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Unit 2: Modeling Biochemical Networks with Multiple Components and Stochastic Behavior

Project 2 Report

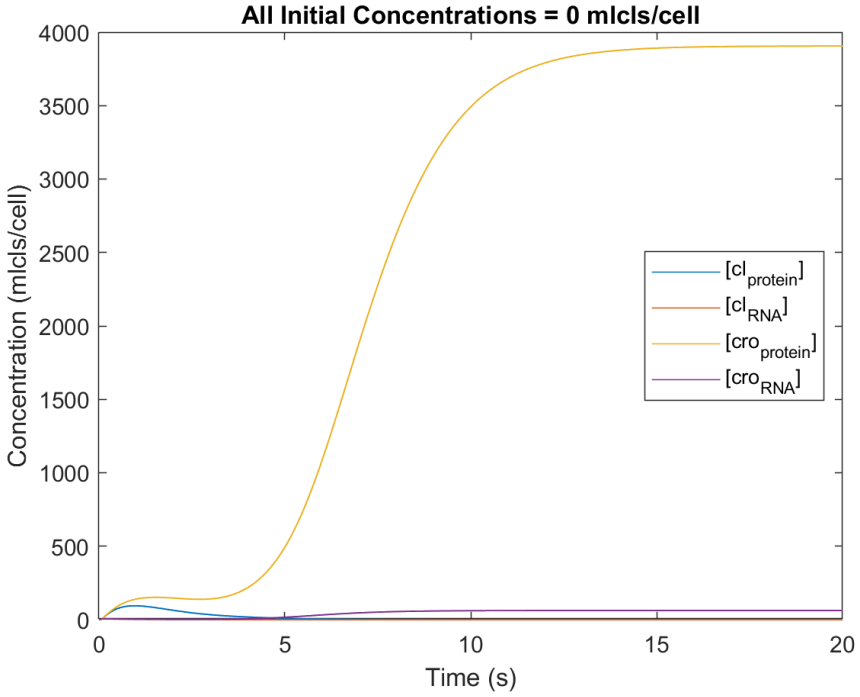
Part A: Deterministic model of the *cro–cI* genetic network

1. Implementing a model of the two transcription factors, cI and cro, involved in the cell-fate decision to enter lysis or lysogeny. In all cases, the constants are as follows:

   $\chi_{cI,rna} = \chi_{cI,prot} = 1.2\ \mathrm{s}^{-1}$ $\chi_{cro,rna} = \chi_{cro,prot} = 0.8\ s^{-1}$,

   $\omega_{cI} = \mu_{cI} = \omega_{cro} = \mu_{cro} = 50\ \mathrm{s}^{-1}$ $K_{cI,1/2} = K_{cro,1/2} = 10\ \frac{\text{molecules}}{\text{cell}} \cdot \mathrm{s}^{-1}$

   (a) Figure A1a: This plot shows a simulation with all initial concentrations set to 0. All four concentrations in molecules per cell were plotted as a function of time in seconds. A simulation length of 20s includes the final steady state of the system.



The degradation rates of cI protein and RNA are greater than those of cro protein and RNA ($1.2\ s^{-1} > 0.8\ s^{-1}$). Figure A1a shows an initial lag period where the cI protein concentration begins to increase, but the difference in degradation rates causes the concentrations of cro protein and RNA to surpass those of cI. Since cro protein represses transcription of cI protein, this in effect causes cI protein and RNA concentrations to fall to nearly zero. The final behavior of this plot shows a very high cro protein concentration that eventually reaches a steady state at about 3900 molecules/cell. The cro RNA concentration also reaches a steady state. In this simulation, the infected bacteria predominantly enter the lytic cycle, due to the abundance of cro protein. This high concentration of cro protein blocks the cells from entering the lysogenic cycle due to its repressive nature.

(b) Figure A1b: This plot shows a simulation starting with 20 molecules/cell of cro_{rna} and all other concentrations set to 0. All four concentrations in molecules per cell were plotted as a function of time in seconds. A simulation length of 20s was chosen to show the final steady state of the system.

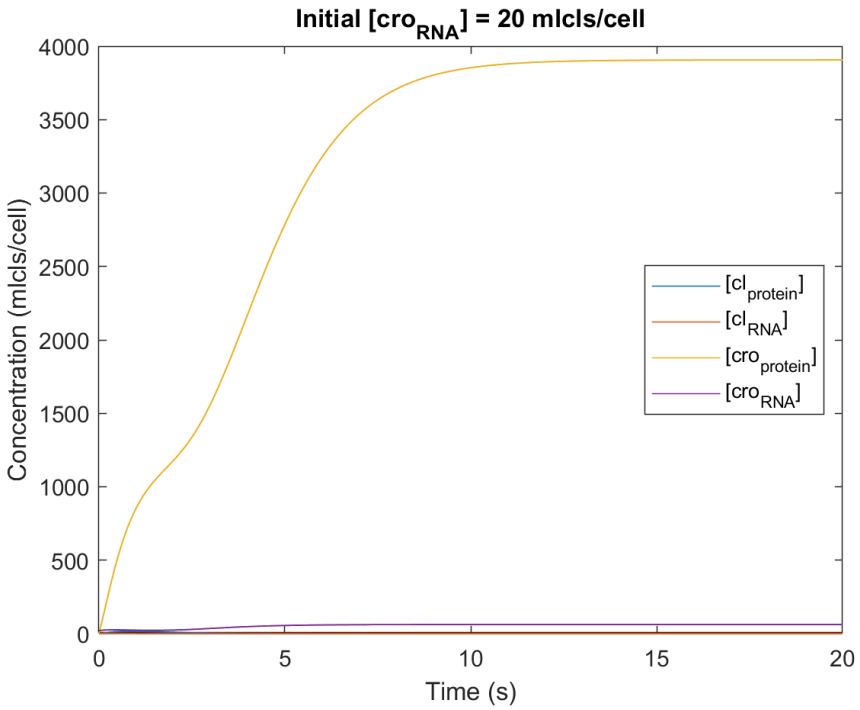


Figure A1b shows similar end behavior as Figure A1a, with a very high cro protein concentration that eventually reaches a steady state at about 3900 molecules/cell. The cro RNA concentration also reaches a steady state. The main distinction between Figures A1a and A1b is that the initial supply of cro RNA producing cro protein omits the initial lag period where cI protein is increasing. cI transcription is inhibited almost immediately as the simulation begins at time 0. Therefore, cI protein and RNA concentrations fall to nearly zero. Along with the lower degradation rates of cro protein and RNA, the initial abundance of cro RNA ensured that cro protein dominated. As in the previous simulation, the infected

bacteria predominantly enter the lytic cycle. The high concentration of cro protein represses lysogeny.

(c) Figure A1c: This plot shows a simulation starting with 50 molecules/cell of cI_{rna} and all other concentrations set to 0. All four concentrations in molecules per cell were plotted as a function of time in seconds. A simulation length of 20s was chosen to show the final steady state of the system.

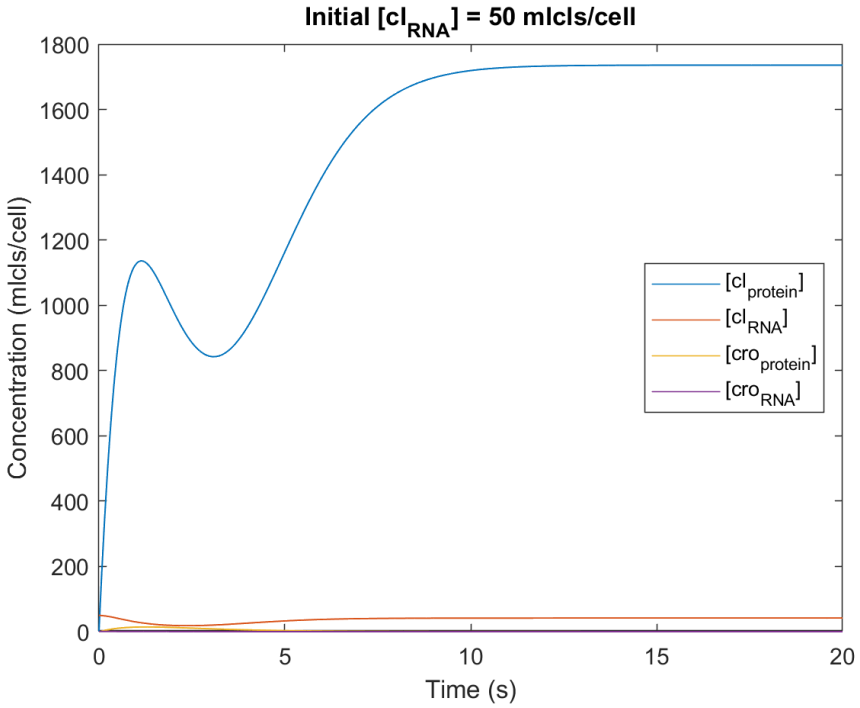
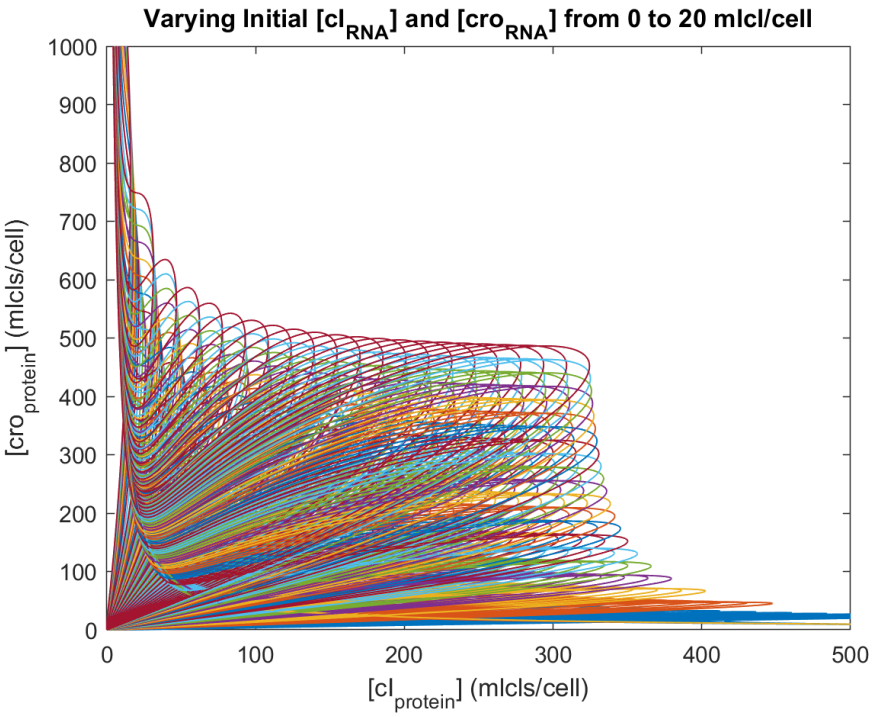


Figure A1c shows a different end behavior than Figures A1a and A1b. There is first a lag phase where the initial abundance of cI RNA produces cI protein that represses transcription of cro protein. The cro protein and RNA concentrations remain at nearly zero, while the cI protein dominates and reaches a steady state concentration at roughly 1750 molecules per cell. The cI RNA concentration also reaches a steady

state. cro transcription is continually inhibited by the high concentration of cI protein. In this simulation, the infected bacteria predominantly enter the lysogenic cycle, due to the abundance of cI protein. This high concentration of cI protein blocks the cells from entering the lytic cycle due to its repressive nature.

2. The simulation from question 1 was repeated with varying initial concentrations of cro and cI RNA. Initial concentrations of both cro and cI proteins were zero in all cases.

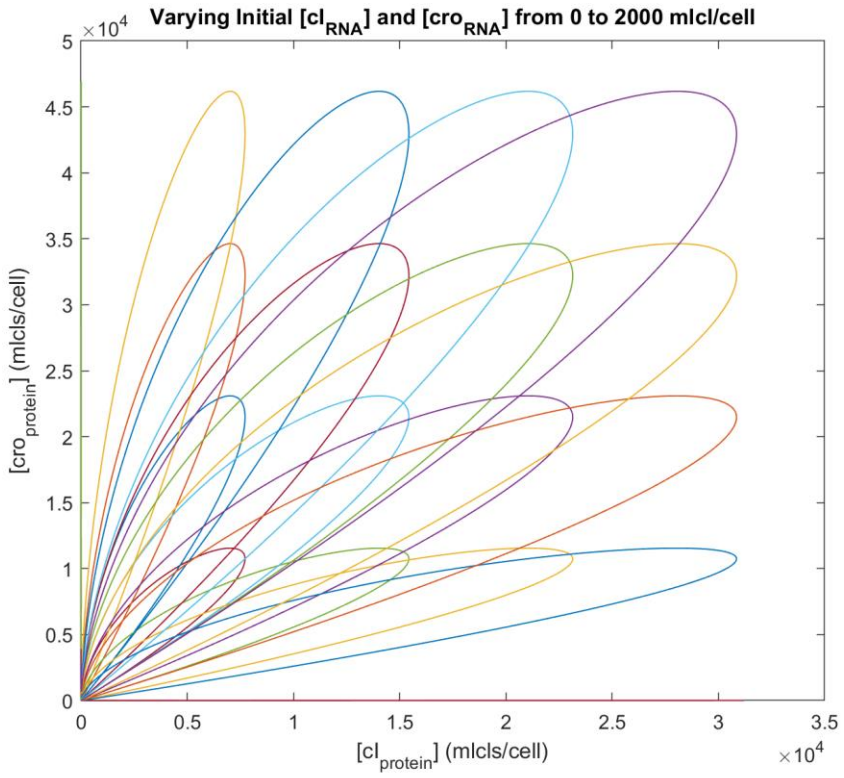
   (a) Figure A2a: The initial concentrations of cI and cro RNA were varied from 0 to 20 molecules per cell, in intervals of 1. The trajectories of all combinations were plotted in a phase plane of cro protein concentration as a function of cI protein concentration.



Since the trajectories of over 400 combinations of initial cro and cI RNA concentrations are plotted in Figure A2a, the individual curves and their associated arrays needed to be consulted in order to understand this plot. As somewhat visible,

all curves begin concentrations of 0 for both proteins. Most of the curves increase in both protein concentrations, then greatly decrease in cI protein concentration and move upward along the y-axis toward a very high steady state cro protein concentration. This shows most simulations result in lysis. A few of the curves increase in cI protein concentration and very slightly in cro protein concentration before moving rightward along the x-axis toward a high steady state cI protein concentration. This shows few simulations result in lysogeny. By analyzing individual concentrations, it is clear that a high initial cI RNA concentration compared to cro RNA concentration is required for cI protein to dominate and lysogeny to occur. For example, an initial [cI_{rna}] of 20 mlcl/cell requires an initial [cro_{rna}] of 2 mlcl/cell in order for cI protein to dominate. If [cro_{rna}] is 3 mlcl/cell in such a case, cro protein will dominate. Similar results exist for other combinations. Even if initial [cro_{rna}] is 0, initial [cI_{rna}] must be at least 6 mlcl/cell in order for cI protein to dominate and lysogeny to occur. It is clearly shown that for an infection to lead to lysogeny in a system with the given constant parameter values, the initial concentration of cI RNA must be very high with respect to the initial concentration of cro RNA. A typical infection has an initial concentration of 0 for all molecules involved, because the phage inserts only its DNA into the bacteria. In this system, a typical infection is expected to result in the cell entering the lytic cycle.

