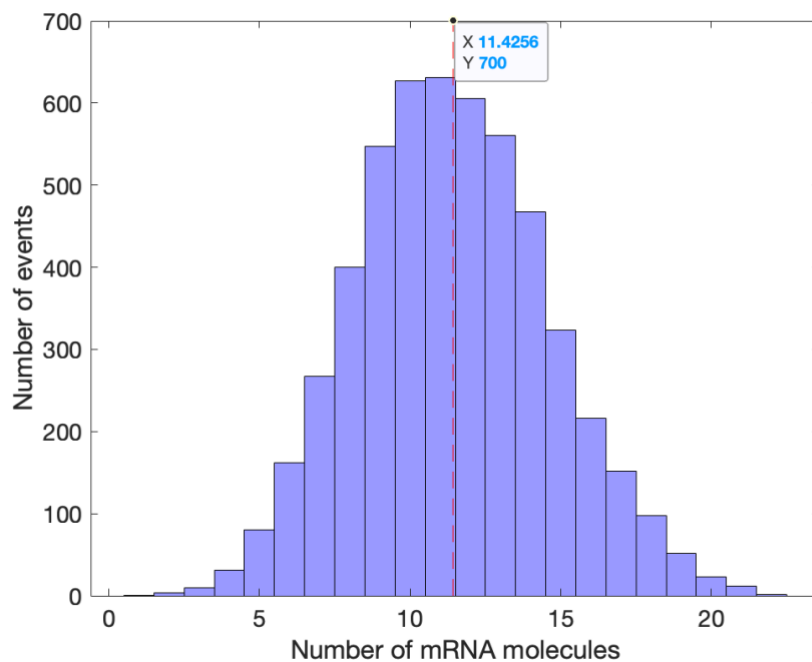
Baseline Run

Running the simulation for the stochastic transcription model at baseline:

The state vector, in this case the one dimensional [M], fluctuates over time

In the non-transient dynamics, the distribution of M is centered around ~11.4:

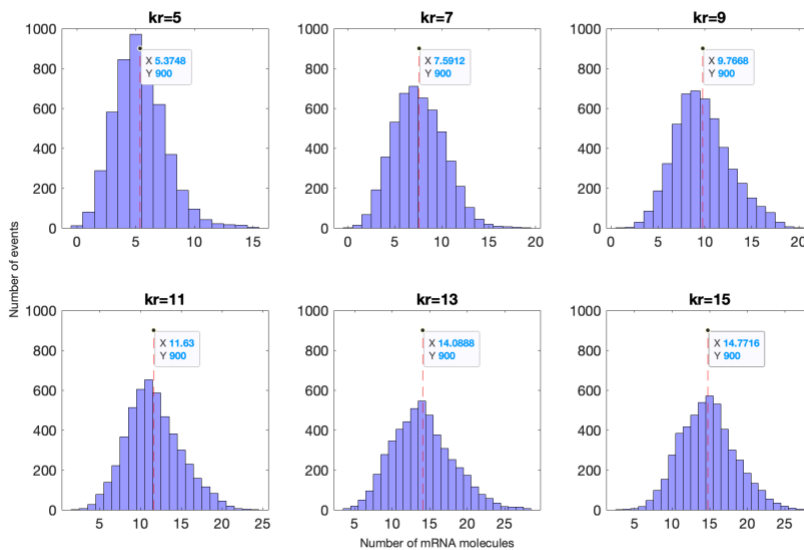The deterministic form of this model is:

$$\dot{M} = k_r - \delta_r M$$

For this model at steady state:

$$\dot{M} = 0 \implies k_r = \delta_r M \implies M^* = \frac{k_r}{\delta_r}$$

For the baseline run, this is equal to 10/1=10, which is close to the mean of the histogram of non-transient M values above.

