Homework Cover Sheet

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Homework # (Unit): module 2

I did the project completely on my own. I did not discuss any of the problems with anyone in the class and did not share any of my work with others. However, I did make extensive use of class text(s), (mini)lectures, Wikipedia, and MathWorks.

By signing below, I attest that the statements made above represent a complete accounting of the materials I used in completing this assignment. I understand that the failure to disclose the use of any resource is an act of academic dishonesty subject to penalty by the Academic Judiciary.

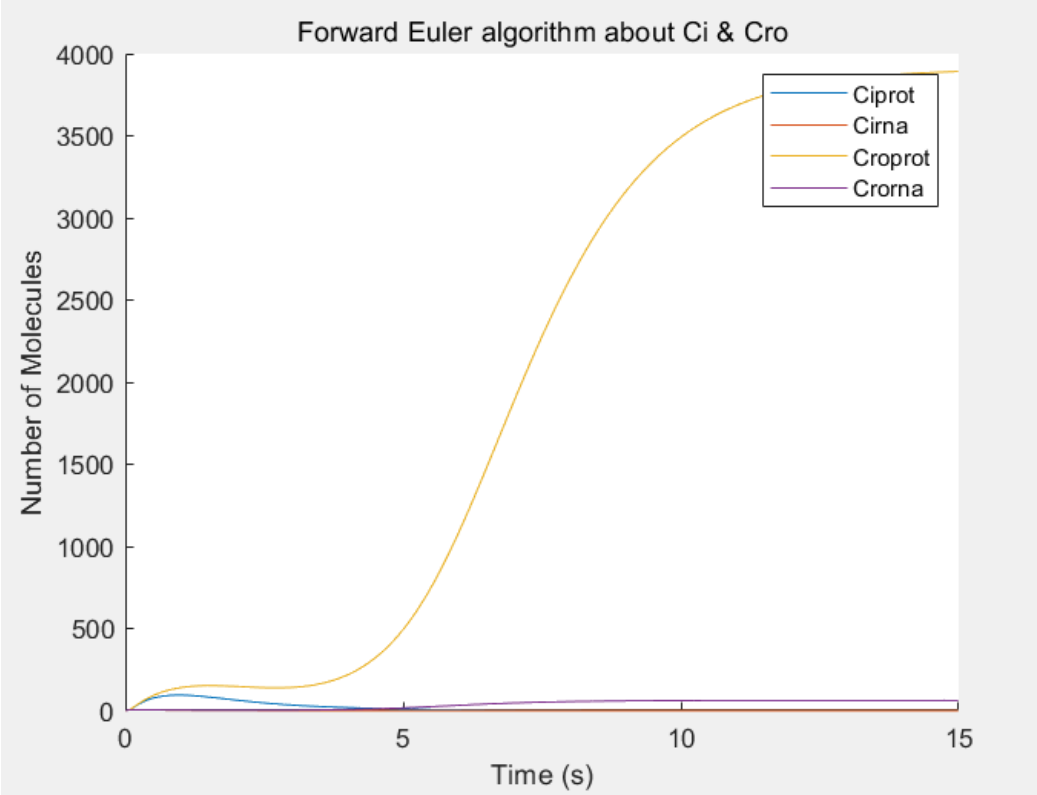
Signature: David Hwang

Date: Feb 24 2024

Part A

1.

Since all the plots in cases 1&2&3 seem to reach a plateau after 15, I set the total length 15(s).