(b) Figure A2b: The initial concentrations of cI and cro RNA were varied from 0 to 2000 molecules per cell, in intervals of 500. The trajectories of all combinations were plotted in a phase plane of cro protein concentration as a function of cI protein concentration.



As in Figure A2a, Figure A2b was analyzed in more depth by looking into individual curves and their associated arrays. Just as in the previous figure, most simulations result in the cell entering lysis because cro protein dominates and approaches a high steady state end concentration. A very high initial cI RNA concentration compared to the initial cro RNA concentration is required for the curve to approach the lysogenic steady state, which is at $[cI_{prot}]$ = 1735.8 mlcl/cell and $[cro_{prot}]$ = 0.1296 mlcl/cell. Only four of the simulations seemed to end up in that state. All four had initial $[cro_{rna}]$ = 0 and initial $[cI_{rna}]$ was 500, 1000, 1500, or 2000

mlcl/cell. All other simulations appeared to result in the cell entering the lytic cycle. The lytic steady state is at [cI_{prot}] = 0.0114 mlcl/cell and [cro_{prot}] = 3906.2 mlcl/cell. Even in the case where initial [cI_{rna}] was 2000 mlcl/cell and initial [cro_{rna}] was 500 mlcl/cell, cro protein dominated. As stated previously, a typical infection where initial concentration is 0 for all molecules is expected to result in the cell entering the lytic cycle.

3. *This question is addressed in all the above discussions next to the appropriate figures.*
4. This model would be changed to describe a bacteria under stress by increasing the degradation rate of cI protein, $\chi_{cI,prot}$. Stressful conditions elevate degradation of the cI protein. As the concentration of the protein decreases, its hold on lysogeny and blockage of lysis are released. A decreased concentration of cI proteins blocking transcription of cro protein allows cro protein to dominate and block cI transcription. The cell then enters the lytic cycle. Starting with the stable lysogenic state (characterized as having a [cI_{prot}] = 1735.8 mlcl/cell, [cro_{prot}] = 0.1296 mlcl/cell, [cI_{rna}] = 41.6597 mlcl/cell, and [cro_{rna}] = 0.0021 mlcl/cell) the degradation constant can be slowly increased until the end behavior of the simulation is not to return to the lysogenic steady state, but to approach the lytic state. It should be noted that the lysogenic and lytic steady states would not be the same as in the original simulation once the cI protein degradation constant has been altered.

Figure A4: This plot shows a simulation starting at the lysogenic steady state. All four concentrations in molecules per cell were plotted as a function of time in seconds. A simulation length of 300s was chosen to show the final steady state of the system.

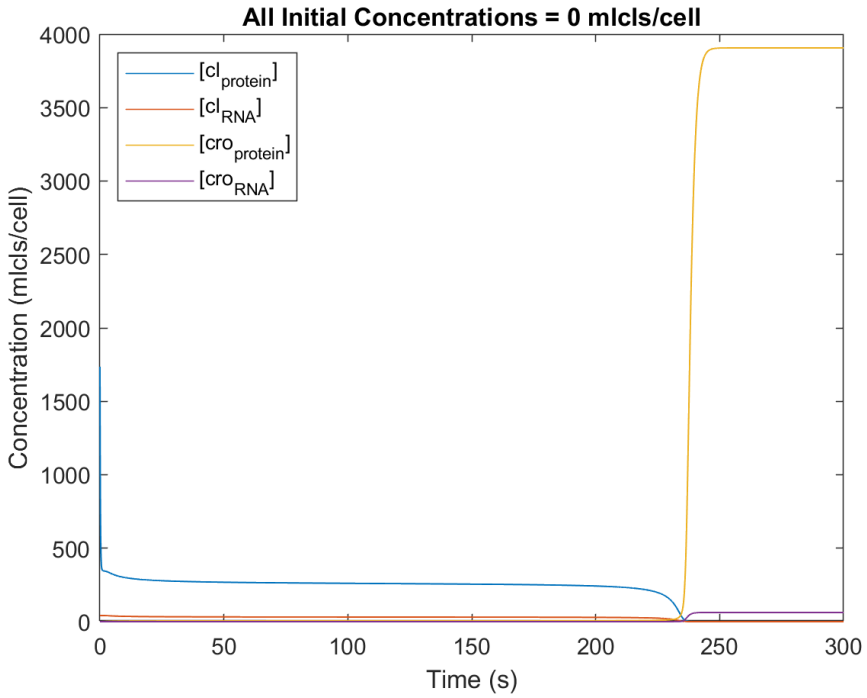
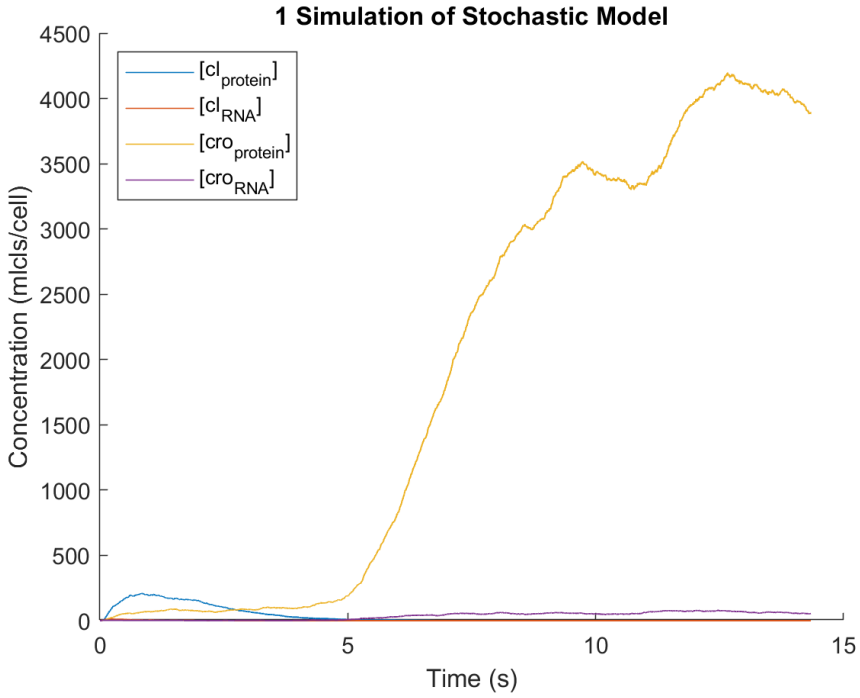


Figure A4 shows the rapid changes in protein concentrations as a result of stress-induced degradation of the lysogenic protein cI. In order to achieve this switch from lysogeny to lysis, the degradation rate of cI was increased to 6.02 mlcl/cell · s^{-1} from the original 1.2 mlcl/cell · s^{-1}. This indicates that the stress-induced aspect of this degradation was 4.82 mlcl/cell · s^{-1} in order to achieve the switch to lysis. As seen in this figure, the cI protein concentration decreases at roughly 230s, in tandem with a dramatic increase in cro protein concentration. As the cro protein concentration increased quickly, the cI protein concentration decreased quickly. This is because the abundance of cro protein very effectively blocked transcription of cI protein, bringing its concentration down to

nearly zero. The system quickly reached the lytic steady state where the cro protein concentration is roughly 3900 mlcl/cell.

Part B: Stochastic model of the *cro–cI* genetic network

1. Figure B1: The stochastic model was implemented using the same constants as for the deterministic model and using Gillespie's algorithm. All initial concentrations were set to zero. The simulation was run for 50,000 steps. All four concentrations in molecules per cell were plotted as a function of time in seconds.



As expected from Figure A1a, a simulation with all initial concentrations starting at 0 mlcl/cell is expected to enter the lytic state. In Figure B1, cro protein dominated and cI protein concentration decreased to nearly zero. The difference between the two figures is that the previous simulation lacks the random components that are characteristic of the

stochastic model used to simulate Figure B1. Rather than approaching a lytic steady state and remaining constant at that value, the end behavior of this plot is more dynamic. This better represents the process in a biological context, because molecules are dynamic. An equilibrium state in biology does not mean that the concentrations of all molecules are constant and unchanging. There are still many fluctuations due to randomness, but the average concentration is constant among various instances of this steady state.

2. Figure B2a: To further show that the average concentration is consistent among multiple simulations of the equilibrium state, this simulation was repeated 20 times. All four concentrations in molecules per cell were plotted as a function of time in seconds.

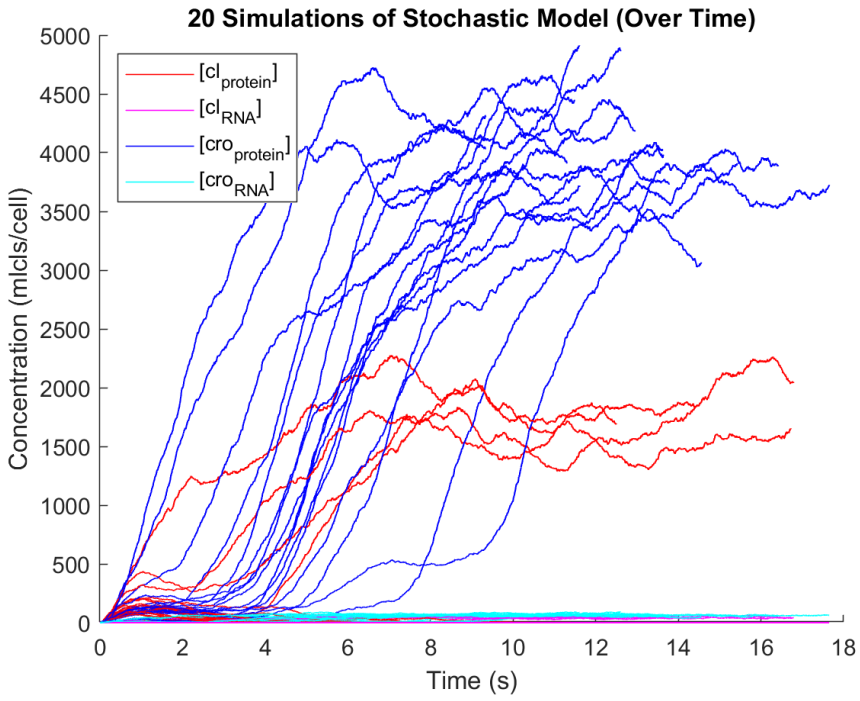


Figure B2a shows the effect of the random components of the stochastic model. In Figure B1, cro protein dominated and the cell entered the lytic cycle. In this figure, it is shown that many of the simulations approach the lytic steady state, but some also approach the

lysogenic steady state. The cro protein dominated in many of the simulations, but the cI protein also dominated in some of the simulations. Among curves that approach a common steady state, there is a lot of variation and random fluctuation. However, it is clear that there is an average concentration that all the curves are generally near.

Figure B2b: The trajectories of all 20 simulations were plotted in a phase plane of cro protein concentration as a function of cI protein concentration.

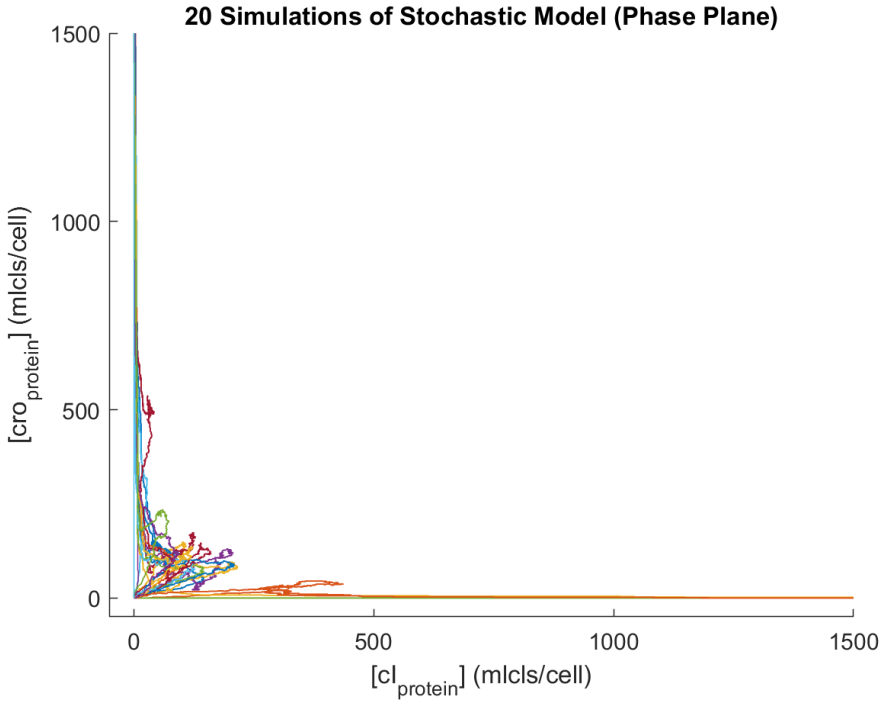


Figure B2b also shows that cro protein dominated in many of the simulations, but the cI protein also dominated in some of the simulations. Simulations that entered lysis ended along the y-axis, with high [cro_{prot}] and low [cI_{prot}]. Simulations that entered lysogeny ended along the x-axis, with low [cro_{prot}] and high [cI_{prot}]. The curves all approach lytic or lysogenic steady states with high concentration of the dominant protein.

3. The simulation was repeated 20 times with starting concentrations of 20 molecules of either cro or cI RNA.

   (a) Initial [cro_{rna}] = 20 mlcl/cell

   Figure B3a: The simulation was repeated 20 times with initially only 20 molecules of cro RNA. All four concentrations in molecules per cell were plotted as a function of time in seconds.

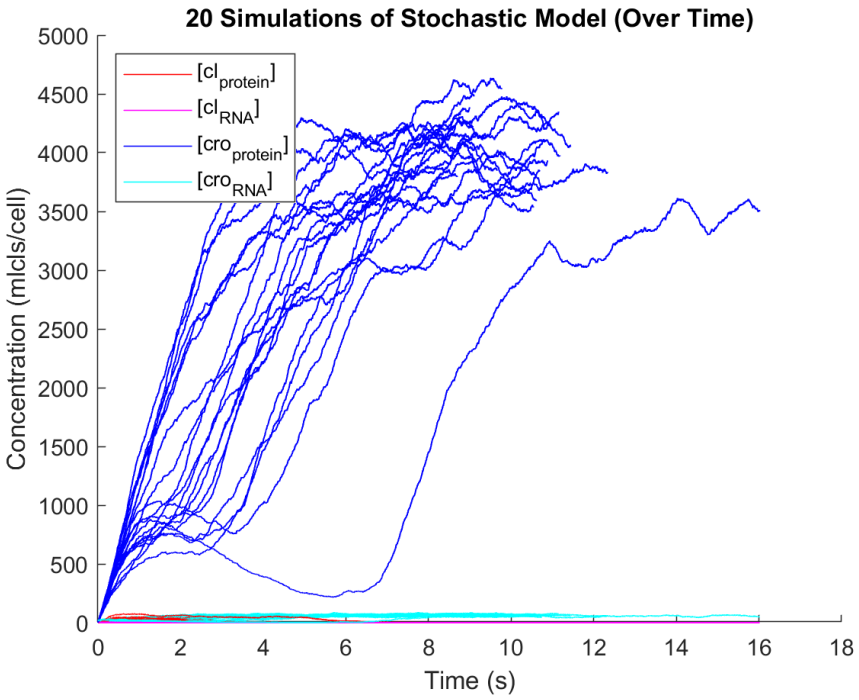


   Figure B3a shows that with an initial abundance of cro RNA, all simulations entered the lytic cycle. Once again, there is a lot of fluctuation between the 20 simulations, but they all generally approach the same average concentration in the end. Due to the stochastic nature of the model, there may be some outliers such as the one curve that exhibits a significant lag period before approaching the lytic steady state.

Figure B3b: The trajectories of all 20 simulations were plotted in a phase plane of cro protein concentration as a function of cI protein concentration.

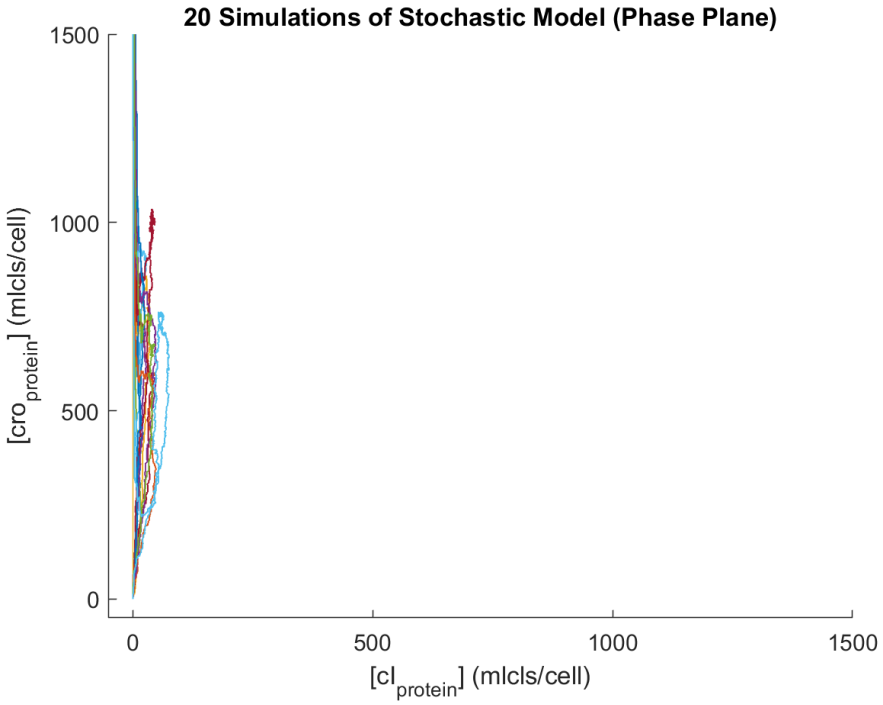


Figure B3b also shows that most simulations will enter the lytic cycle, as shown by all trajectories ending along the y-axis. All simulations end with high [cro_{prot}] and low [cI_{prot}]. All curves approach the lytic steady state characterized by a very high concentration of the dominant cro protein.

(b) Initial [cI_{rna}] = 20 mlcl/cell

Figure B3c: The simulation was repeated 20 times with initially only 20 molecules of cI RNA. All four concentrations in molecules per cell were plotted as a function of time in seconds.

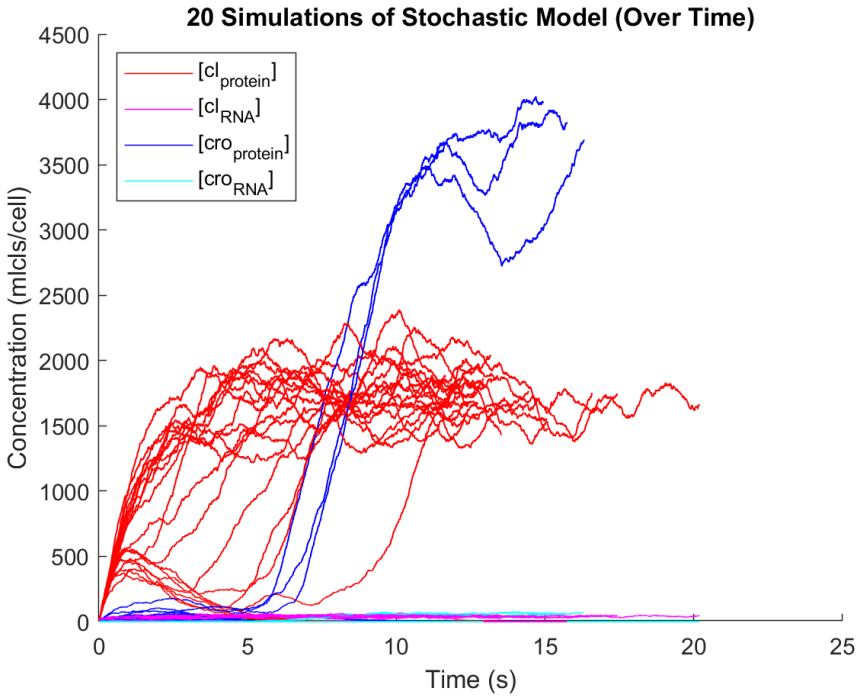


Figure B3c shows that with an initial abundance of cI RNA, most simulations entered the lysogenic cycle. It is clear that a few of the simulations entered the lytic cycle. This is once again due to the stochastic nature of the model. The high degradation rate of cI protein and RNA has been previously observed to make it more difficult for cI protein to dominate over cro protein. This is why none of the simulations in Figure B3a entered lysogeny, but a substantial number of simulations here entered lysis. There is a lot of fluctuation among the simulations that approach a common steady state, but they all generally approach the same average concentration in the end.

Figure B3d: The trajectories of all 20 simulations were plotted in a phase plane of cro protein concentration as a function of cI protein concentration.

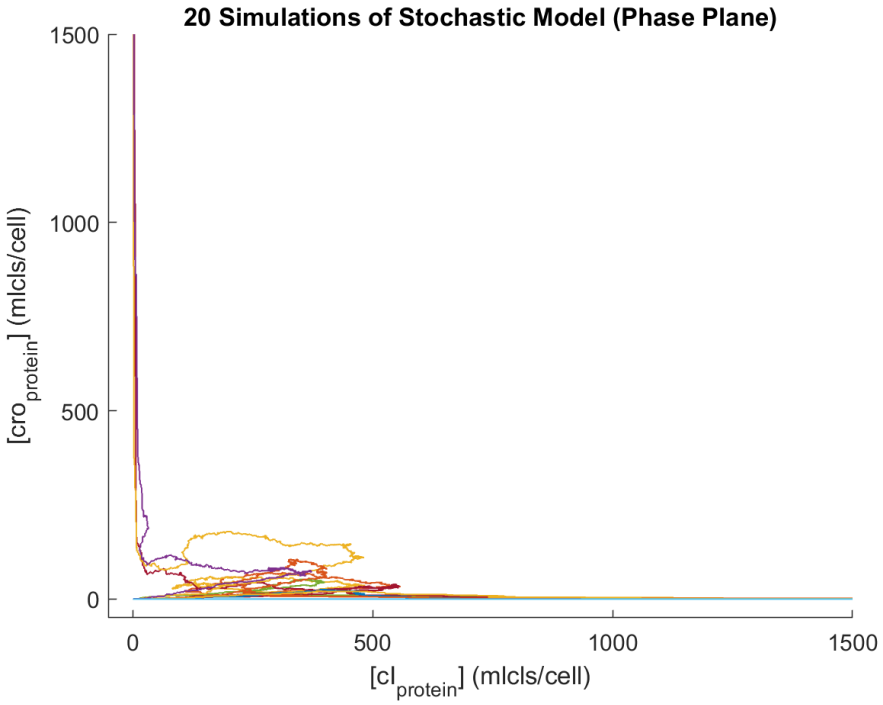


Figure B3b also shows that most simulations entered the lysogenic cycle but a few of the simulations entered the lytic cycle. Most of the trajectories end along the x-axis, but a few end along the y-axis. Most simulations end with low [cro_{prot}] and high [cI_{prot}]. Those curves approach the lysogenic steady state characterized by a very high concentration of the dominant cI protein. The remaining few curves approach the lytic steady state with a very high concentration of cro protein.

4. Figure B4a: This plot shows 20 simulations with 100,000 steps starting at the lysogenic steady state. All four concentrations in molecules per cell were plotted as a function of time in seconds.

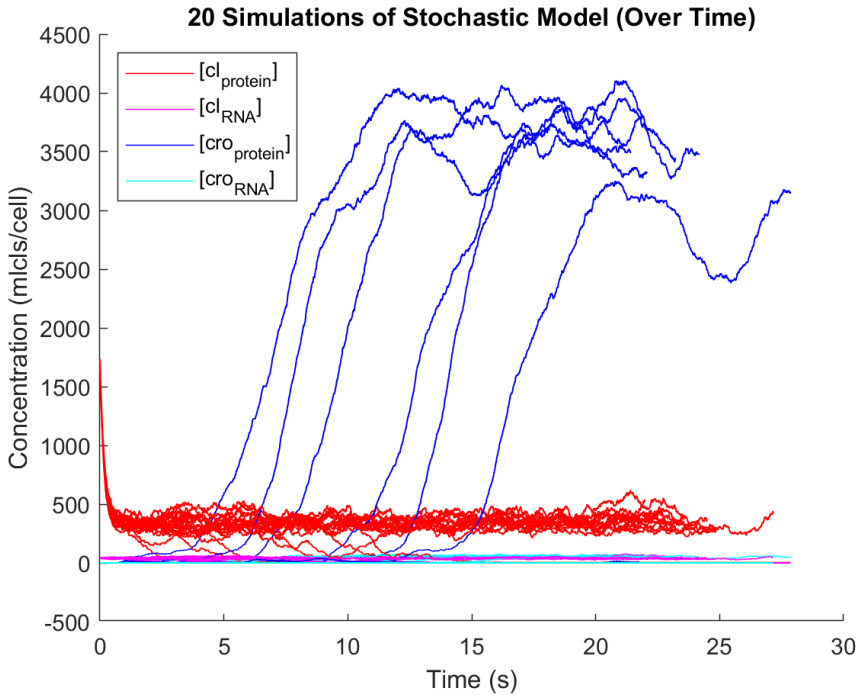
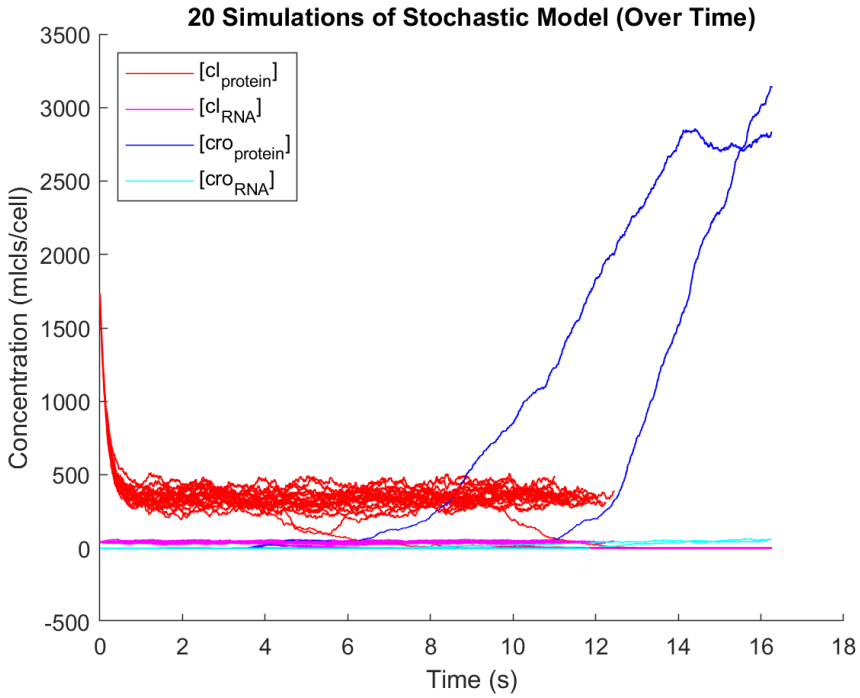


Figure B4b: This plot shows 20 simulations with 50,000 steps starting at the lysogenic steady state. All four concentrations in molecules per cell were plotted as a function of time in seconds.



In Part A question 4, the smallest possible stress-induced cI protein degradation rate that switched the system from lysogeny to lysis was chosen. In Figure 4A, the system strongly approached the lytic steady state. However, Figure B4A exemplifies that in a biological system, variation is very common. In a real bacterial colony experiencing stressful conditions, some of the cells may be undergoing lysis and some may be undergoing lysogeny. That is what is occurring in Figure B4A, as this small amount of stress was enough to cause some of the cells to switch, but not all.

The length of the simulation is certainly significant. In comparing Figure B4b, which was simulated with half as many steps, to Figure B4a, it is clear that the latter better represents the end behaviors of the simulations. Figure B4b does not offer the whole

picture of the simulated system. It likely only shows some of the simulations that switch to lysis, because other simulations may have switched after more reactions occurred. It also does not show the end behaviors of the simulations well, as the steady states these molecules approach are far less apparent.

Figure B4c: The trajectories of all 20 simulations were plotted in a phase plane of cro protein concentration as a function of cI protein concentration.

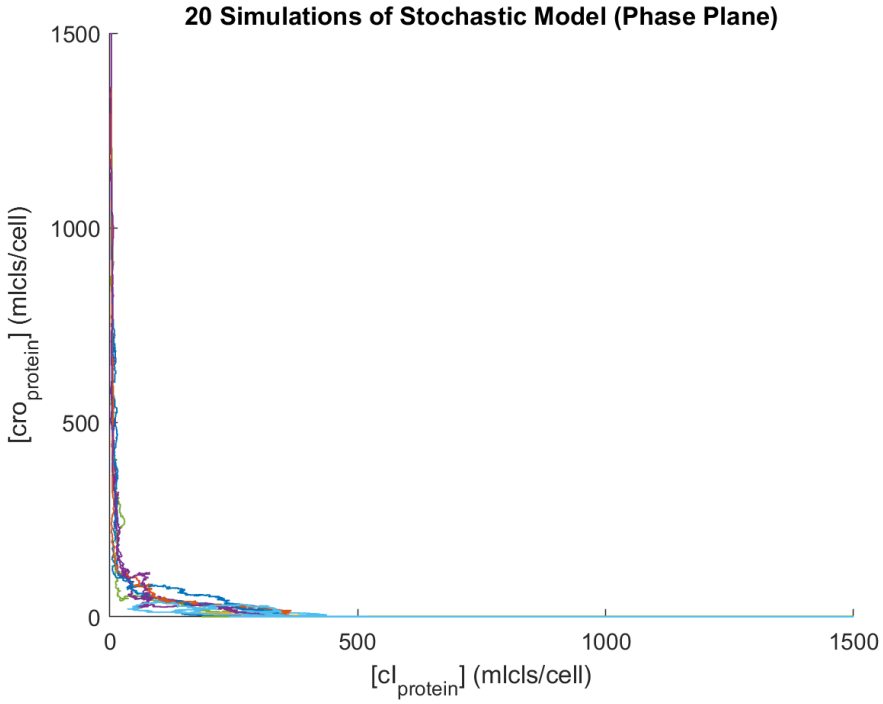


Figure B4c also shows that some simulations switched from the lysogenic cycle to the lytic but many of the simulations remained in the lysogenic cycle. Some of the trajectories end along the y-axis, but many end along the x-axis. Some simulations that switched to lysis end with high [cro_{prot}] and low [cI_{prot}]. Those curves approach the lytic steady state characterized by a very high concentration of the dominant cro protein. The

remaining curves approach the lysogenic steady state with a very high concentration of cI protein.

5. *Specific examples comparing stochastic and deterministic results can be found in the discussions of Figures B1 and B4a. This is a continuation of those discussions but is more general.*

   The results of the stochastic model were far more variable and fluctuated greatly, compared to those seen in the deterministic case. The results of the stochastic model are more in line with what occurs in a biological system. In a real biological system, many fluctuations occur due to chance, but the general reaction path is consistent among various simulations. Unlike the deterministic model, the stochastic model accounts for this. Rather than approaching precise steady states and remaining constant at those values, the end behaviors of the stochastic plots were more dynamic. An equilibrium state in biology means that the concentrations of all molecules are generally consistent around an average value, not actually constant. On the other hand, the constant and unchanging nature of steady states in the deterministic plots helped to definitively determine whether the concentrations reached a specific steady state. Many simulations and reaction steps are needed for such a visualization in the stochastic plots, while this can be accomplished with one 20 second simulation using a deterministic model. I think both models are useful in different ways. The deterministic model is very useful to visualize the mathematical context of the models and better understand their behavior through quantitative analysis. However, it is important to consult the stochastic model to visualize the bigger picture and how the system would behave in a real biological context. This can be used to better fine-tune the model, for example to ensure that the elevated degradation

constant definitively causes a stress-induced switch in all cells in an infected bacterial colony, not just some of them.

Contents

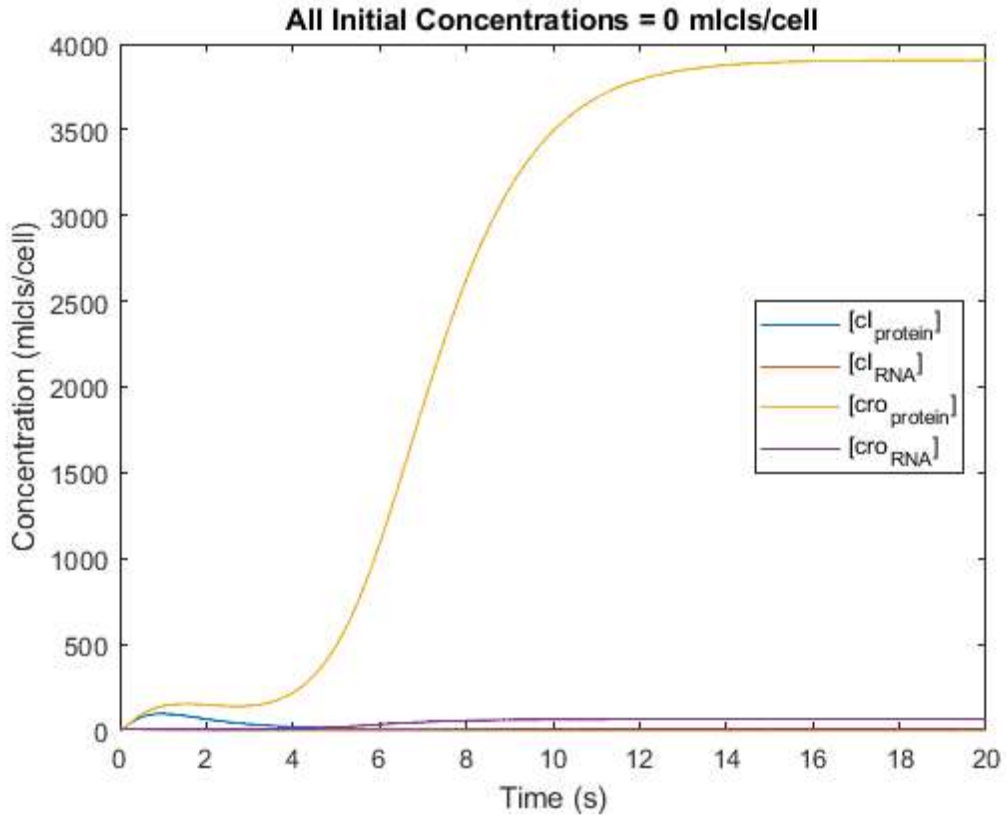
Part A: Deterministic model of the cro-cI genetic network

```
clear
close all
```

1.(a) (all initial concentrations 0)

```
clear

XcI_rna = 1.2; % 1/s
XcI_prot = 1.2; % 1/s
Xcro_rna = 0.8; % 1/s
Xcro_prot = 0.8; % 1/s
wcI = 50; % 1/s
ucI = 50; % 1/s
wcro = 50; % 1/s
ucro = 50; % 1/s
KcI = 10; % mlcl/cell*s
Kcro = 10; % mlcl/cell*s

deltaT = 0.01; % s
maxT = 20; % s
numiterations = maxT/deltaT;
t = 0:deltaT:maxT;

fig1 = figure(1);
cIprot = zeros(size(t));
cIrna = zeros(size(t));
croprot = zeros(size(t));
crorna = zeros(size(t));
cIprot(1) = 0; % initial concentration
cIrna(1) = 0; % initial concentration
croprot(1) = 0; % initial concentration
crorna(1) = 0; % initial concentration

for i = 1:numiterations
    dcIprotdt = (wcI*cIrna(i)) - (XcI_prot*cIprot(i));
    dcIrnadt = ucI*(1 - ((croprot(i)^2) / ((Kcro^2) + (croprot(i)^2)))) - XcI_rna*cIrna(i);
    dcroprotdt = (wcro*crorna(i)) - (Xcro_prot*croprot(i));
    dcrornadt = ucro*(1 - ((cIprot(i)^2) / ((KcI^2) + (cIprot(i)^2)))) - Xcro_rna*crorna(i);

    cIprot(i+1) = cIprot(i) + dcIprotdt*deltaT;
    cIrna(i+1) = cIrna(i) + dcIrnadt*deltaT;
```

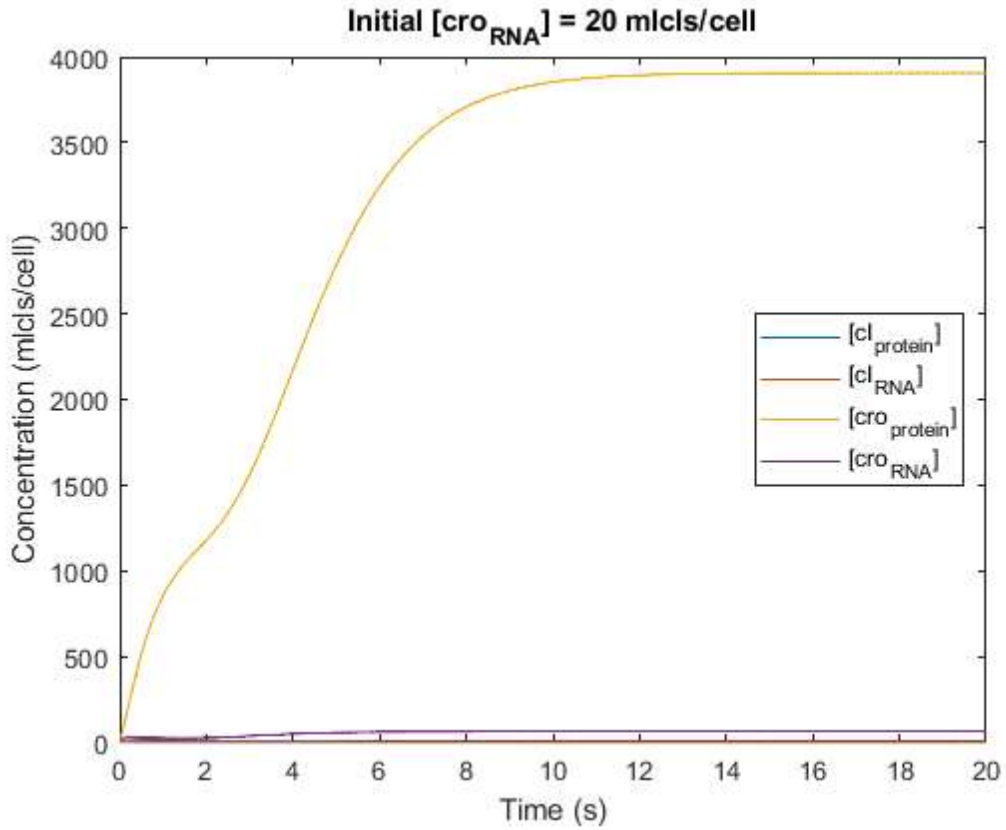
```
    croprot(i+1) = croprot(i) + dcroprotdt*deltaT;
    crorna(i+1) = crorna(i) + dcrornadt*deltaT;
end

plot(t, cIprot)
hold on
plot(t, cIrna)
plot(t, croprot)
plot(t, crorna)
xlabel('Time (s)')
ylabel('Concentration (mlcls/cell)')
title('All Initial Concentrations = 0 mlcls/cell')
legend('[cI_{protein}]', '[cI_{RNA}]', '[cro_{protein}]', '[cro_{RNA}]', 'Location', 'east')
hold off
```



1.(b) (initial crorna 20)

```
clear

XcI_rna = 1.2; % 1/s
XcI_prot = 1.2; % 1/s
Xcro_rna = 0.8; % 1/s
Xcro_prot = 0.8; % 1/s
wcI = 50; % 1/s
ucI = 50; % 1/s
wcro = 50; % 1/s
ucro = 50; % 1/s
KcI = 10; % mlcl/cell*s
Kcro = 10; % mlcl/cell*s

deltaT = 0.01; % s
```

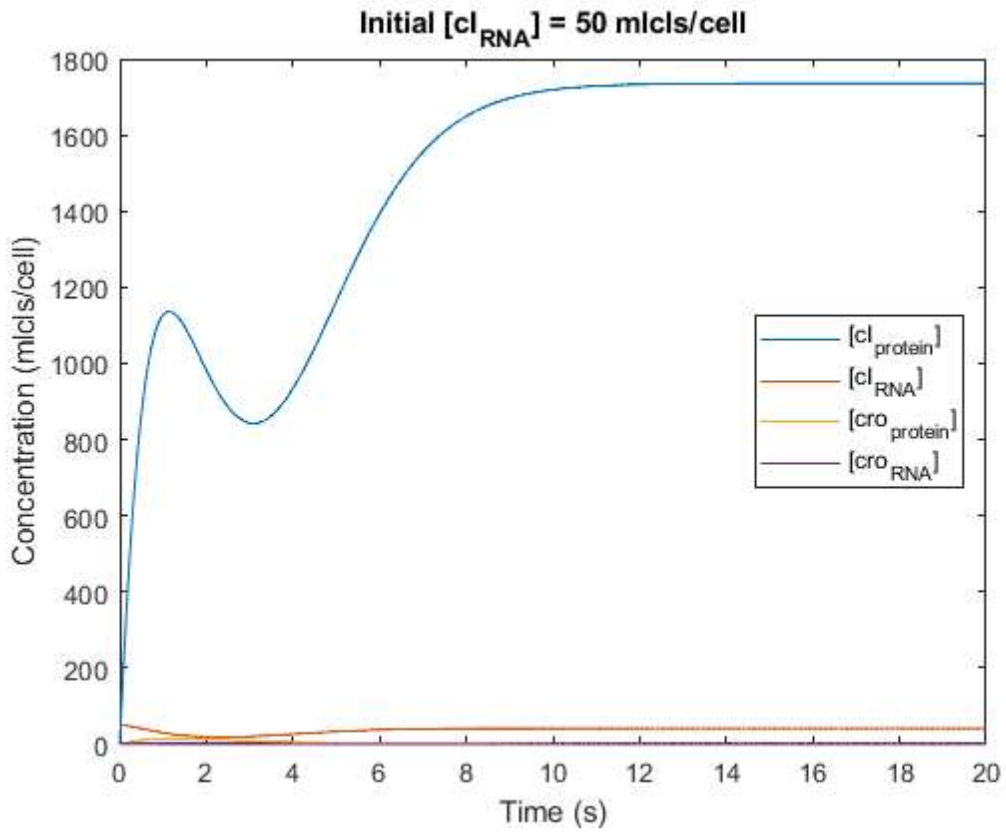
```
maxT = 20; % s
numiterations = maxT/deltaT;
t = 0:deltaT:maxT;

fig2 = figure(2);
cIprot = zeros(size(t));
cIrna = zeros(size(t));
croprot = zeros(size(t));
crorna = zeros(size(t));
cIprot(1) = 0; % initial concentration
cIrna(1) = 0; % initial concentration
croprot(1) = 0; % initial concentration
crorna(1) = 20; % initial concentration

for i = 1:numiterations
    dcIprotdt = (wcI*cIrna(i)) - (XcI_prot*cIprot(i));
    dcIrnadt = ucI*(1 - ((croprot(i)^2) / ((Kcro^2) + (croprot(i)^2)))) - XcI_rna*cIrna(i);
    dcroprotdt = (wcro*crorna(i)) - (Xcro_prot*croprot(i));
    dcrornadt = ucro*(1 - ((cIprot(i)^2) / ((KcI^2) + (cIprot(i)^2)))) - Xcro_rna*crorna(i);

    cIprot(i+1) = cIprot(i) + dcIprotdt*deltaT;
    cIrna(i+1) = cIrna(i) + dcIrnadt*deltaT;
    croprot(i+1) = croprot(i) + dcroprotdt*deltaT;
    crorna(i+1) = crorna(i) + dcrornadt*deltaT;
end

plot(t, cIprot)
hold on
plot(t, cIrna)
plot(t, croprot)
plot(t, crorna)
xlabel('Time (s)')
ylabel('Concentration (mlcls/cell)')
title('Initial [cro_{RNA}] = 20 mlcls/cell')
legend('[cI_{protein}]', '[cI_{RNA}]', '[cro_{protein}]', '[cro_{RNA}]', 'Location', 'east')
hold off
```



1.(c) (initial cI rna 50)

```
clear

XcI_rna = 1.2; % 1/s
XcI_prot = 1.2; % 1/s
Xcro_rna = 0.8; % 1/s
Xcro_prot = 0.8; % 1/s
wcI = 50; % 1/s
ucI = 50; % 1/s
wcro = 50; % 1/s
ucro = 50; % 1/s
KcI = 10; % mlcl/cell*s
Kcro = 10; % mlcl/cell*s

deltaT = 0.01; % s
maxT = 20; % s
numiterations = maxT/deltaT;
t = 0:deltaT:maxT;

fig3 = figure(3);
cIprot = zeros(size(t));
cIrna = zeros(size(t));
croprot = zeros(size(t));
crorna = zeros(size(t));
cIprot(1) = 0; % initial concentration
cIrna(1) = 50; % initial concentration
croprot(1) = 0; % initial concentration
crorna(1) = 0; % initial concentration

for i = 1:numiterations
```

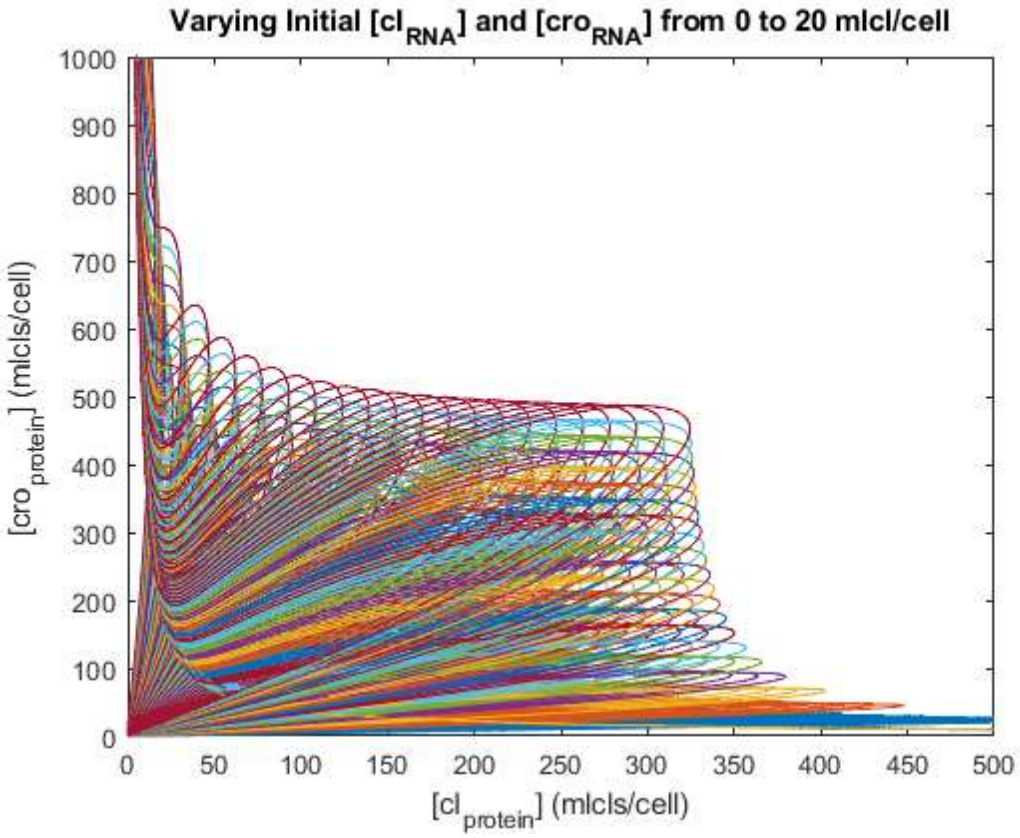
```
    dcIprotdt = (wcI*cIrna(i)) - (XcI_prot*cIprot(i));
    dcIrnadt = ucI*(1 - ((croprot(i)^2) / ((Kcro^2) + (croprot(i)^2)))) - XcI_rna*cIrna(i);
    dcroprotdt = (wcro*crorna(i)) - (Xcro_prot*croprot(i));
    dcrornadt = ucro*(1 - ((cIprot(i)^2) / ((KcI^2) + (cIprot(i)^2)))) - Xcro_rna*crorna(i);

    cIprot(i+1) = cIprot(i) + dcIprotdt*deltaT;
    cIrna(i+1) = cIrna(i) + dcIrnadt*deltaT;
    croprot(i+1) = croprot(i) + dcroprotdt*deltaT;
    crorna(i+1) = crorna(i) + dcrornadt*deltaT;
end

plot(t, cIprot)
hold on
plot(t, cIrna)
plot(t, croprot)
plot(t, crorna)
xlabel('Time (s)')
ylabel('Concentration (mlcls/cell)')
title('Initial [cI_{RNA}] = 50 mlcls/cell')
legend('[cI_{protein}]', '[cI_{RNA}]', '[cro_{protein}]', '[cro_{RNA}]', 'Location', 'east')
hold off
```



2. (a) (initial cIrna & crorna 0 to 20)

```
clear

XcI_rna = 1.2; % 1/s
XcI_prot = 1.2; % 1/s
Xcro_rna = 0.8; % 1/s
Xcro_prot = 0.8; % 1/s
wcI = 50; % 1/s
```

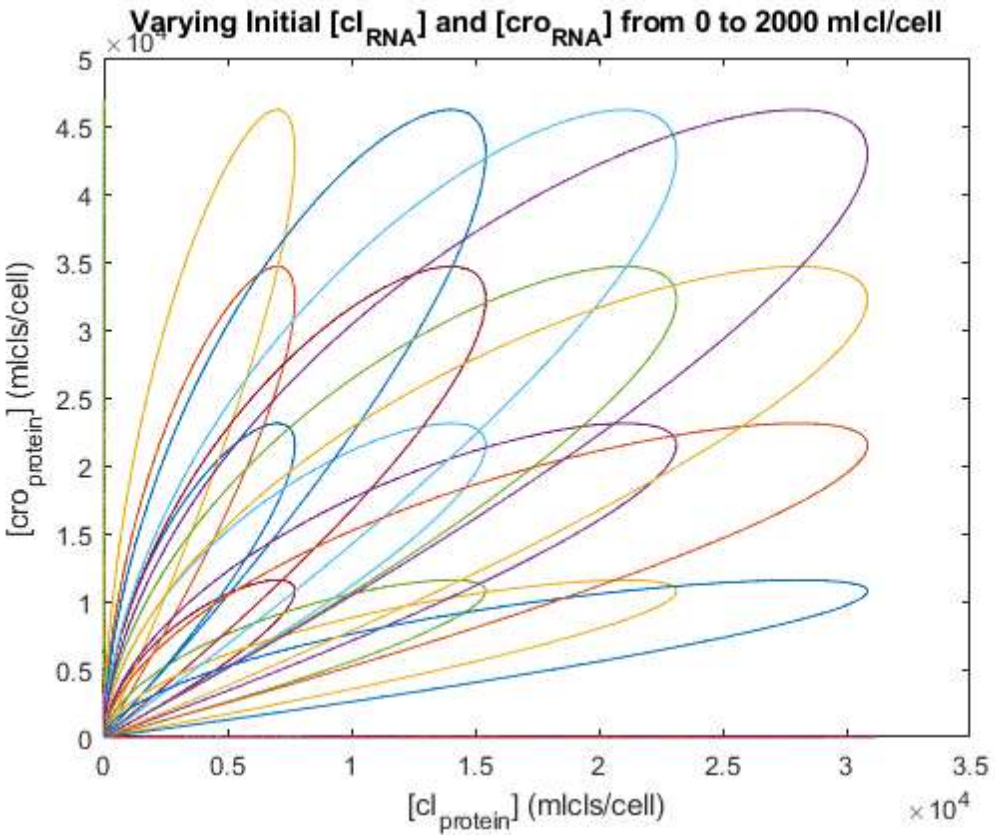
```
ucI = 50; % 1/s
wcro = 50; % 1/s
ucro = 50; % 1/s
KcI = 10; % mlcl/cell*s
Kcro = 10; % mlcl/cell*s

deltaT = 0.01; % s
maxT = 50; % s
numiterations = maxT/deltaT;
t = 0:deltaT:maxT;

fig4 = figure(4);
for cIrna_0 = 0:20 % initial concentration (mlcls/cell)
    for crorna_0 = 0:20 % initial concentration (mlcls/cell)
        cIprot = zeros(size(t));
        cIrna = zeros(size(t));
        croprot = zeros(size(t));
        crorna = zeros(size(t));
        cIprot(1) = 0; % initial concentration
        cIrna(1) = cIrna_0; % initial concentration
        croprot(1) = 0; % initial concentration
        crorna(1) = crorna_0; % initial concentration

        for i = 1:numiterations
            dcIprotdt = (wcI*cIrna(i)) - (XcI_prot*cIprot(i));
            dcIrnadt = ucI*(1 - ((croprot(i)^2) / ((Kcro^2) + (croprot(i)^2)))) - XcI_rna*cIrna(i);
            dcroprotdt = (wcro*crorna(i)) - (Xcro_prot*croprot(i));
            dcrornadt = ucro*(1 - ((cIprot(i)^2) / ((KcI^2) + (cIprot(i)^2)))) - Xcro_rna*crorna(i);

            cIprot(i+1) = cIprot(i) + dcIprotdt*deltaT;
            cIrna(i+1) = cIrna(i) + dcIrnadt*deltaT;
            croprot(i+1) = croprot(i) + dcroprotdt*deltaT;
            crorna(i+1) = crorna(i) + dcrornadt*deltaT;
        end
        plot(cIprot, croprot)
        hold on
    end
end
xlabel('[cI_{protein}] (mlcls/cell)')
ylabel('[cro_{protein}] (mlcls/cell)')
title('Varying Initial [cI_{RNA}] and [cro_{RNA}] from 0 to 20 mlcl/cell')
xlim([0 500])
ylim([0 1000])
hold off
```



2. (b) (initial clrna & crorna 0 to 2000)

```
clear

XcI_rna = 1.2; % 1/s
XcI_prot = 1.2; % 1/s
Xcro_rna = 0.8; % 1/s
Xcro_prot = 0.8; % 1/s
wcI = 50; % 1/s
ucI = 50; % 1/s
wcro = 50; % 1/s
ucro = 50; % 1/s
KcI = 10; % mlcl/cell*s
Kcro = 10; % mlcl/cell*s

deltaT = 0.01; % s
maxT = 100; % s
numiterations = maxT/deltaT;
t = 0:deltaT:maxT;

fig5 = figure(5);
for cIrna_0 = 0:500:2000 % initial concentration (mlcls/cell)
    for crorna_0 = 0:500:2000 % initial concentration (mlcls/cell)
        cIprot = zeros(size(t));
        cIrna = zeros(size(t));
        croprot = zeros(size(t));
        crorna = zeros(size(t));
        cIprot(1) = 0; % initial concentration
        cIrna(1) = cIrna_0; % initial concentration
        croprot(1) = 0; % initial concentration
        crorna(1) = crorna_0; % initial concentration
```

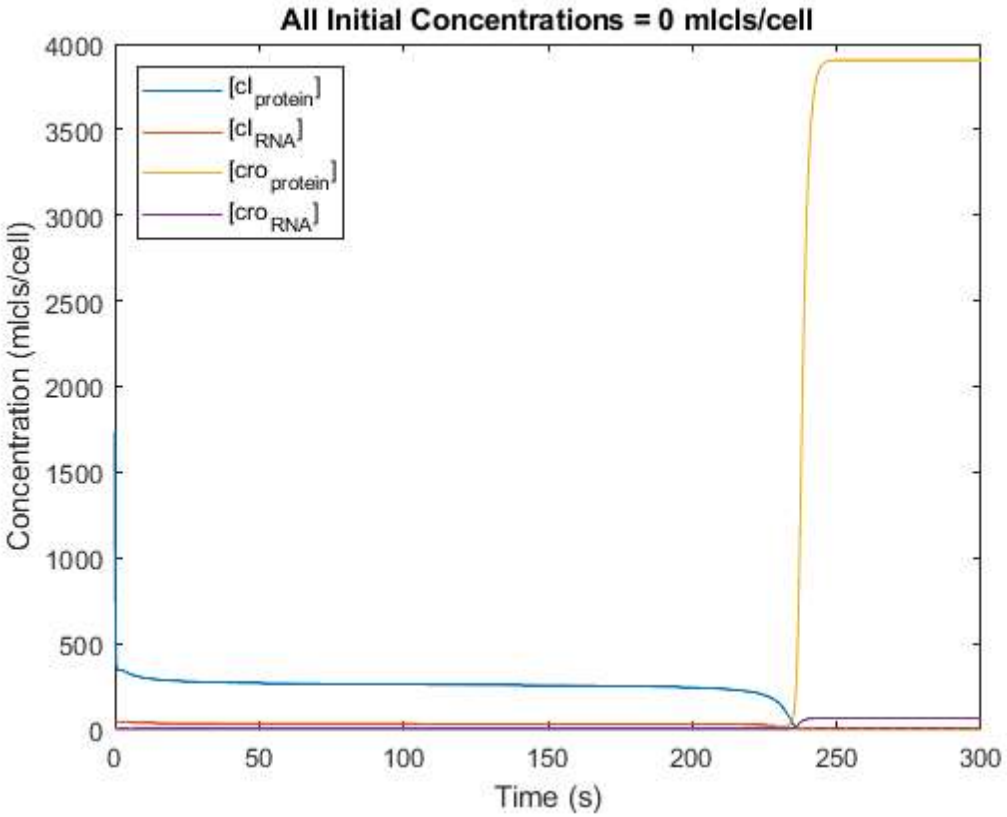
```
        for i = 1:numiterations
            dcIprotdt = (wcI*cIrna(i)) - (XcI_prot*cIprot(i));
            dcIrnadt = ucI*(1 - ((croprot(i)^2) / ((Kcro^2) + (croprot(i)^2)))) - XcI_rna*cIrna(i);
            dcroprotdt = (wcro*crorna(i)) - (Xcro_prot*croprot(i));
            dcrornadt = ucro*(1 - ((cIprot(i)^2) / ((KcI^2) + (cIprot(i)^2)))) - Xcro_rna*crorna(i);

            cIprot(i+1) = cIprot(i) + dcIprotdt*deltaT;
            cIrna(i+1) = cIrna(i) + dcIrnadt*deltaT;
            croprot(i+1) = croprot(i) + dcroprotdt*deltaT;
            crorna(i+1) = crorna(i) + dcrornadt*deltaT;
        end
        plot(cIprot, croprot)
        hold on
    end
end
xlabel('[cI_{protein}] (mlcls/cell)')
ylabel('[cro_{protein}] (mlcls/cell)')
title('Varying Initial [cI_{RNA}] and [cro_{RNA}] from 0 to 2000 mlcl/cell')
hold off
```



4.

```
clear
close all

XcI_rna = 1.2; % 1/s
XcI_prot = 6.02; % 1/s
Xcro_rna = 0.8; % 1/s
Xcro_prot = 0.8; % 1/s
wcI = 50; % 1/s
```

```
ucI = 50; % 1/s
wcro = 50; % 1/s
ucro = 50; % 1/s
KcI = 10; % mlcl/cell*s
Kcro = 10; % mlcl/cell*s

deltaT = 0.01; % s
maxT = 300; % s
numiterations = maxT/deltaT;
t = 0:deltaT:maxT;

fig1 = figure(1);
cIprot = zeros(size(t));
cIrna = zeros(size(t));
croprot = zeros(size(t));
crorna = zeros(size(t));
cIprot(1) = 1735.8; % initial concentration
cIrna(1) = 41.6597; % initial concentration
croprot(1) = 0.1296; % initial concentration
crorna(1) = 0.0021; % initial concentration

for i = 1:numiterations
    dcIprotdt = (wcI*cIrna(i)) - (XcI_prot*cIprot(i));
    dcIrnadt = ucI*(1 - ((croprot(i)^2) / ((Kcro^2) + (croprot(i)^2)))) - XcI_rna*cIrna(i);
    dcroprotdt = (wcro*crorna(i)) - (Xcro_prot*croprot(i));
    dcrornadt = ucro*(1 - ((cIprot(i)^2) / ((KcI^2) + (cIprot(i)^2)))) - Xcro_rna*crorna(i);

    cIprot(i+1) = cIprot(i) + dcIprotdt*deltaT;
    cIrna(i+1) = cIrna(i) + dcIrnadt*deltaT;
    croprot(i+1) = croprot(i) + dcroprotdt*deltaT;
    crorna(i+1) = crorna(i) + dcrornadt*deltaT;
end

plot(t, cIprot)
hold on
plot(t, cIrna)
plot(t, croprot)
plot(t, crorna)
xlabel('Time (s)')
ylabel('Concentration (mlcls/cell)')
title('All Initial Concentrations = 0 mlcls/cell')
legend('[cI_{protein}]', '[cI_{RNA}]', '[cro_{protein}]', '[cro_{RNA}]', 'Location', 'northwest')
hold off
```



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Part B: Stochastic model of the cro-cI genetic network

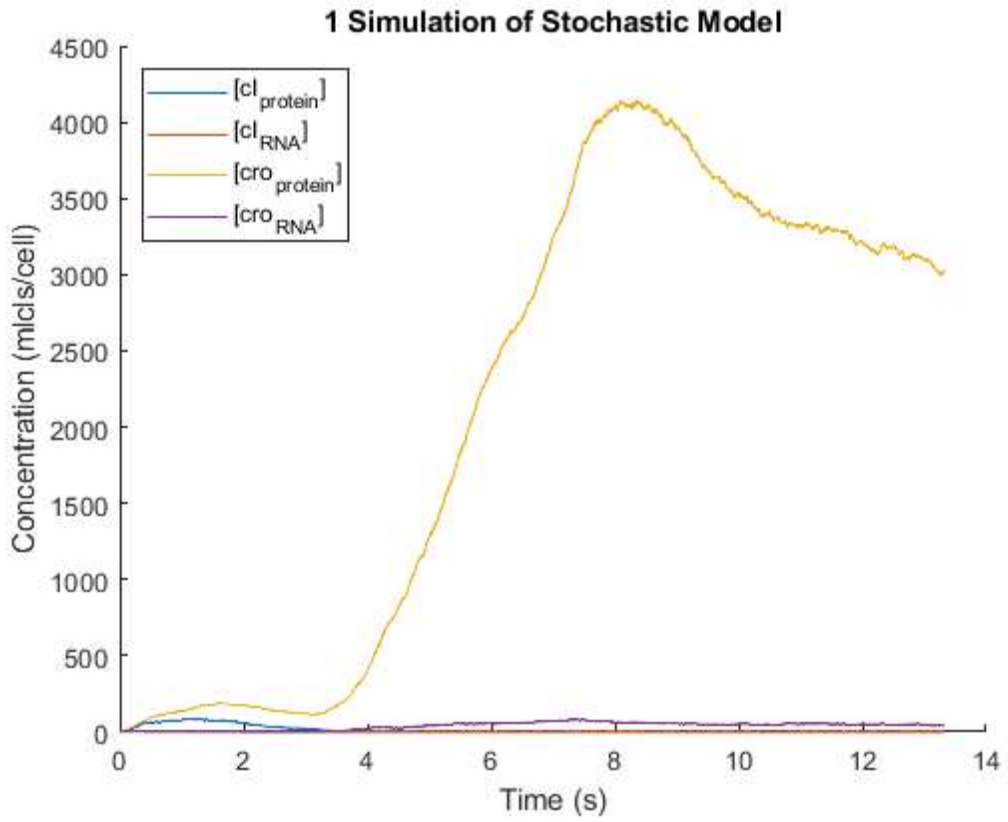
Contents

1. One simulation

```
clear
close all

XcI_rna = 1.2; % 1/s
XcI_prot = 1.2; % 1/s
Xcro_rna = 0.8; % 1/s
Xcro_prot = 0.8; % 1/s
wcI = 50; % 1/s
ucI = 50; % 1/s
wcro = 50; % 1/s
ucro = 50; % 1/s
KcI = 10; % mlcl/cell*s
Kcro = 10; % mlcl/cell*s

steps = 50000;
time_points(1) = 0;

cIprot = zeros(1,steps);
cIrna = zeros(1,steps);
croprot = zeros(1,steps);
crorna = zeros(1,steps);
cIprot(1) = 0; % initial concentration
cIrna(1) = 0; % initial concentration
croprot(1) = 0; % initial concentration
crorna(1) = 0; % initial concentration

v1 = zeros(1,steps);
v2 = zeros(1,steps);
v3 = zeros(1,steps);
v4 = zeros(1,steps);
v5 = zeros(1,steps);
v6 = zeros(1,steps);
v7 = zeros(1,steps);
v8 = zeros(1,steps);

for i = 1:(steps-1)
    v1 = wcI*cIrna(i);
    v2 = XcI_prot*cIprot(i);
    v3 = ucI*(1- ( ((croprot(i))^2) / ((Kcro^2)+((croprot(i))^2)) ));
    v4 = XcI_rna*cIrna(i);
    v5 = wcro*crorna(i);
    v6 = Xcro_prot*croprot(i);
```

```
    v7 = ucro*(1- ( ((cIprot(i))^2) / ((KcI^2)+((cIprot(i))^2)) ));
    v8 = Xcro_rna*crorna(i);
    vtotal = v1+v2+v3+v4+v5+v6+v7+v8; %calc total rxn rate

    y = rand();
    tau = -log(y)/(vtotal); %calc time to next rxn
    time_points(i+1) = time_points(i) + tau;

    y_mod = vtotal*rand();
    if y_mod <= v1
        cIprot(i+1) = cIprot(i) + 1; %cIprot syn
        cIrna(i+1) = cIrna(i);
        croprot(i+1) = croprot(i);
        crorna(i+1) = crorna(i);
    elseif y_mod <= (v1 + v2)
        cIprot(i+1) = cIprot(i) - 1; %cIprot deg
        cIrna(i+1) = cIrna(i);
        croprot(i+1) = croprot(i);
        crorna(i+1) = crorna(i);
    elseif y_mod <= (v1 + v2 + v3)
        cIprot(i+1) = cIprot(i);
        cIrna(i+1) = cIrna(i) + 1; %cIrna syn
        croprot(i+1) = croprot(i);
        crorna(i+1) = crorna(i);
    elseif y_mod <= (v1 + v2 + v3 + v4)
        cIprot(i+1) = cIprot(i);
        cIrna(i+1) = cIrna(i) - 1; %cIrna deg
        croprot(i+1) = croprot(i);
        crorna(i+1) = crorna(i);
    elseif y_mod <= (v1 + v2 + v3 + v4 + v5)
        cIprot(i+1) = cIprot(i);
        cIrna(i+1) = cIrna(i);
        croprot(i+1) = croprot(i) + 1; %croprot syn
        crorna(i+1) = crorna(i);
    elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6)
        cIprot(i+1) = cIprot(i);
        cIrna(i+1) = cIrna(i);
        croprot(i+1) = croprot(i) - 1; %croprot deg
        crorna(i+1) = crorna(i);
    elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6 + v7)
        cIprot(i+1) = cIprot(i);
        cIrna(i+1) = cIrna(i);
        croprot(i+1) = croprot(i);
        crorna(i+1) = crorna(i) + 1; %crorna syn
    elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6 + v7 + v8)
        cIprot(i+1) = cIprot(i);
        cIrna(i+1) = cIrna(i);
        croprot(i+1) = croprot(i);
        crorna(i+1) = crorna(i) - 1; %crorna deg
    else
        Disp('error');

    end
end

fig6 = figure(6);
hold on
plot(time_points, cIprot)
```

```
plot(time_points, cIrna)
plot(time_points, croprot)
plot(time_points, crorna)
xlabel('Time (s)')
ylabel('Concentration (mlcls/cell)')
title('1 Simulation of Stochastic Model')
legend('[cI_{protein}]', '[cI_{RNA}]', '[cro_{protein}]', '[cro_{RNA}]', 'Location','northwest')
hold off
```

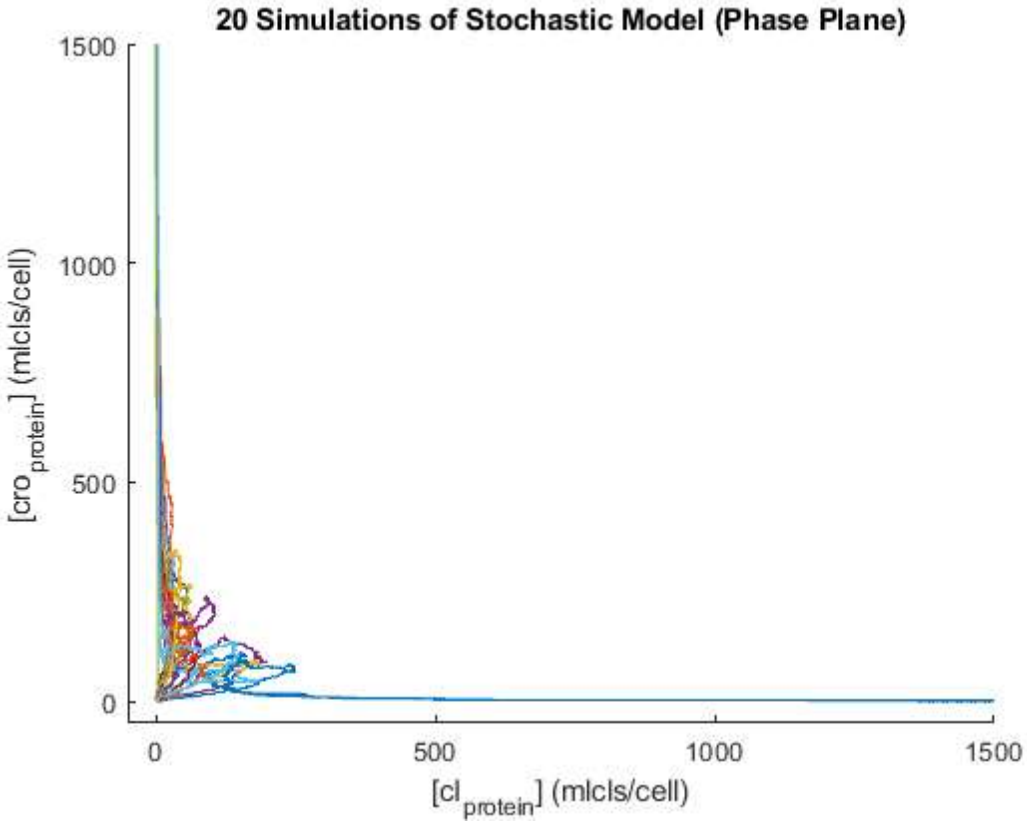


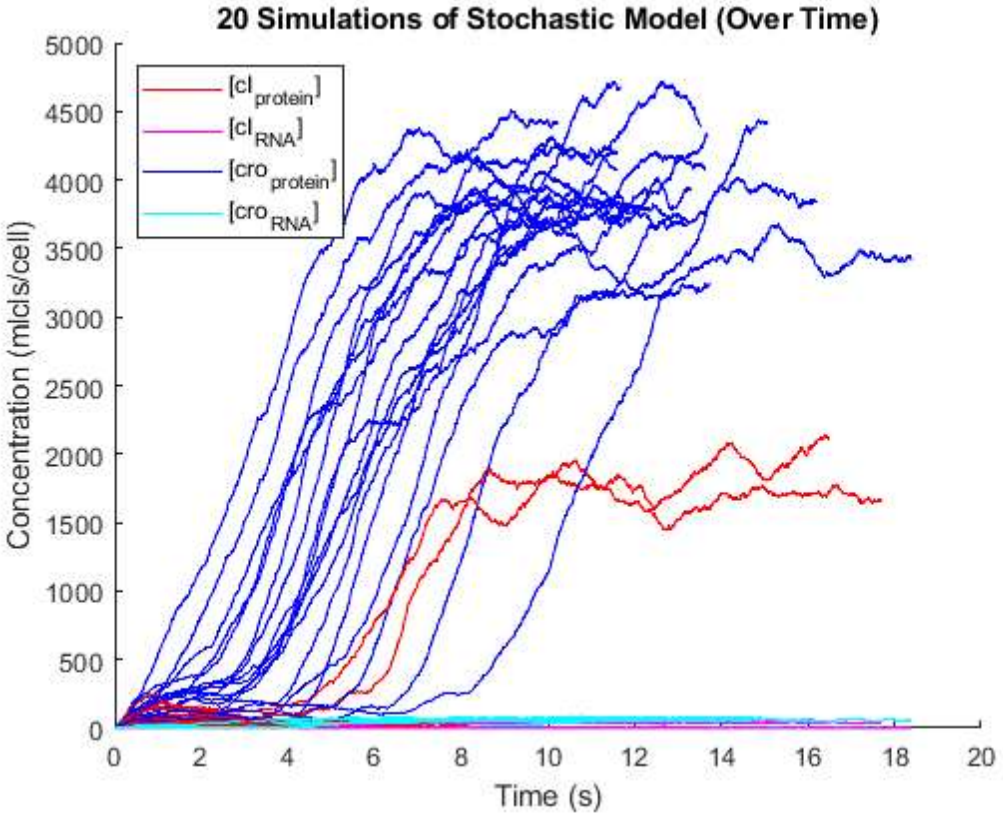
2. 20 simulations

```
clear
close all

XcI_rna = 1.2; % 1/s
XcI_prot = 1.2; % 1/s
Xcro_rna = 0.8; % 1/s
Xcro_prot = 0.8; % 1/s
wcI = 50; % 1/s
ucI = 50; % 1/s
wcro = 50; % 1/s
ucro = 50; % 1/s
KcI = 10; % mlcl/cell*s
Kcro = 10; % mlcl/cell*s

steps = 50000;
time_points(1) = 0;

cIprot = zeros(1,steps);
cIrna = zeros(1,steps);
croprot = zeros(1,steps);
```

```
crorna = zeros(1,steps);
cIprot(1) = 0; % initial concentration
cIrna(1) = 0; % initial concentration
croprot(1) = 0; % initial concentration
crorna(1) = 0; % initial concentration

v1 = zeros(1,steps);
v2 = zeros(1,steps);
v3 = zeros(1,steps);
v4 = zeros(1,steps);
v5 = zeros(1,steps);
v6 = zeros(1,steps);
v7 = zeros(1,steps);
v8 = zeros(1,steps);

fig7 = figure(7);
fig8 = figure(8);
for s = 1:20
    for i = 1:(steps-1)
        v1 = wcI*cIrna(i);
        v2 = XcI_prot*cIprot(i);
        v3 = ucI*(1- ( ((croprot(i))^2) / ((Kcro^2)+((croprot(i))^2)) ));
        v4 = XcI_rna*cIrna(i);
        v5 = wcro*crorna(i);
        v6 = Xcro_prot*croprot(i);
        v7 = ucro*(1- ( ((cIprot(i))^2) / ((KcI^2)+((cIprot(i))^2)) ));
        v8 = Xcro_rna*crorna(i);
        vtotal = v1+v2+v3+v4+v5+v6+v7+v8; %calc total rxn rate

        y = rand();
        tau = -log(y)/(vtotal); %calc time to next rxn
        time_points(i+1) = time_points(i) + tau;

        y_mod = vtotal*rand();
        if y_mod <= v1
            cIprot(i+1) = cIprot(i) + 1; %cIprot syn
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2)
            cIprot(i+1) = cIprot(i) - 1; %cIprot deg
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i) + 1; %cIrna syn
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i) - 1; %cIrna deg
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i) + 1; %croprot syn
```

```
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i) - 1; %croprot deg
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6 + v7)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i) + 1; %crorna syn
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6 + v7 + v8)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i) - 1; %crorna deg
        else
            Disp('error');

        end
    end

    set(0, 'CurrentFigure', fig7)
    hold on
    plot(cIprot, croprot)

    set(0, 'CurrentFigure', fig8)
    hold on
    plot(time_points, cIprot, 'r')
    plot(time_points, cIrna, 'm')
    plot(time_points, croprot, 'b')
    plot(time_points, crorna, 'c')
end

set(0, 'CurrentFigure', fig7)
xlabel('[cI_{protein}] (mlcls/cell)')
ylabel('[cro_{protein}] (mlcls/cell)')
title('20 Simulations of Stochastic Model (Phase Plane)')
xlim([-50 1500])
ylim([-50 1500])
hold off

set(0, 'CurrentFigure', fig8)
xlabel('Time (s)')
ylabel('Concentration (mlcls/cell)')
title('20 Simulations of Stochastic Model (Over Time)')
legend('[cI_{protein}]', '[cI_{RNA}]', '[cro_{protein}]', '[cro_{RNA}]', 'Location','northwest')
hold off
```





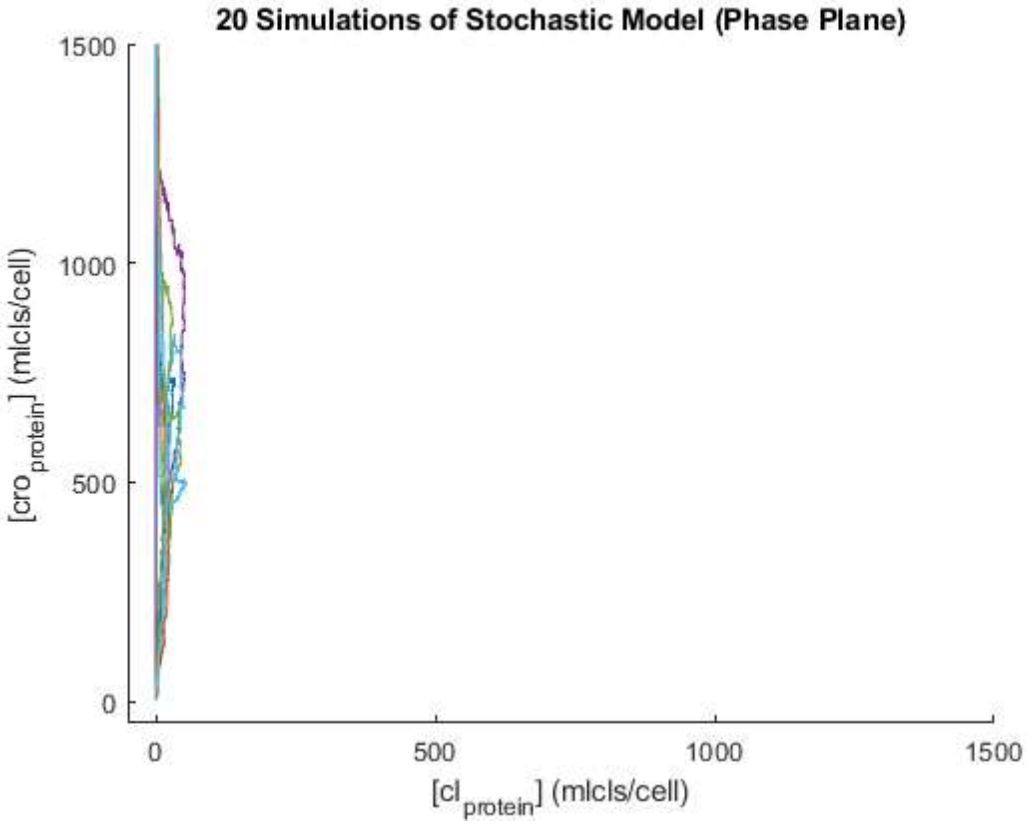
3. crorna0 = 20

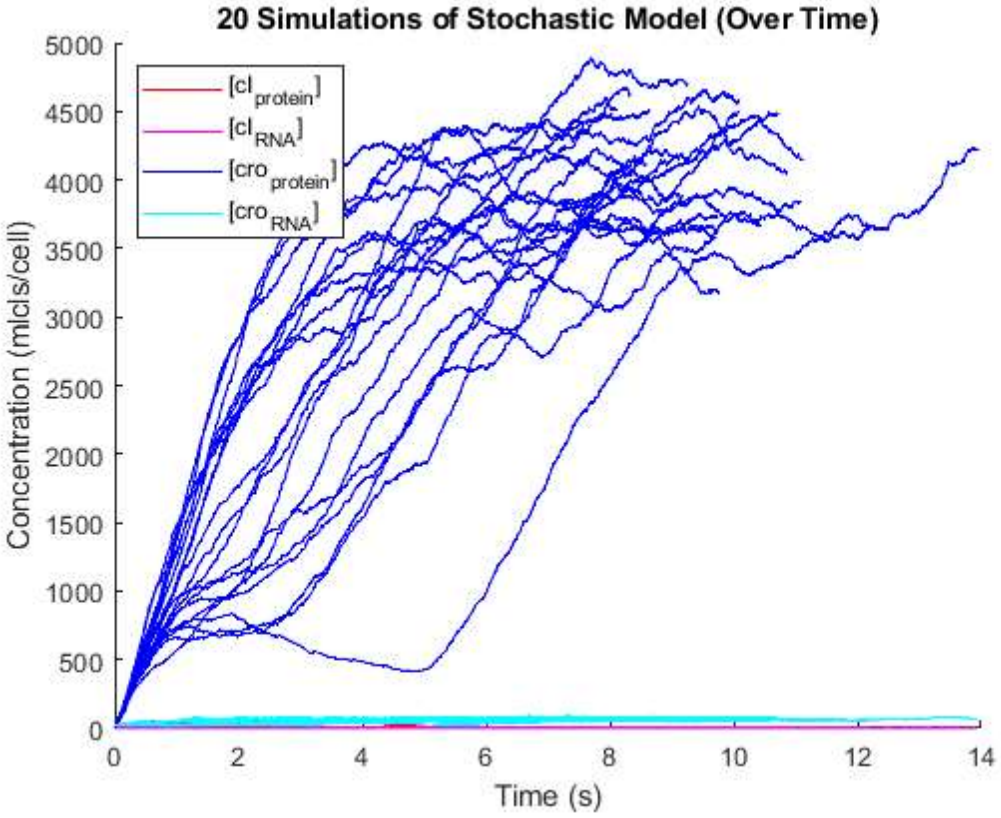
```
clear
close all
```

```
XcI_rna = 1.2; % 1/s
XcI_prot = 1.2; % 1/s
Xcro_rna = 0.8; % 1/s
Xcro_prot = 0.8; % 1/s
wcI = 50; % 1/s
ucI = 50; % 1/s
wcro = 50; % 1/s
ucro = 50; % 1/s
KcI = 10; % mlcl/cell*s
Kcro = 10; % mlcl/cell*s

steps = 50000;
time_points(1) = 0;

cIprot = zeros(1,steps);
cIrna = zeros(1,steps);
croprot = zeros(1,steps);
crorna = zeros(1,steps);
cIprot(1) = 0; % initial concentration
cIrna(1) = 0; % initial concentration
croprot(1) = 0; % initial concentration
crorna(1) = 20; % initial concentration

v1 = zeros(1,steps);
v2 = zeros(1,steps);
v3 = zeros(1,steps);
v4 = zeros(1,steps);
v5 = zeros(1,steps);
v6 = zeros(1,steps);
v7 = zeros(1,steps);
v8 = zeros(1,steps);

fig9 = figure(9);
fig10 = figure(10);
for s = 1:20
    for i = 1:(steps-1)
        v1 = wcI*cIrna(i);
        v2 = XcI_prot*cIprot(i);
        v3 = ucI*(1- ( ((croprot(i))^2) / ((Kcro^2)+((croprot(i))^2)) ));
        v4 = XcI_rna*cIrna(i);
        v5 = wcro*crorna(i);
        v6 = Xcro_prot*croprot(i);
        v7 = ucro*(1- ( ((cIprot(i))^2) / ((KcI^2)+((cIprot(i))^2)) ));
        v8 = Xcro_rna*crorna(i);
        vtotal = v1+v2+v3+v4+v5+v6+v7+v8; %calc total rxn rate

        y = rand();
        tau = -log(y)/(vtotal); %calc time to next rxn
        time_points(i+1) = time_points(i) + tau;

        y_mod = vtotal*rand();
        if y_mod <= v1
            cIprot(i+1) = cIprot(i) + 1; %cIprot syn
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2)
            cIprot(i+1) = cIprot(i) - 1; %cIprot deg
```

```
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i) + 1; %cIrna syn
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i) - 1; %cIrna deg
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i) + 1; %croprot syn
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i) - 1; %croprot deg
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6 + v7)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i) + 1; %crorna syn
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6 + v7 + v8)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i) - 1; %crorna deg
        else
            Disp('error');

        end
    end

    set(0, 'CurrentFigure', fig9)
    hold on
    plot(cIprot, croprot)

    set(0, 'CurrentFigure', fig10)
    hold on
    plot(time_points, cIprot, 'r')
    plot(time_points, cIrna, 'm')
    plot(time_points, croprot, 'b')
    plot(time_points, crorna, 'c')
end

set(0, 'CurrentFigure', fig9)
xlabel('[cI_{protein}] (mlcls/cell)')
ylabel('[cro_{protein}] (mlcls/cell)')
title('20 Simulations of Stochastic Model (Phase Plane)')
xlim([-50 1500])
ylim([-50 1500])
hold off
```

```
set(0, 'CurrentFigure', fig10)
xlabel('Time (s)')
ylabel('Concentration (mlcls/cell)')
title('20 Simulations of Stochastic Model (Over Time)')
legend('[cI_{protein}]', '[cI_{RNA}]', '[cro_{protein}]', '[cro_{RNA}]', 'Location','northwest')
hold off
```





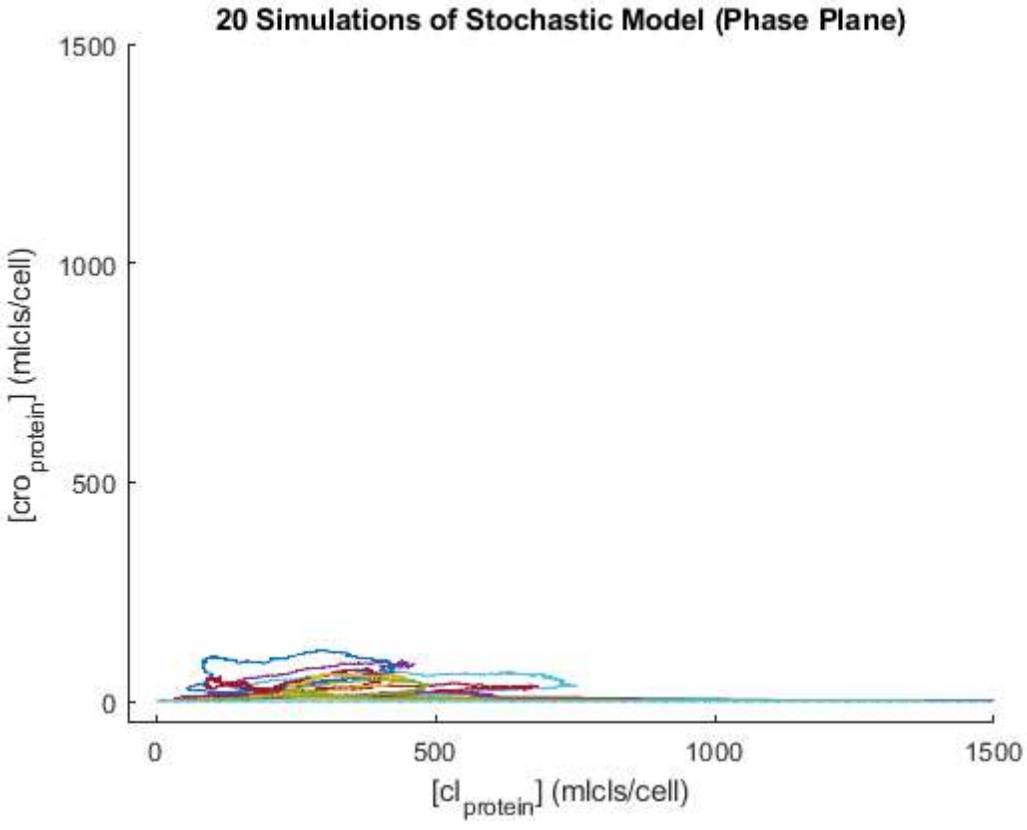
3. clrna0 = 20

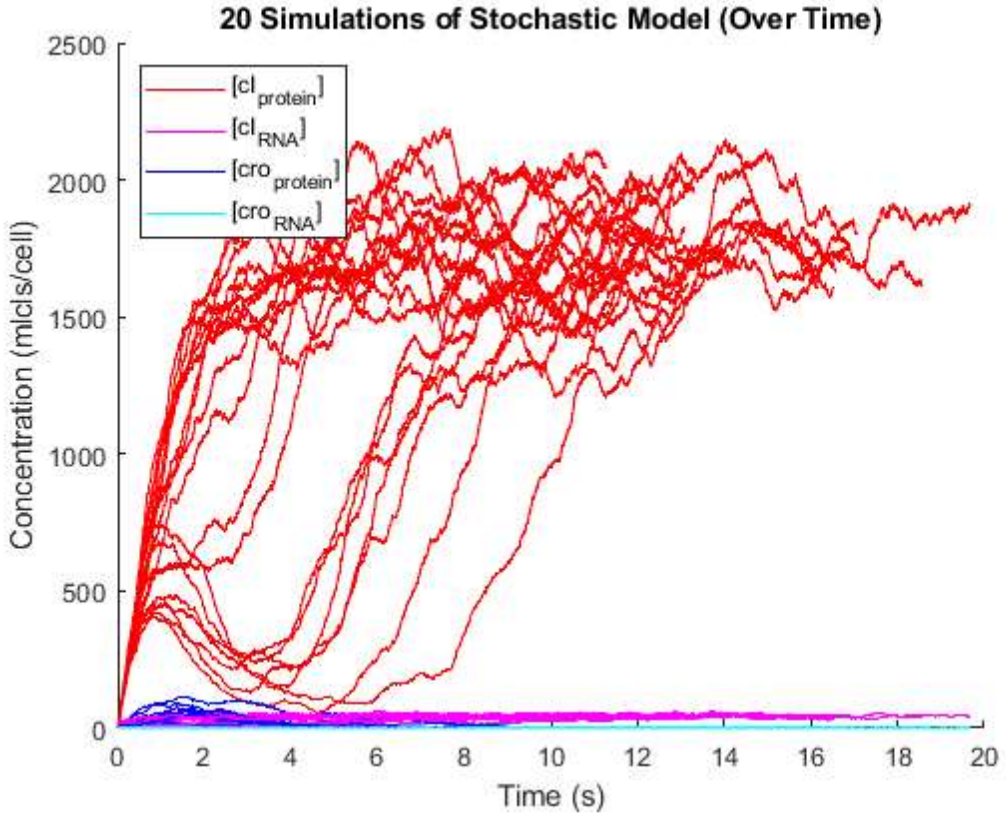
```
clear
close all
```

```
XcI_rna = 1.2; % 1/s
XcI_prot = 1.2; % 1/s
Xcro_rna = 0.8; % 1/s
Xcro_prot = 0.8; % 1/s
wcI = 50; % 1/s
ucI = 50; % 1/s
wcro = 50; % 1/s
ucro = 50; % 1/s
KcI = 10; % mlcl/cell*s
Kcro = 10; % mlcl/cell*s

steps = 50000;
time_points(1) = 0;

cIprot = zeros(1,steps);
cIrna = zeros(1,steps);
croprot = zeros(1,steps);
crorna = zeros(1,steps);
cIprot(1) = 0; % initial concentration
cIrna(1) = 20; % initial concentration
croprot(1) = 0; % initial concentration
crorna(1) = 0; % initial concentration

v1 = zeros(1,steps);
v2 = zeros(1,steps);
v3 = zeros(1,steps);
v4 = zeros(1,steps);
v5 = zeros(1,steps);
v6 = zeros(1,steps);
v7 = zeros(1,steps);
v8 = zeros(1,steps);

fig11 = figure(11);
fig12 = figure(12);
for s = 1:20
    for i = 1:(steps-1)
        v1 = wcI*cIrna(i);
        v2 = XcI_prot*cIprot(i);
        v3 = ucI*(1- ( ((croprot(i))^2) / ((Kcro^2)+((croprot(i))^2)) ));
        v4 = XcI_rna*cIrna(i);
        v5 = wcro*crorna(i);
        v6 = Xcro_prot*croprot(i);
        v7 = ucro*(1- ( ((cIprot(i))^2) / ((KcI^2)+((cIprot(i))^2)) ));
        v8 = Xcro_rna*crorna(i);
        vtotal = v1+v2+v3+v4+v5+v6+v7+v8; %calc total rxn rate

        y = rand();
        tau = -log(y)/(vtotal); %calc time to next rxn
        time_points(i+1) = time_points(i) + tau;

        y_mod = vtotal*rand();
        if y_mod <= v1
            cIprot(i+1) = cIprot(i) + 1; %cIprot syn
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2)
            cIprot(i+1) = cIprot(i) - 1; %cIprot deg
```

```
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i) + 1; %cIrna syn
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i) - 1; %cIrna deg
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i) + 1; %croprot syn
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i) - 1; %croprot deg
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6 + v7)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i) + 1; %crorna syn
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6 + v7 + v8)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i) - 1; %crorna deg
        else
            Disp('error');

        end
    end

    set(0, 'CurrentFigure', fig11)
    hold on
    plot(cIprot, croprot)

    set(0, 'CurrentFigure', fig12)
    hold on
    plot(time_points, cIprot, 'r')
    plot(time_points, cIrna, 'm')
    plot(time_points, croprot, 'b')
    plot(time_points, crorna, 'c')
end

set(0, 'CurrentFigure', fig11)
xlabel('[cI_{protein}] (mlcls/cell)')
ylabel('[cro_{protein}] (mlcls/cell)')
title('20 Simulations of Stochastic Model (Phase Plane)')
xlim([-50 1500])
ylim([-50 1500])
hold off
```

```
set(0, 'CurrentFigure', fig12)
xlabel('Time (s)')
ylabel('Concentration (mlcls/cell)')
title('20 Simulations of Stochastic Model (Over Time)')
legend('[cI_{protein}]', '[cI_{RNA}]', '[cro_{protein}]', '[cro_{RNA}]', 'Location','northwest')
hold off
```





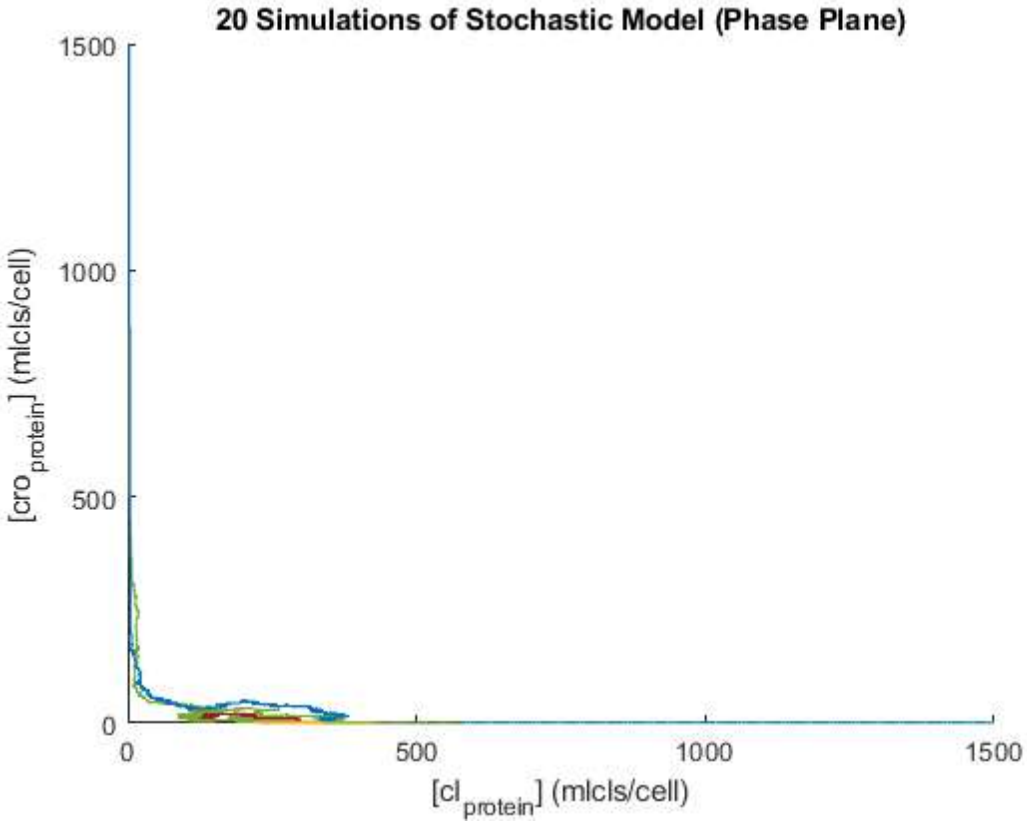
4.

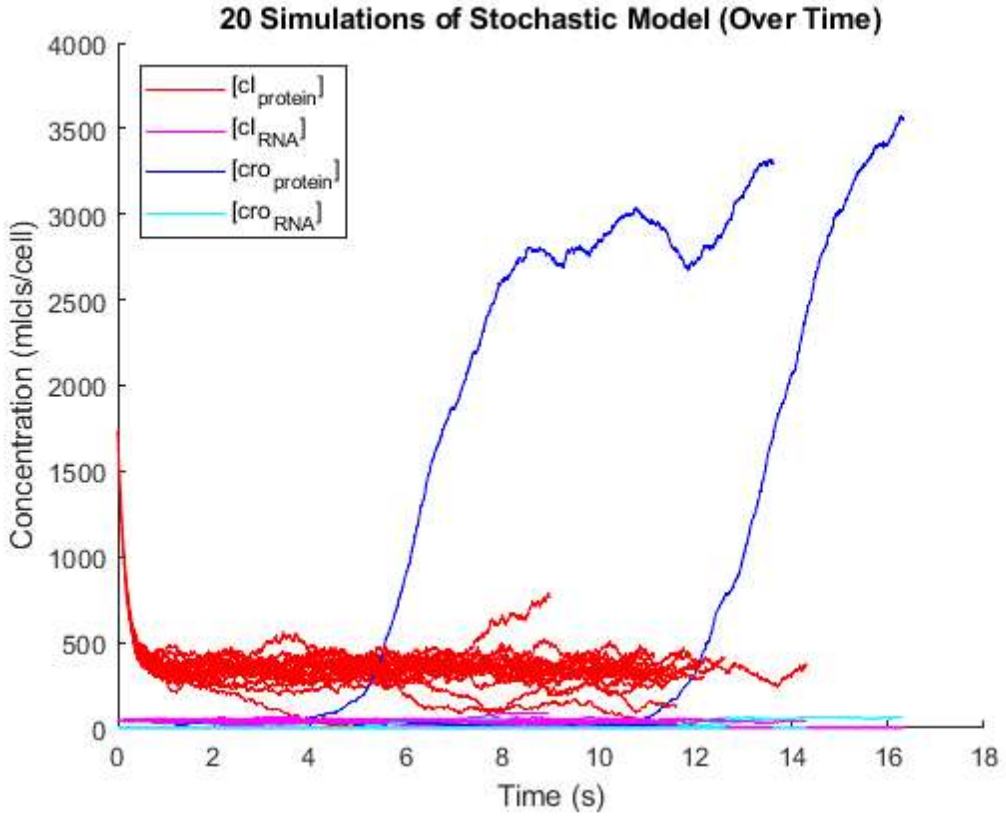
```
clear
close all
```

```
XcI_rna = 1.2; % 1/s
XcI_prot = 6.02; % 1/s
Xcro_rna = 0.8; % 1/s
Xcro_prot = 0.8; % 1/s
wcI = 50; % 1/s
ucI = 50; % 1/s
wcro = 50; % 1/s
ucro = 50; % 1/s
KcI = 10; % mlcl/cell*s
Kcro = 10; % mlcl/cell*s

steps = 50000;
time_points(1) = 0;

cIprot = zeros(1,steps);
cIrna = zeros(1,steps);
croprot = zeros(1,steps);
crorna = zeros(1,steps);
cIprot(1) = 1735.8; % initial concentration
cIrna(1) = 41.6597; % initial concentration
croprot(1) = 0.1296; % initial concentration
crorna(1) = 0.0021; % initial concentration

v1 = zeros(1,steps);
v2 = zeros(1,steps);
v3 = zeros(1,steps);
v4 = zeros(1,steps);
v5 = zeros(1,steps);
v6 = zeros(1,steps);
v7 = zeros(1,steps);
v8 = zeros(1,steps);

fig14 = figure(14);
fig15 = figure(15);
for s = 1:20
    for i = 1:(steps-1)
        v1 = wcI*cIrna(i);
        v2 = XcI_prot*cIprot(i);
        v3 = ucI*(1- ( ((croprot(i))^2) / ((Kcro^2)+((croprot(i))^2)) ));
        v4 = XcI_rna*cIrna(i);
        v5 = wcro*crorna(i);
        v6 = Xcro_prot*croprot(i);
        v7 = ucro*(1- ( ((cIprot(i))^2) / ((KcI^2)+((cIprot(i))^2)) ));
        v8 = Xcro_rna*crorna(i);
        vtotal = v1+v2+v3+v4+v5+v6+v7+v8; %calc total rxn rate

        y = rand();
        tau = -log(y)/(vtotal); %calc time to next rxn
        time_points(i+1) = time_points(i) + tau;

        y_mod = vtotal*rand();
        if y_mod <= v1
            cIprot(i+1) = cIprot(i) + 1; %cIprot syn
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2)
            cIprot(i+1) = cIprot(i) - 1; %cIprot deg
```

```
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i) + 1; %cIrna syn
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i) - 1; %cIrna deg
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i) + 1; %croprot syn
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i) - 1; %croprot deg
            crorna(i+1) = crorna(i);
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6 + v7)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i) + 1; %crorna syn
        elseif y_mod <= (v1 + v2 + v3 + v4 + v5 + v6 + v7 + v8)
            cIprot(i+1) = cIprot(i);
            cIrna(i+1) = cIrna(i);
            croprot(i+1) = croprot(i);
            crorna(i+1) = crorna(i) - 1; %crorna deg
        else
            Disp('error');

        end
    end

    set(0, 'CurrentFigure', fig14)
    hold on
    plot(cIprot, croprot)

    set(0, 'CurrentFigure', fig15)
    hold on
    plot(time_points, cIprot, 'r')
    plot(time_points, cIrna, 'm')
    plot(time_points, croprot, 'b')
    plot(time_points, crorna, 'c')
end

set(0, 'CurrentFigure', fig14)
xlabel('[cI_{protein}] (mlcls/cell)')
ylabel('[cro_{protein}] (mlcls/cell)')
title('20 Simulations of Stochastic Model (Phase Plane)')
xlim([0 1500])
ylim([0 1500])
hold off
```

```
set(0, 'CurrentFigure', fig15)
xlabel('Time (s)')
ylabel('Concentration (mlcls/cell)')
title('20 Simulations of Stochastic Model (Over Time)')
legend('[cI_{protein}]', '[cI_{RNA}]', '[cro_{protein}]', '[cro_{RNA}]', 'Location','northwest')
hold off
```





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