Varying Reaction Rates

Varying the production rate kr, we see that the mean number of M increases. This is expected since the fixed point is proportional to kr:

Looking at the summary statistics of these distributions as a function of kr, we see that the mean is linearly proportional to kr (as expected from the fixed point), and COV is inversely proportional to kr on a log-log scale.
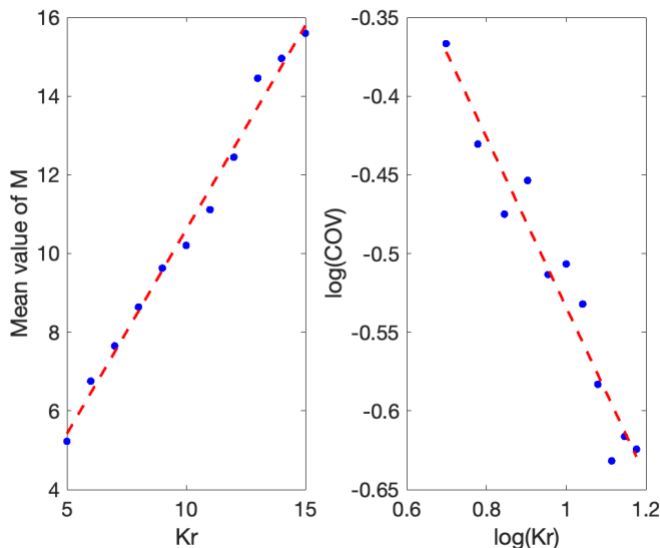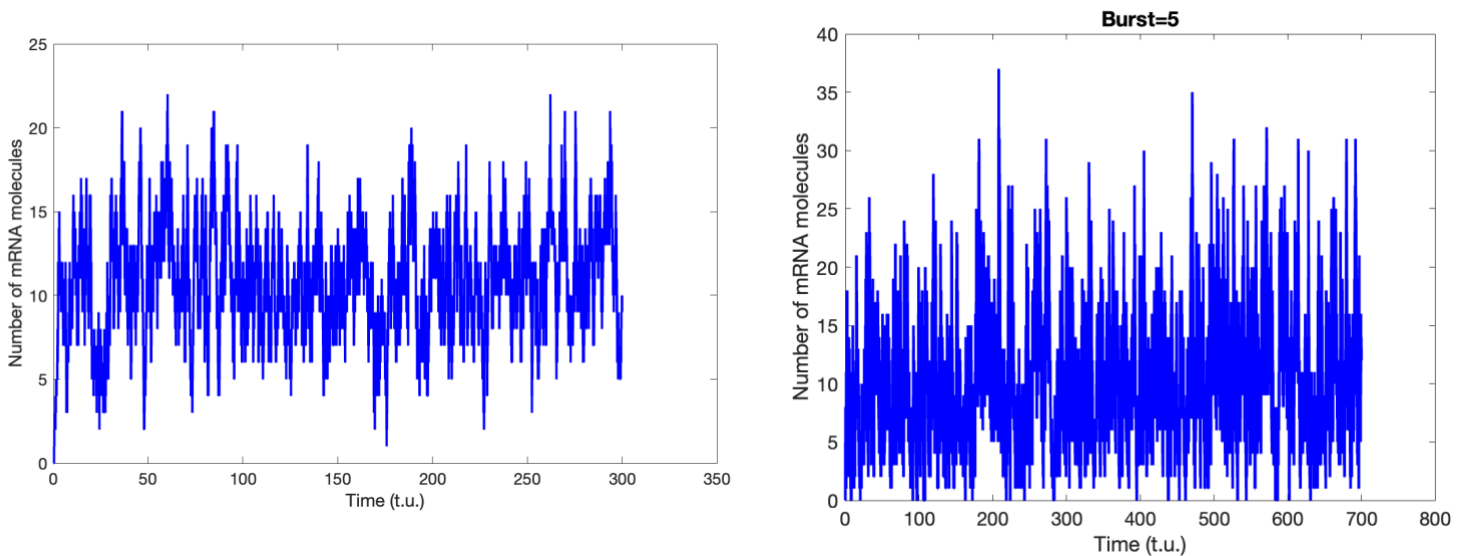
Looking now at the degradation rate instead, we see the same relationships, but this time for 1/dr, since the fixed point of the corresponding deterministic system was inversely proportional to dr:
