**Simple stochastic simulation of repressilator**

20.020

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In this assignment, you will simulate a stochastic model of the repressillator (i.e. ring oscillator) using Matlab. As a template, please download the following Matlab M-files from the wiki:

stochastic\_sim.m

Calculate\_Sum\_Of\_Avals.m

EQ\_Get\_Next\_States.m

The code in these files simulates a single inverter (i.e. repressor/promoter) with an input mRNA that can be set to a particular level, as we discussed in class. First, make sure you can execute the simulation by running “stochastic\_sim”. At the end of the simulation, Matlab will open up seven figure windows that display the behavior of the seven different molecular species during the simulation. Once you have successfully executed the simulation, you should look over the code to familiarize yourself with it.

For this assignment, you will need to extend the inverter simulation to include three genetic inverters connected in a ring topology based on the repressilator paper by Elowitz, *et al* (*Nature* 2000). Since the repressillator works independently of any external input, you should remove the external control over the mRNA input. You only need to include the repressors in the simulation, and do not need to include GFP. You can also assume that all repressors behave in the same manner (i.e. same kinetics, dimerization, cooperative binding). Please state in the code any additional assumptions that you make.

Run the oscillator simulation 3 times each with a duration that achieves at least 10 distinctive oscillations beyond the initial “setup” time. Graph the oscillations (using the concentration of the dimeric form of one of the repressors). What is the maximum value obtained for each of the runs? How long did each run last?