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% case 2 with starting only with 20 molecules of cro RNA present
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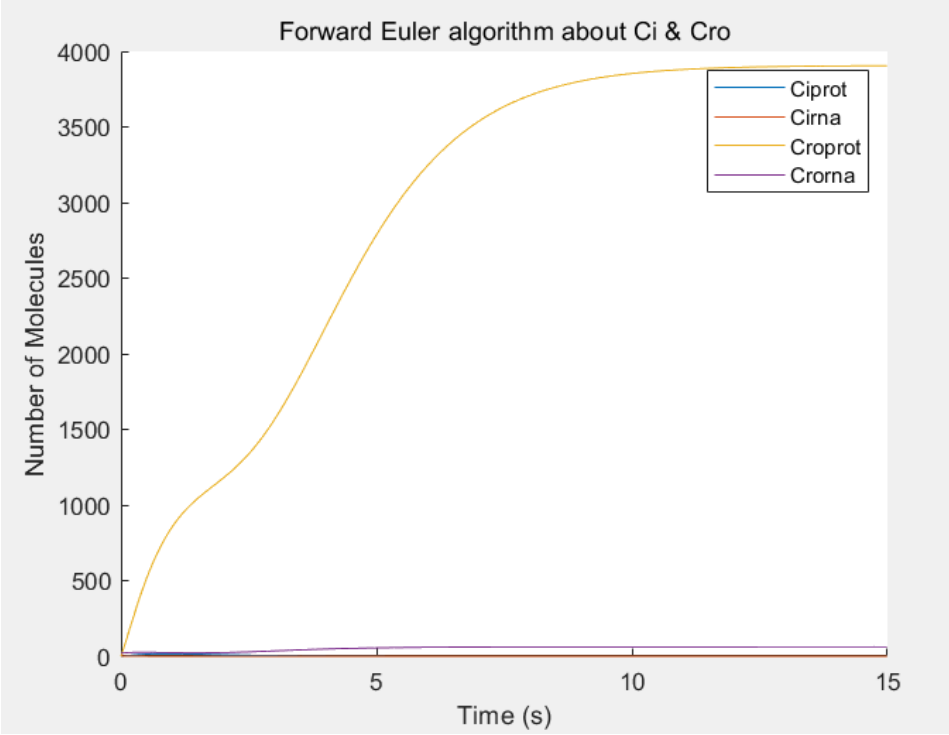

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% case 3 with starting only with 50 molecules of cI RNA present
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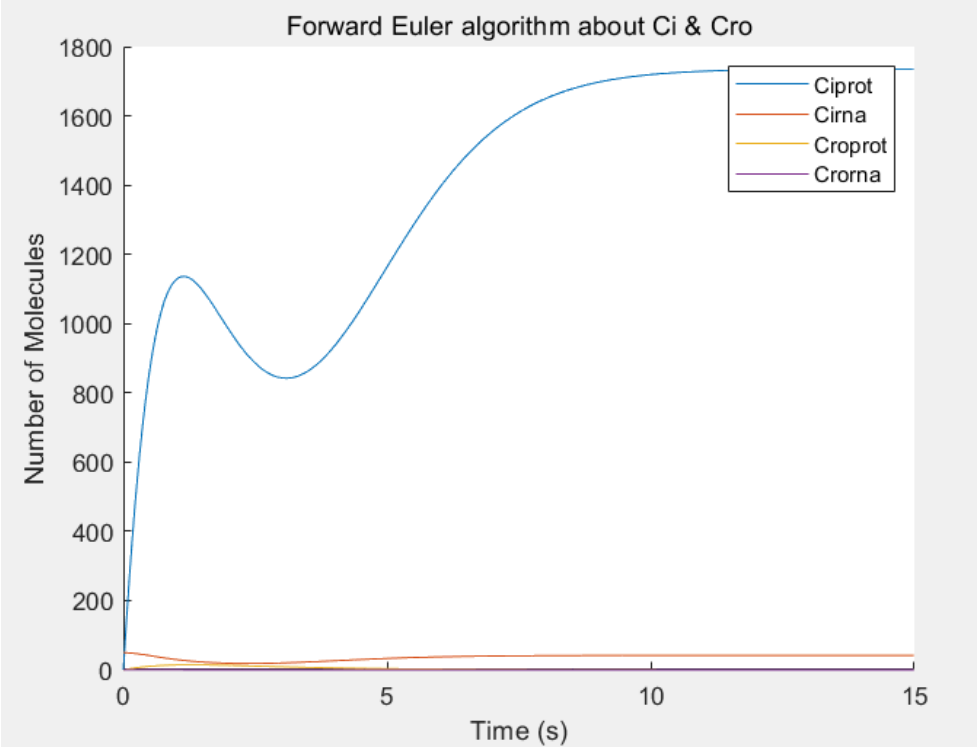

2.

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%%%% 2
%%%% 2-(1)
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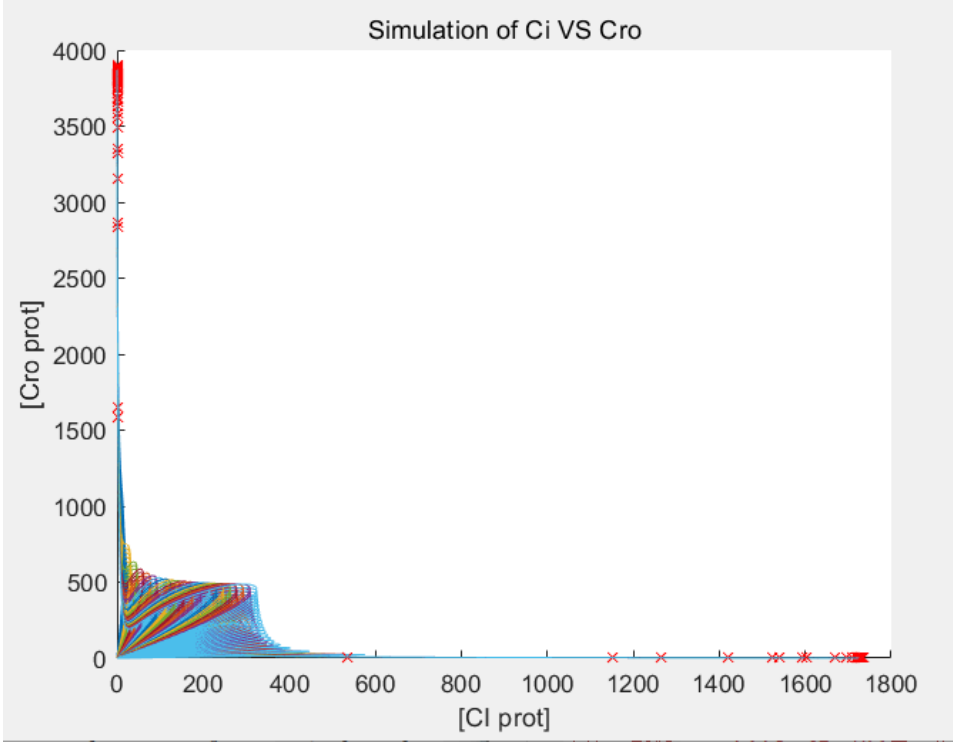
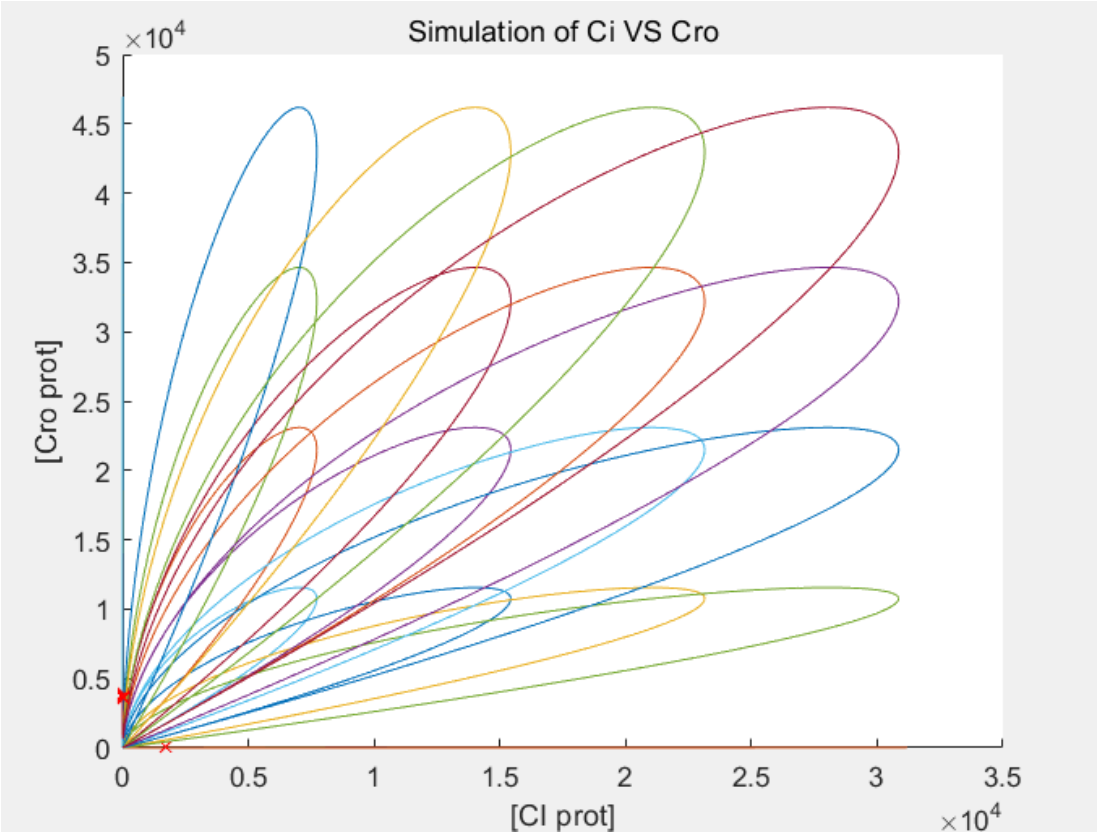


%%%% 2-(2)

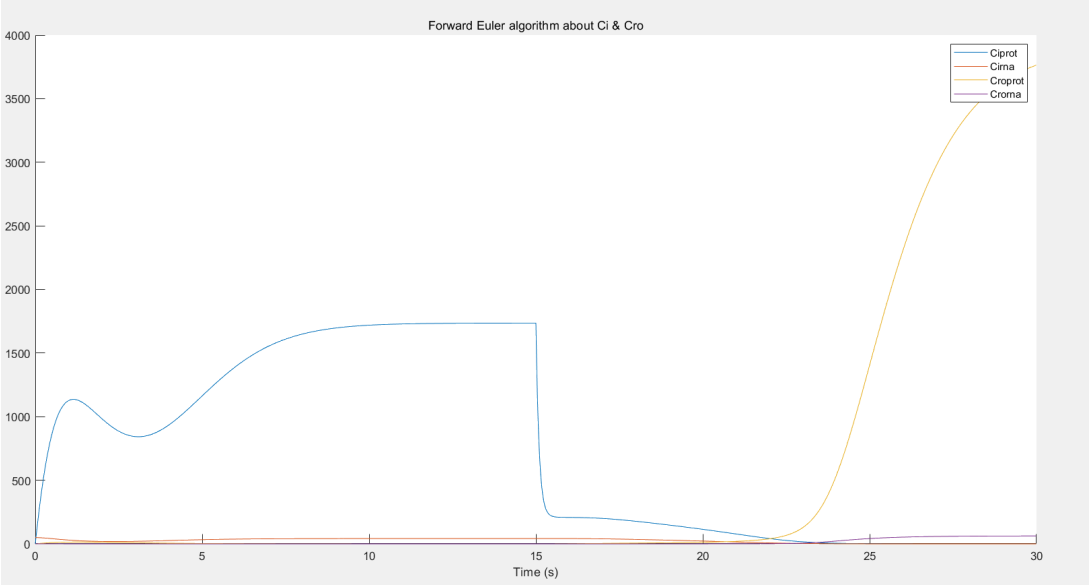


3.

From 1, we found that when we start a simulation with all initial concentrations set to 0, the number of Cro protein molecules increases a lot and this will lead to lysis infection. So basically, when the Cro and CI have the same initial condition(about the number of rna molecules), the infection would be lysis. But when the number of molecules of Ci rna is more than the others, this will lead the infection to lysogeny. However from 2-(2) we can see that there is only one condition that ended up at high [CI prot], this implies that only when we start at the number of CI rna molecules is much more than Cro rna, the infection can become lysogeny and if not, the infection will be lysis as a typical case.

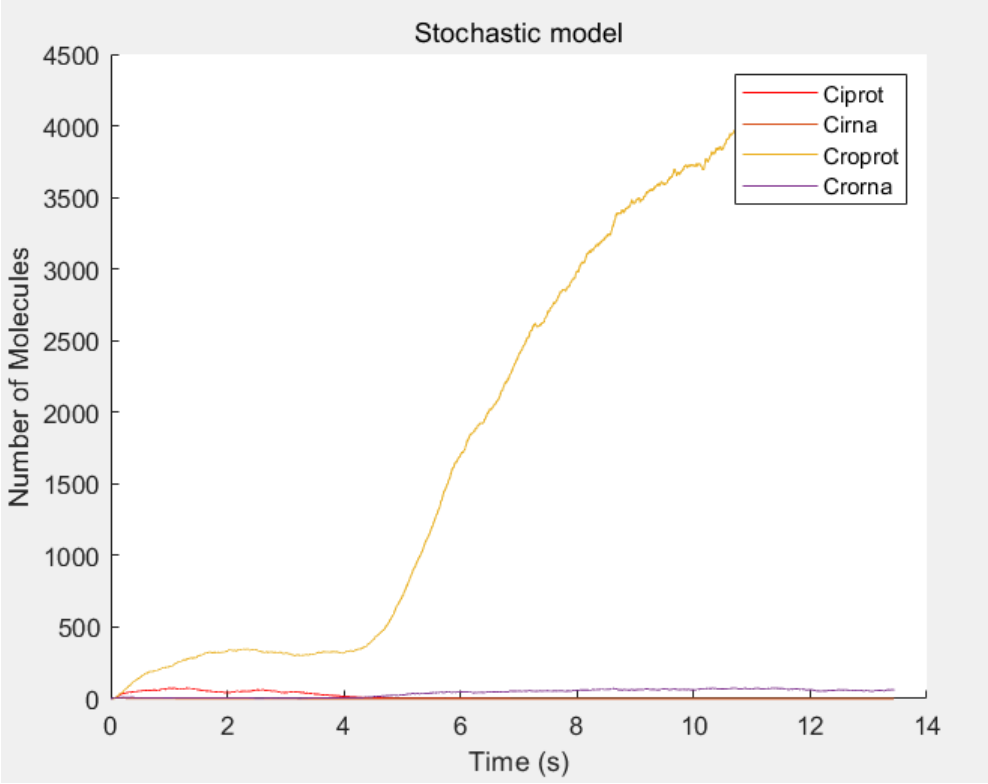
4.

Since stress condition increases degradation of CI protein, a constant (Xci,prot) should be increased. When we start with many Ci RNA molecules, this induces many Ci protein molecules and leads the stable lysogeny. However, if the stress input, Xciprot would increase and this decreases the number of Ci proteins and increases the number of Cro proteins. So the state can be changed to lysis even when we are in a stable lysogenic state. I changed Xci,prot from 1.2 to 10 when the states were in stable lysogeny.



Part B

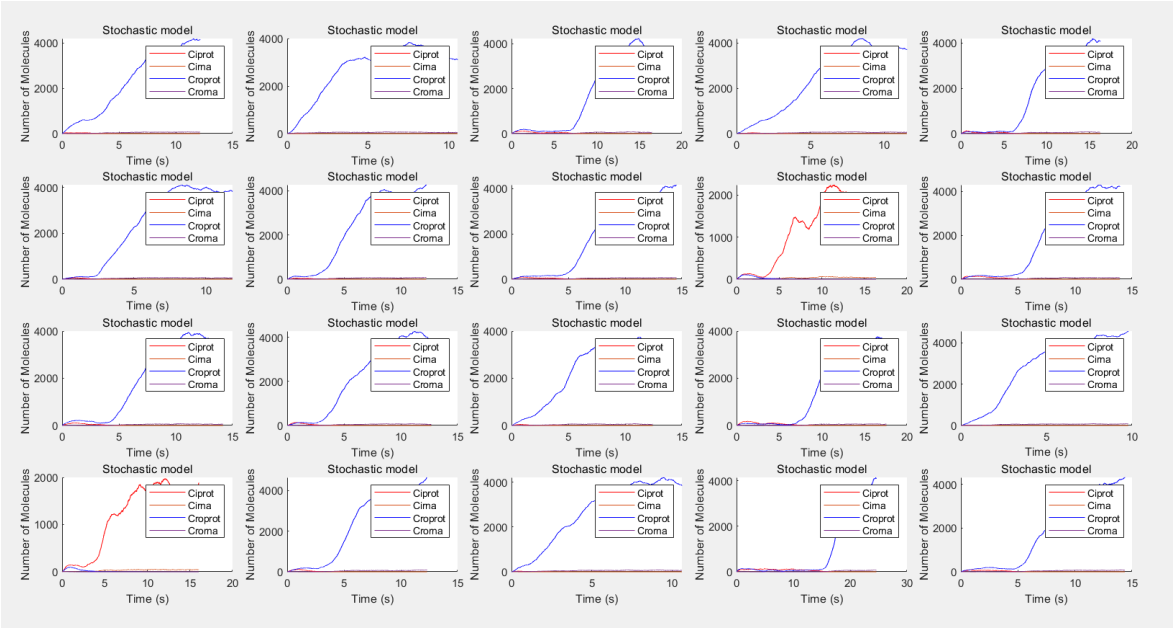
1.

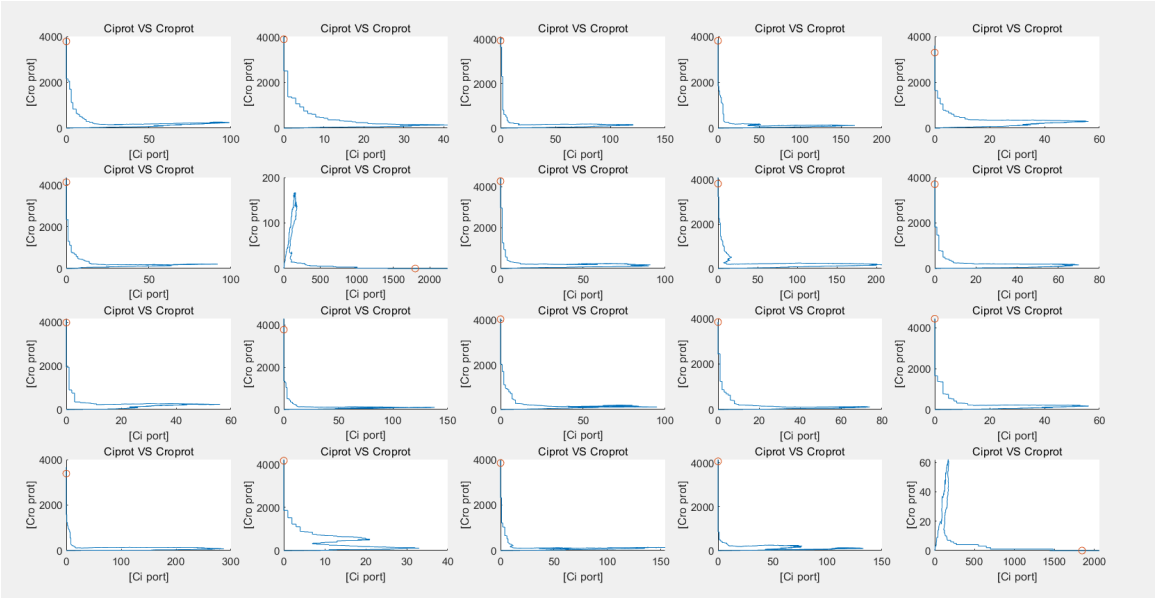


Starting with all concentrations equal to zero, the number of molecules of cro increases the most and the infection state becomes lysis. It can be seen from the graph that when the number of molecules of Ci protein increases, the slope of the graph of Cro protein decreases. Also, as

soon as Ci decreases, cro increases rapidly. Through this, it can be confirmed that Ci is an inhibitor of cro.

2.



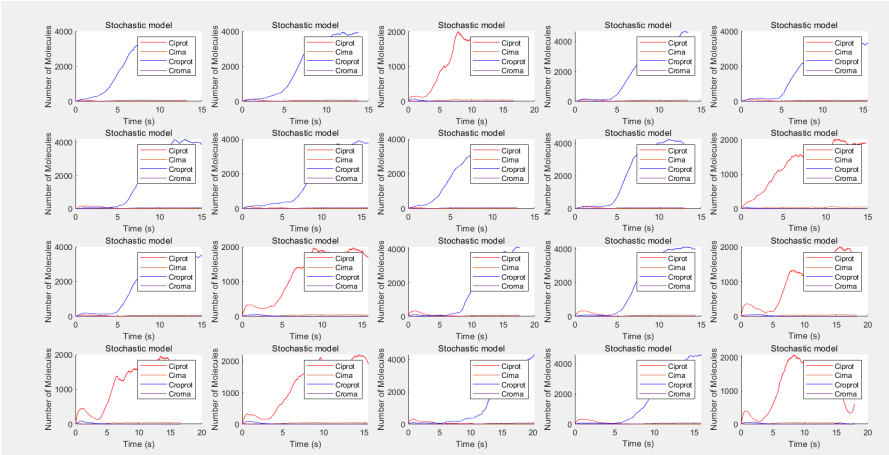


Red circles in the phase plane indicate endpoints.
In most cases, the number of Ci proteins increases and then goes to a lytic state, but sometimes the number of Ci proteins increases and leads to a lysogenic state. In the phase plane, similarly, when we begin with all concentrations equal to 0, in most cases, the states go to lysis. When we see the phase plane graph above, it can be seen that [Ci prot] and [Cro prot] are inversely proportional. And the graph against time also

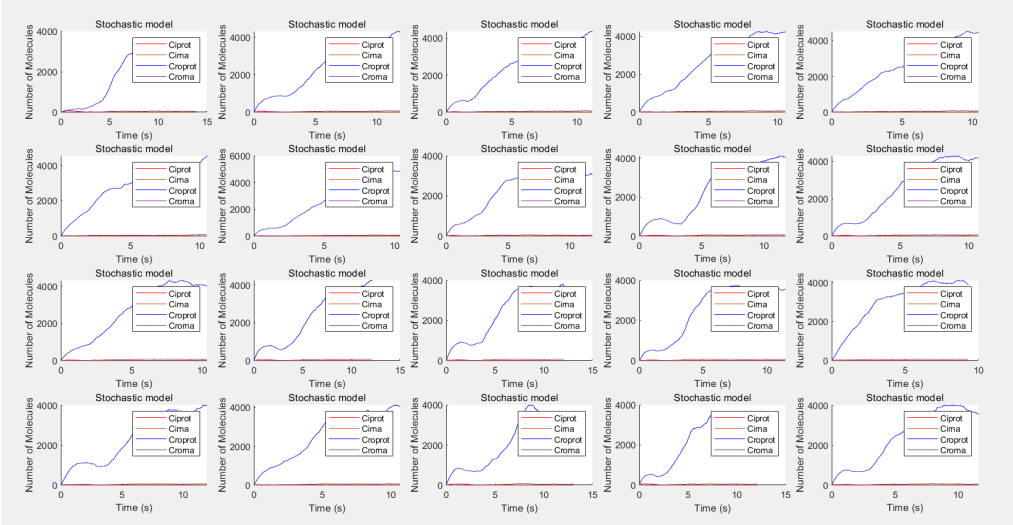
confirmed that there was no case of having a very large number of molecules at the same time as cro and ci. Also, as the number of Cro increases through the phase plane, the number of Ci decreases, and as Ci increases, Cro decreases.

3.

I started with 20 molecules of Ci RNA



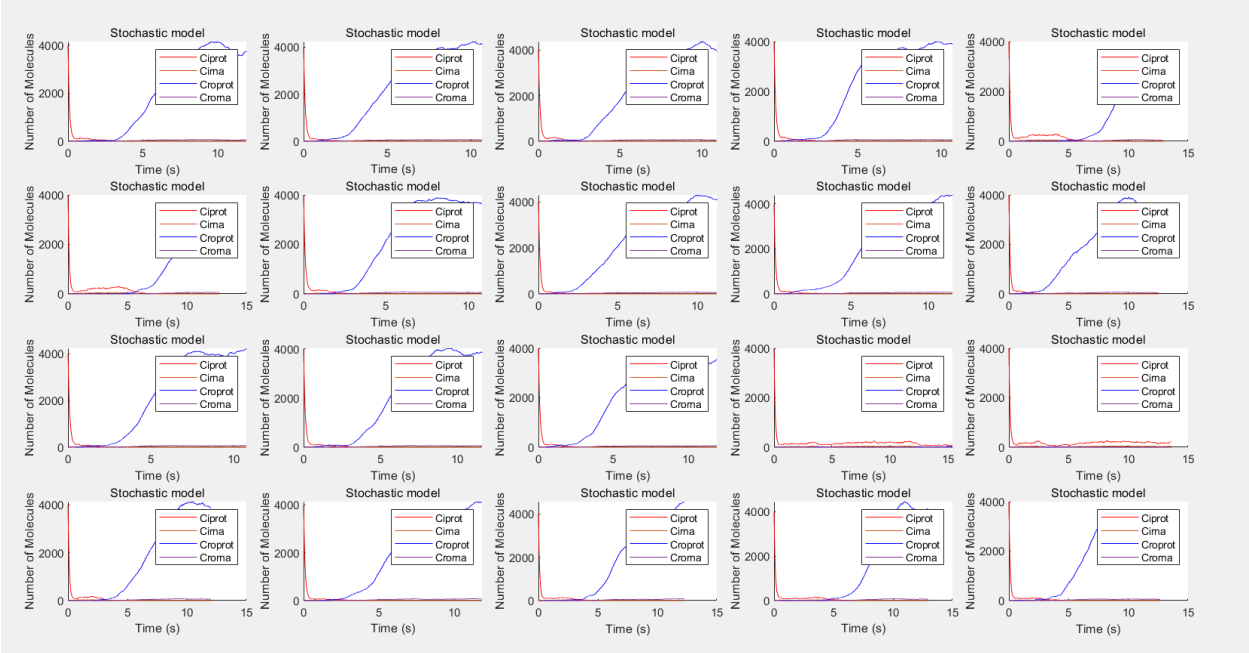
I started with 20 molecules of Cro RNA



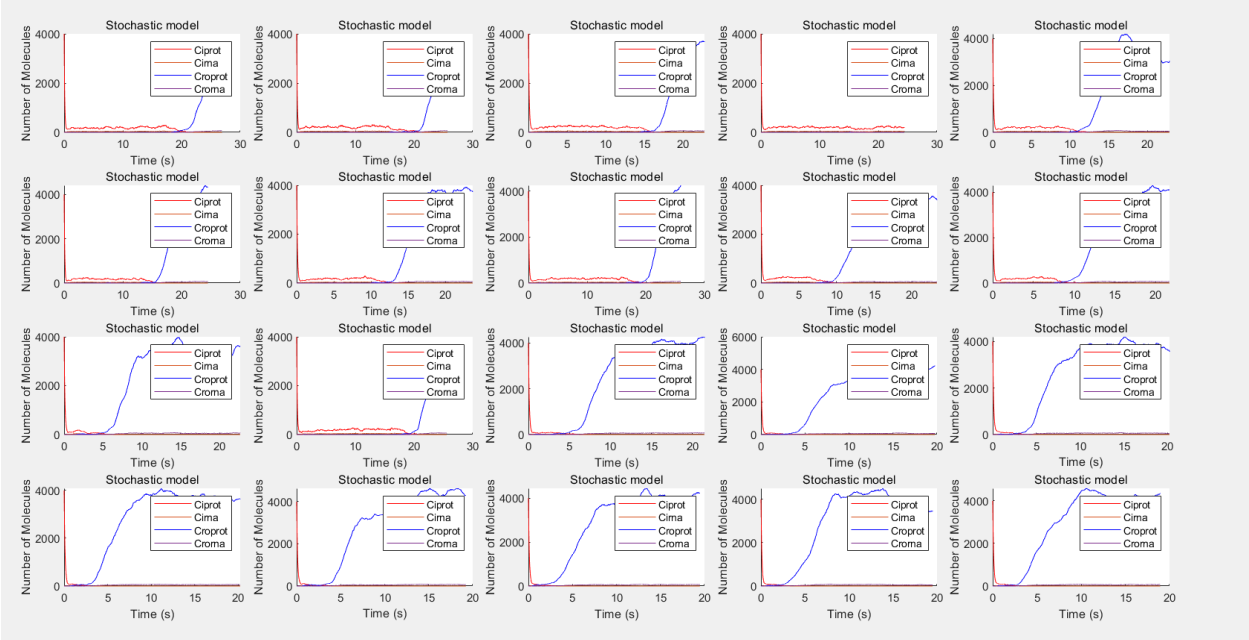
When we set [Ci rna] greater than [Cro rna] for the initial value, the number of ci proteins increased, and the number of cases going to lysogeny increased (the red line means the number of Ci proteins). On the other hand, when the initial value of [Cro rna] is greater than that of [Ci rna], it was confirmed that almost all of the cases went to the state of lysis (the blue line means the number of Cro proteins).

4.

When the number of steps is 50,000



When the number of steps is 100,000



We started the simulation with stable lysogeny with only 40000 Ci protein molecules. When the stress was received and set that the Xciprot increased to 10, we can see that in most cases in the stochastic model, the number of Ci proteins also decreased and the number of Cro proteins increased, converging to stable lysis.

The length of the simulation is significant here. When we run a simulation for 50000 steps, the number of Ci proteins decreased in many cases. However, there were cases where the infection state was not stable because the increase in the number of Cro proteins did not occur yet. In addition, looking at the graphs when the number of steps was set to 100000, it was confirmed that there were cases where the number of Ci protein increased only after 20 seconds and became stable lysis. Therefore, it is necessary to give enough time for the reaction to occur so that we know which stable state it converges to.

5.
Using a deterministic model, it is possible to know through average results what reactions occur and what state these reactions lead to in the biological situation. On the other hand, stochastic models utilize the biological characteristic that molecular interactions occur randomly. Therefore, it shows more realistic results in actual biological situations than a deterministic model. However, stochastic simulations have difficulty obtaining consistent results due to the nature of random probability. So stable results must be obtained by running multiple stochastic simulations or a deterministic model.