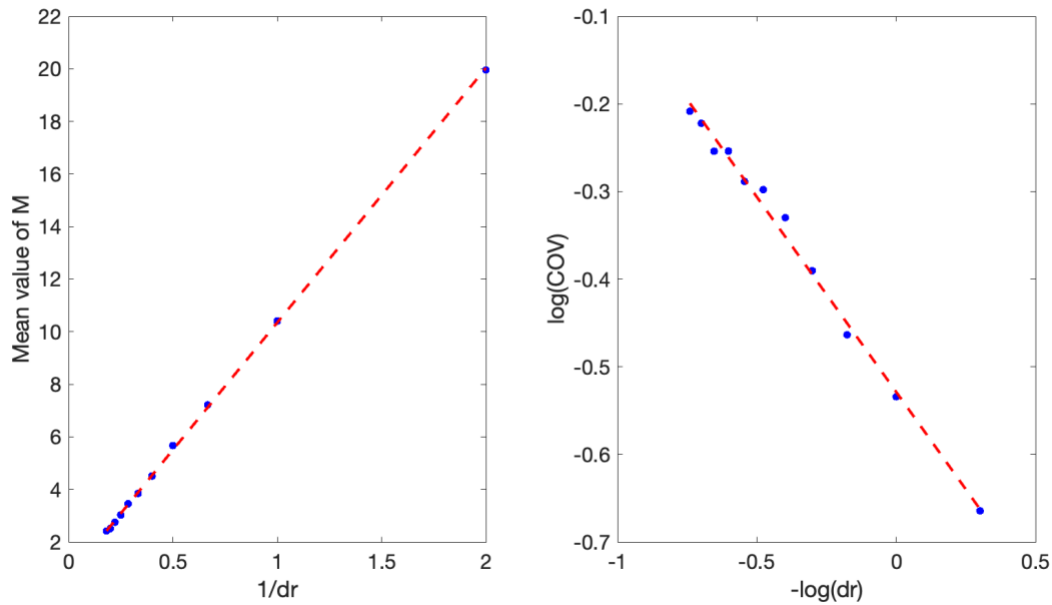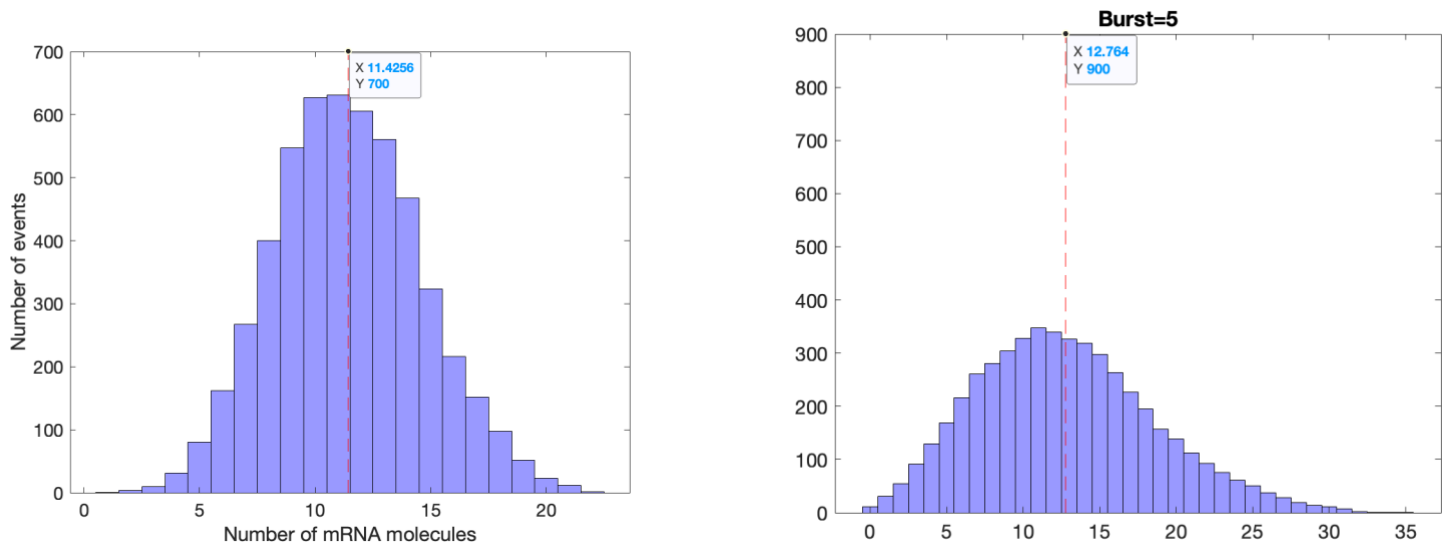

Bursting

If we change the transcription step to a burst of 5 rather than 1 (right), the time trace is much noisier than baseline (left):

This can also be visualized in the histograms (baseline on left, burst=5 on right):

In addition to increasing the noise and slightly increasing the mean, we can also see that the histogram has a long tail in high M, as the large bursts allow for large random effects that build.

This is readily apparent in the frequency domain, where the non-transient time traces show an increase in higher frequency noise as the burst factor increases: