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HW #4

1. A fixed point is the equivalent to a stationary point and is defined by a point where the derivative of all functions on a graph is zero. In this case, it is where the change in protein concentration, as well as the change in mRNA concentration, is zero. To analyze the equations for fixed points, I will solve for each equation resulting in 0 in cases.

For equation 1:

When either ω or [Xrna] are equal to 0, and χprot or [Xprot] is equal to 0, there is a is a null cline for this equation. Additionally, there is a null cline for when $\omega[Xrna] = \chi prot[Xprot]$.

For equation 2:

When either μ or $[Xprot]^2$ are equal to 0, and χrna or [Xrna] is equal to zero, there is a null cline for this equation. Additionally, when $\mu[Xprot]^2/(K_{1/2}^2+[Xprot]^2) = \chi rna[Xrna]$, there is a null cline.

When both null clines intersect, there is a fixed point on the graph. I will list all fixed points.

(1) When $\mu[Xprot]^2/(K_{1/2}^2+[Xprot]^2) = \chi rna[Xrna]$ and $\omega[Xrna] = \chi prot[Xprot]$
(2) When [Xprot] and [Xrna] are both equal to 0
(3) When χprot, χrna, μ, and ω are all equal to 0
(4) When [Xrna], χprot, and μ are all equal to 0
(5) When [Xprot], ω, and χrna are all equal to 0

2.

Code

```
%This program uses the forward euler method to create 3
graphs representing the
%protein and RNA concentrations
a = 0:.01:.1;
%This creates a vector for the time that has passed
b1 = zeros(1,11);
b2 = zeros(1,11);
%This initializes a vector for the population values
b1(1) = 3;
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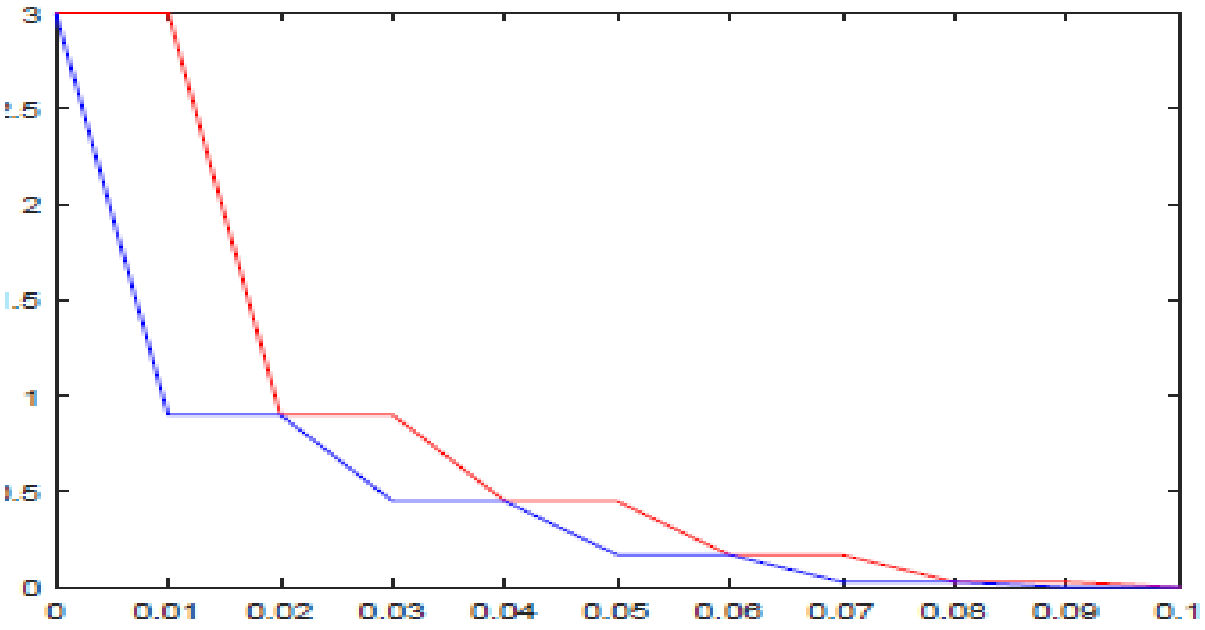
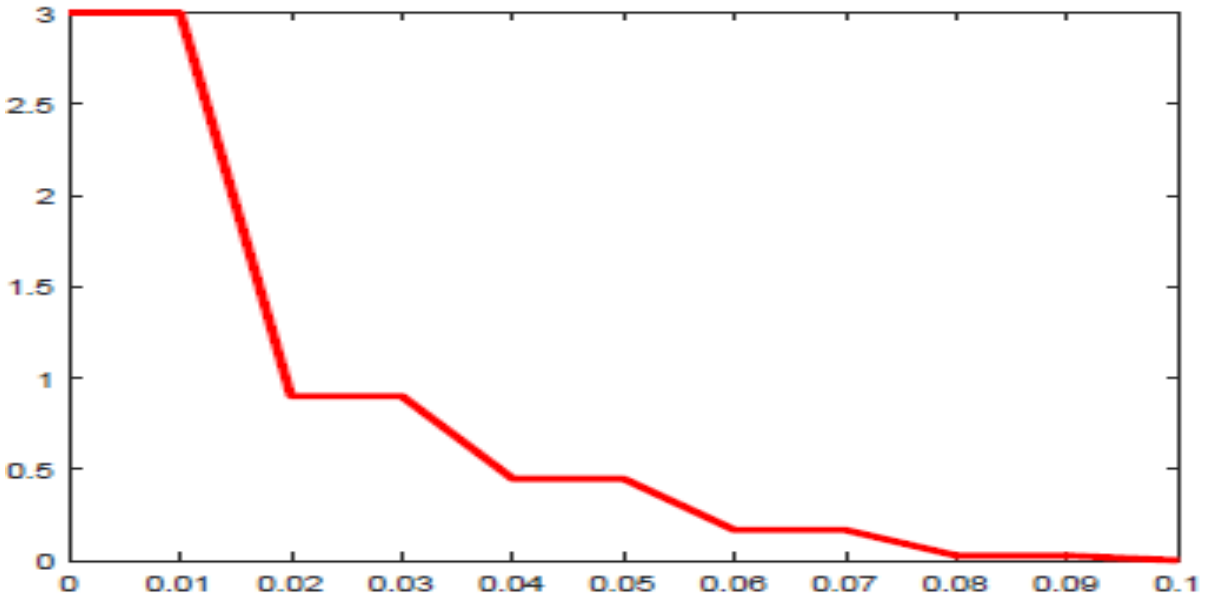
```
b2(1) = 3;
%This sets the initial population
for i = 2:11
    x = b2(i-1)-b1(i-1);
    y = ((b1(i-1))^2)/(1+(b1(i-1))^2)-b2(i-1);
    %This finds the product of the derivative and the
interval of time
    b1(i) = (b1(i-1))+x;
    b2(i) = (b2(i-1))+y;
    %This sums the i-1 value and the derivative times the
interval of time.
end
%This loop inputs values for a vector for the number of
yeast cells after a
%given time interval
fig1 = figure(1);
plot(a,b1,'-r',a,b2,'-b')
fig2 = figure(2);
plot(a,b1,'-r','LineWidth',3.0)
fig3 = figure(3);
plot(a,b2,'-b','LineWidth',3.0)
%This creates all plots with the requested parameters
%and changes the handle of the plotted figures to fig1,2,
and 3
print(fig1,'BothConcentrationsOverTime','-dpdf')
print(fig2,'ConcentrationOfProteinOverTime','-dpdf')
print(fig3,'ConcentrationOfRNAOverTime','-dpdf')
%This saves the figures as a pdf
```

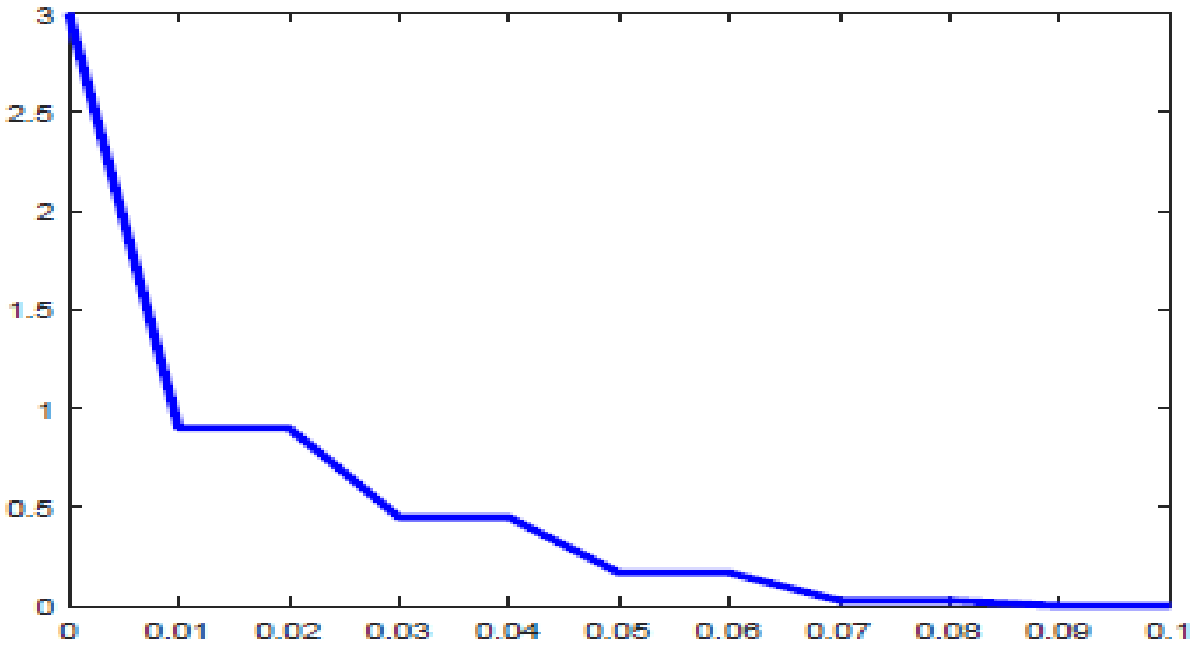
Execution



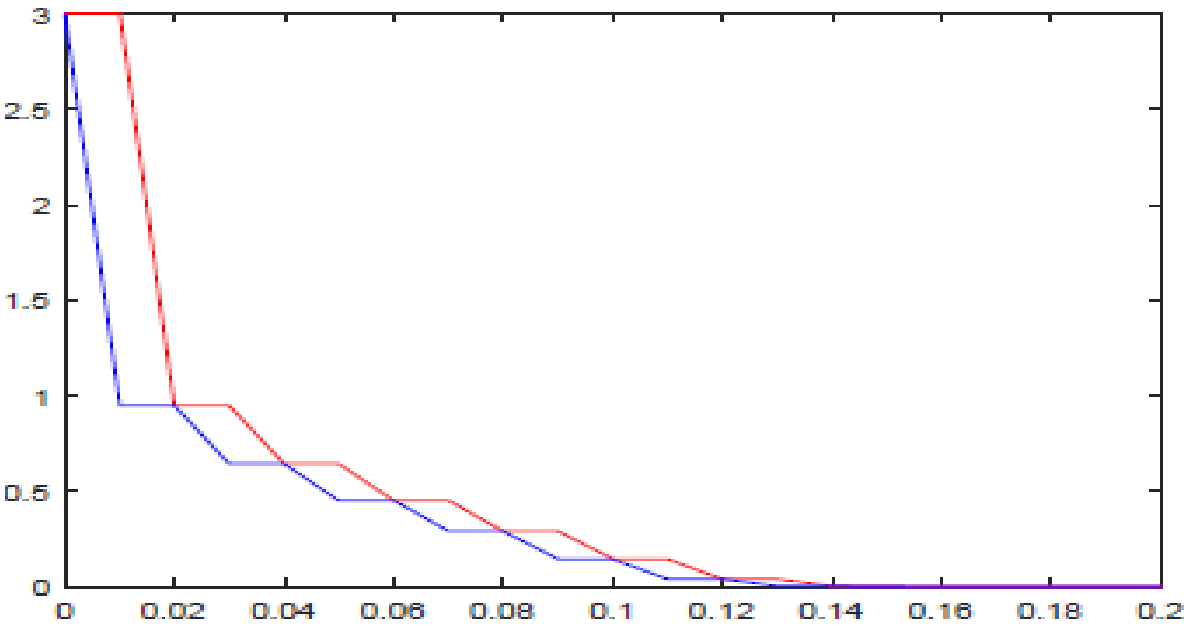
This graph shows both concentrations over time, and it is apparent that the only stationary point exists when both concentrations are 0, when there is a k value of 1. The stationary point is stable.



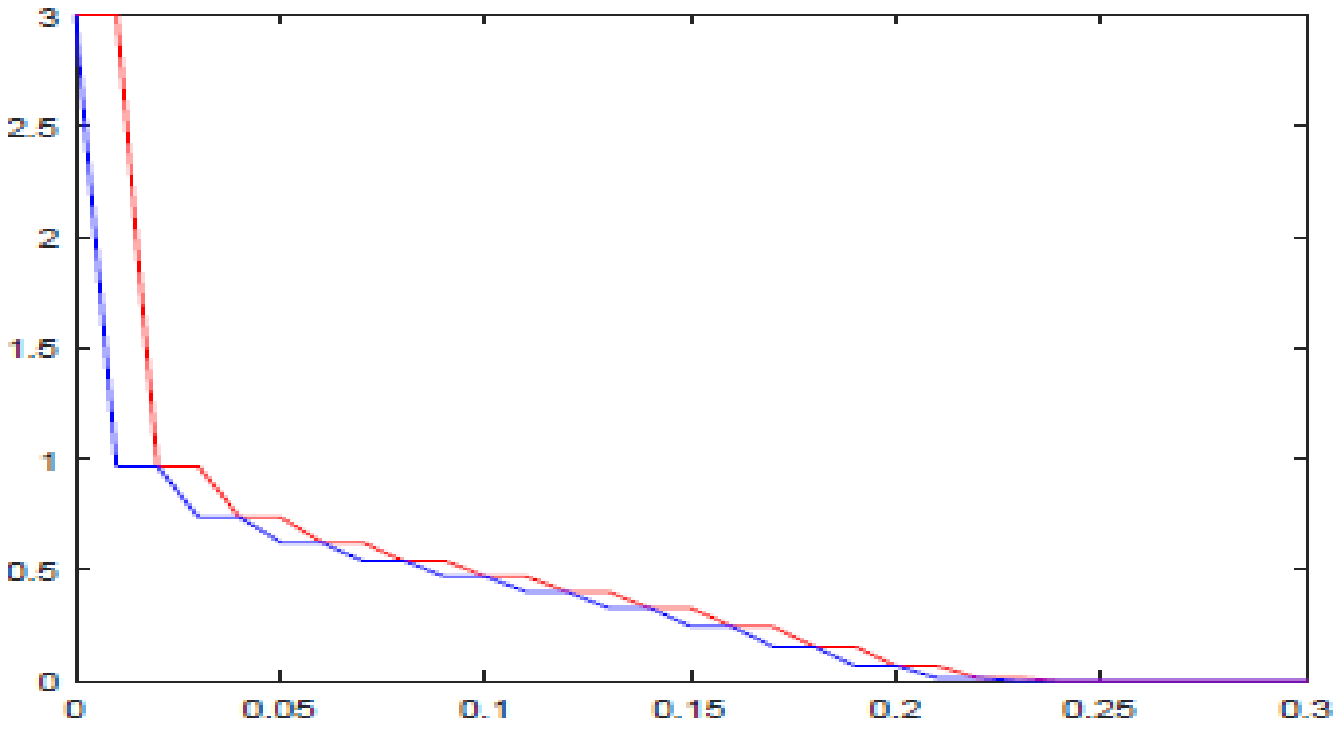
This graph shows the concentration of protein over time.



This graph shows the concentration of RNA over time.



This graph shows both concentrations over time, and it is apparent that the only stationary point exists when both concentrations are 0, when there is a k value of .5. The stationary point is stable.



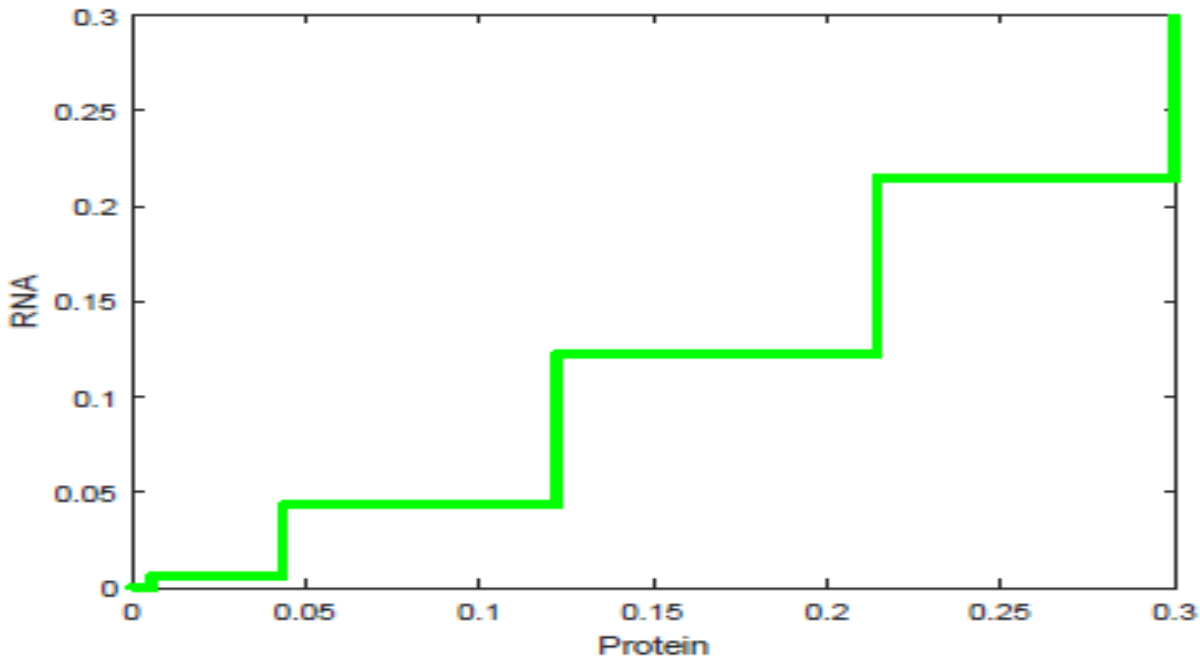
This graph shows both concentrations over time, and it is apparent that the only stationary point exists when both concentrations are 0, when there is a k value of .33. The stationary point is stable.

3.

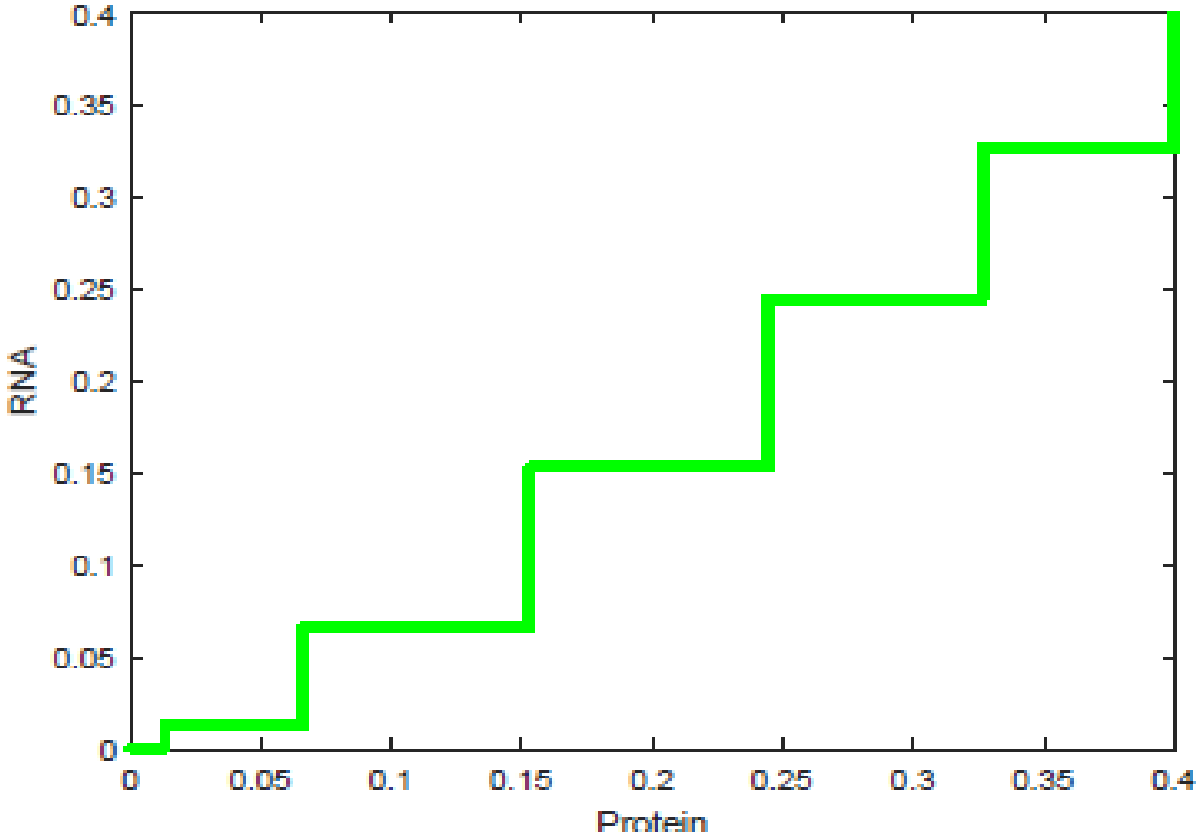
Code

```
%This program uses the forward euler method to create 3
graphs representing the
%protein and RNA concentrations
a = 0:.01:.3;
%This creates a vector for the time that has passed
b1 = zeros(1,31);
b2 = zeros(1,31);
%This initializes a vector for the population values
b1(1) = .1;
b2(1) = .1;
%This sets the initial population
for i = 2:31
    x = b2(i-1)-b1(i-1);
    y = ((b1(i-1))^2)/(.33+(b1(i-1))^2)-b2(i-1);
    %This finds the product of the derivative and the
interval of time
```

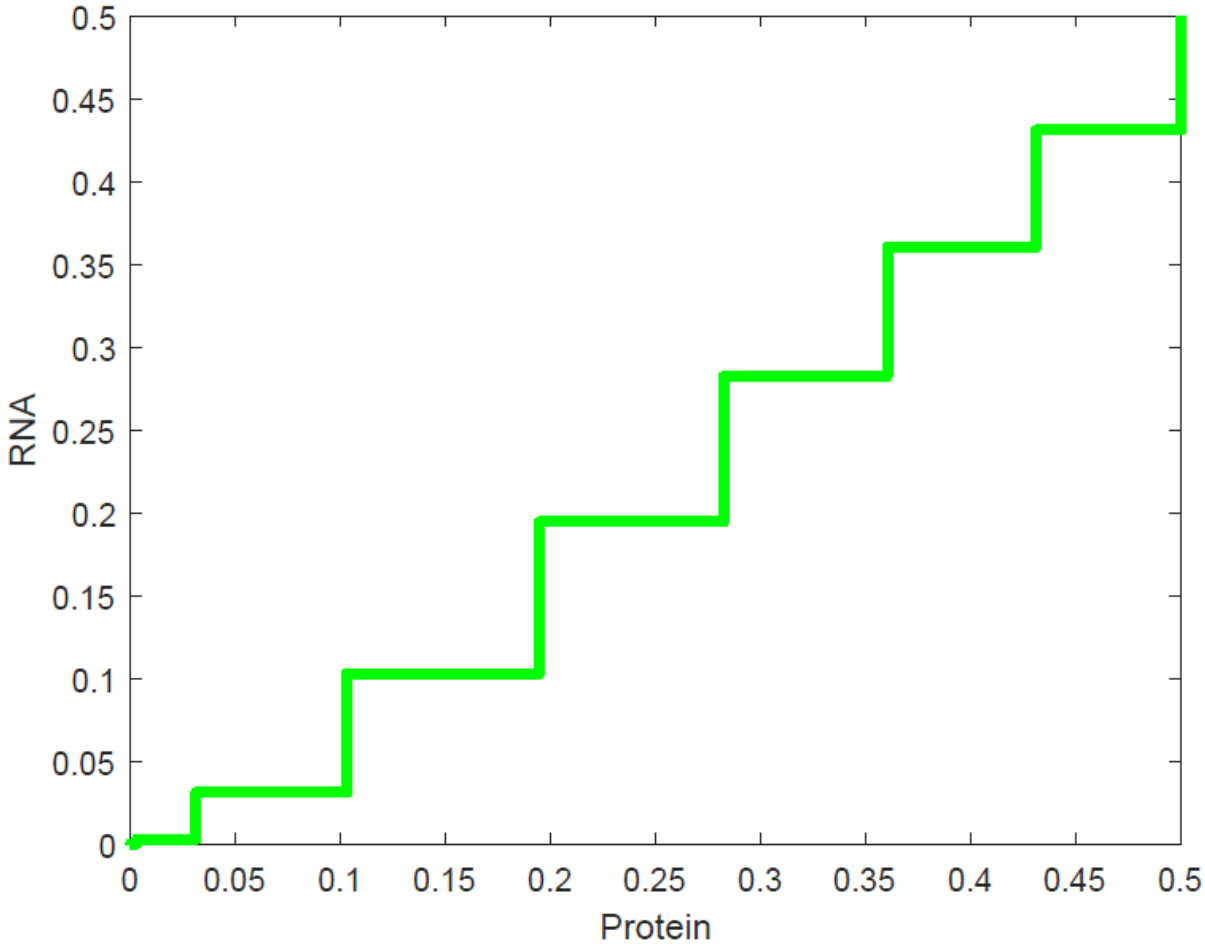
```
    b1(i) = (b1(i-1))+x;
    b2(i) = (b2(i-1))+y;
    %This sums the i-1 value and the derivative times the
interval of time.
end
%This loop inputs values for a vector for the number of
yeast cells after a
%given time interval
fig1 = figure(1);
plot(a,b1,'-r',a,b2,'-b')
fig2 = figure(2);
plot(a,b1,'-r','LineWidth',3.0)
fig3 = figure(3);
plot(a,b2,'-b','LineWidth',3.0)
fig4 = figure(4);
plot(b1,b2,'g','LineWidth',3.0)
xlabel('Protein')
ylabel('RNA')
%This creates all plots with the requested parameters
%and changes the handle of the plotted figures to fig1,2,
and 3
print(fig1,'BothConcentrationsOverTime','-dpdf')
print(fig2,'ConcentrationOfProteinOverTime','-dpdf')
print(fig3,'ConcentrationOfRNAOverTime','-dpdf')
print(fig4,'ConcentrationofProteinVsRNA','-dpdf')
%This saves the figures as a pdf
```



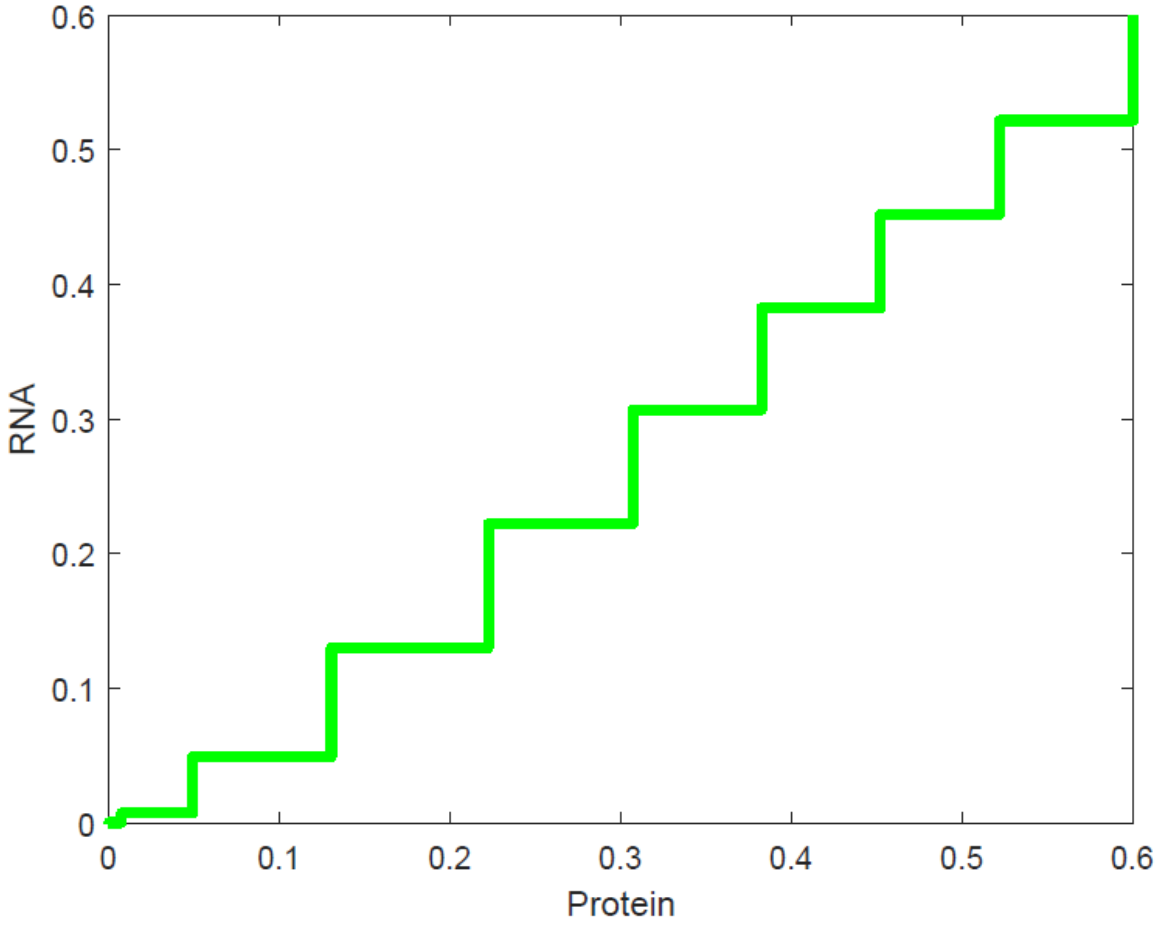
Protein vs RNA at a starting concentration of .3 each



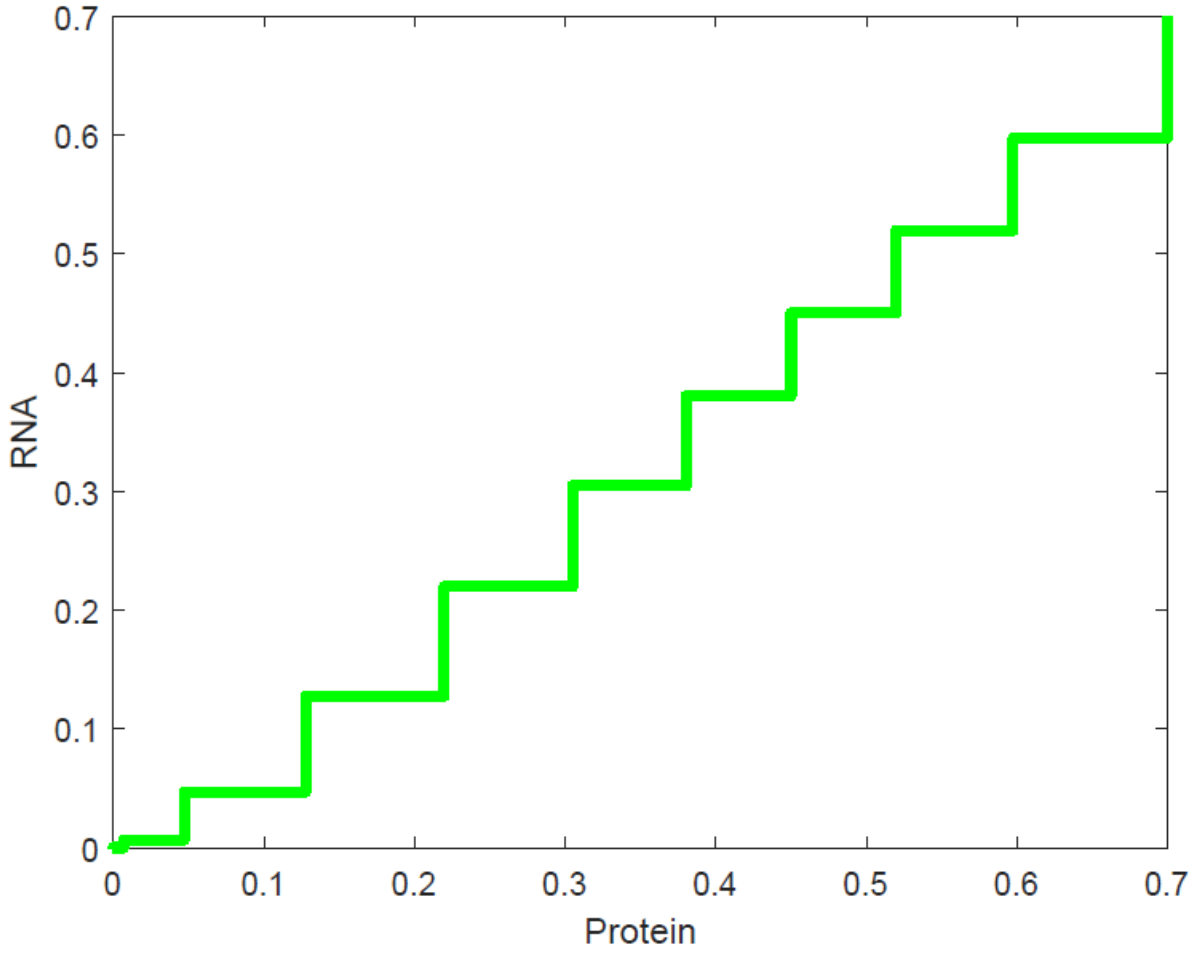
Protein vs RNA at a starting concentration of .4 each



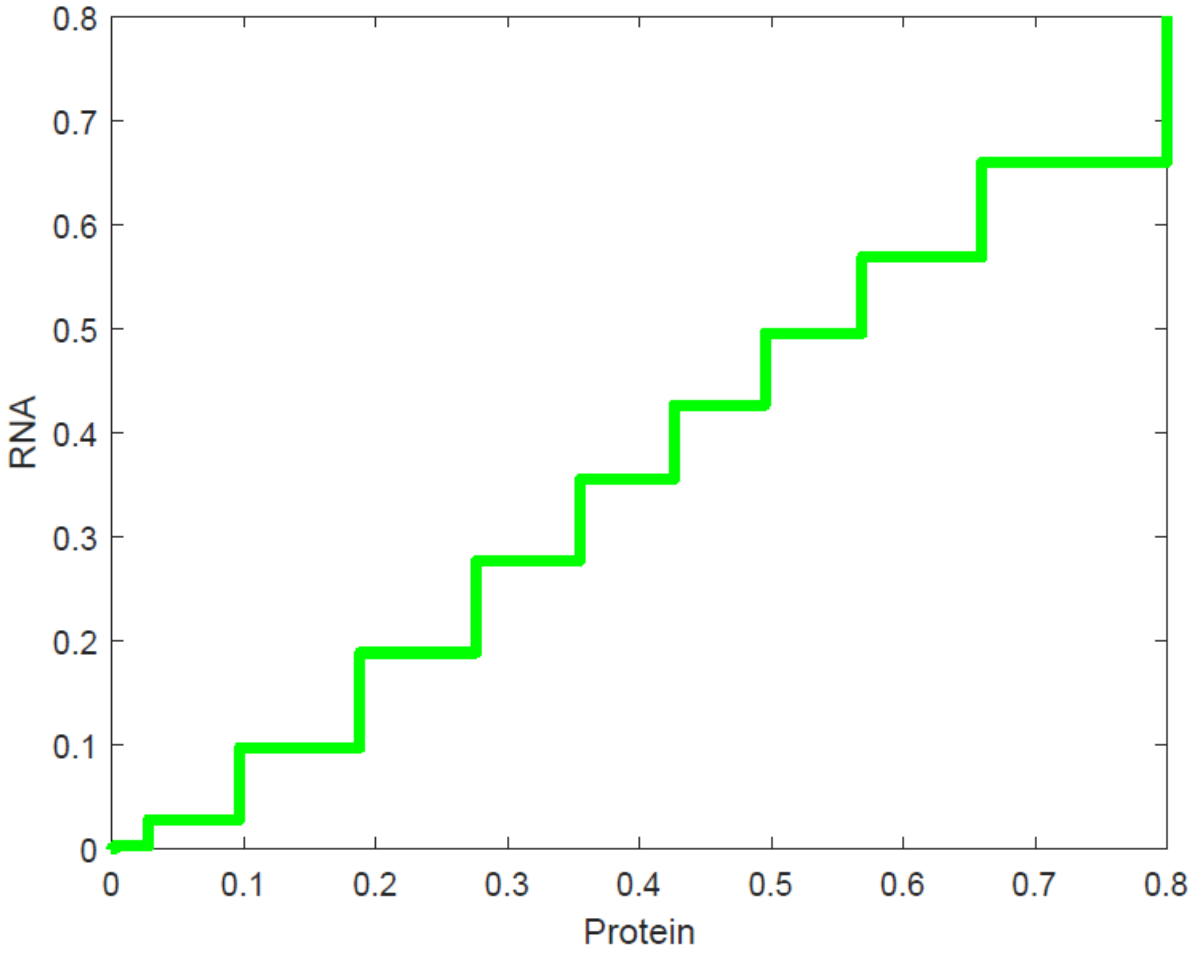
Protein vs RNA at a starting concentration of .5 each



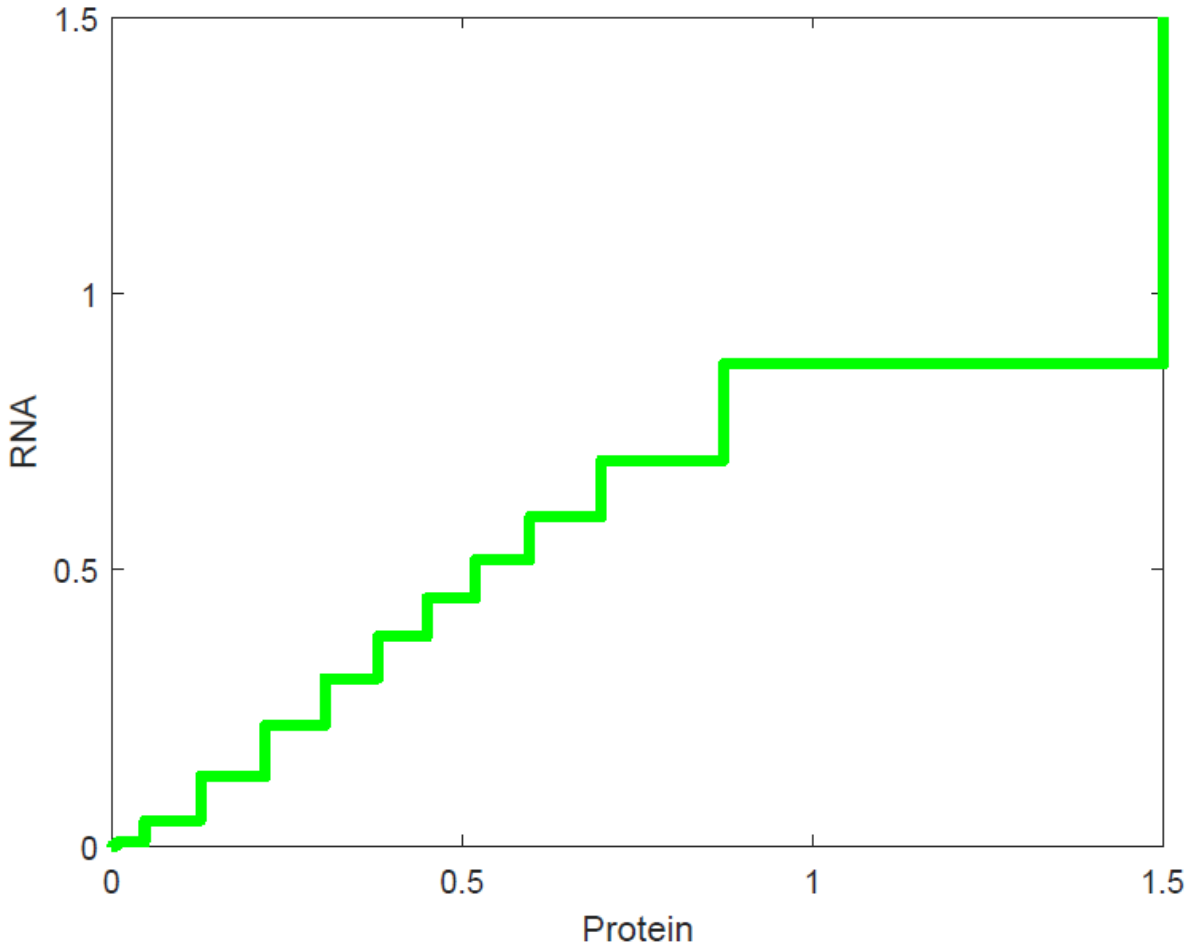
Protein vs RNA at a starting concentration of .6 each



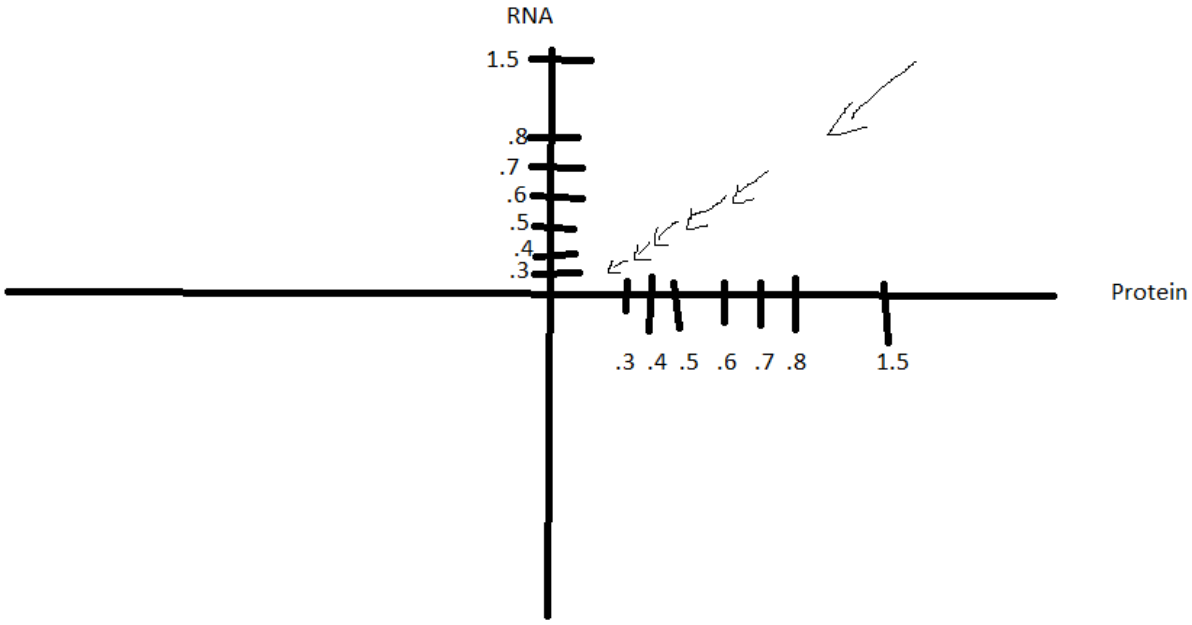
Protein vs RNA at a starting concentration of .7 each



Protein vs RNA at a starting concentration of .8 each

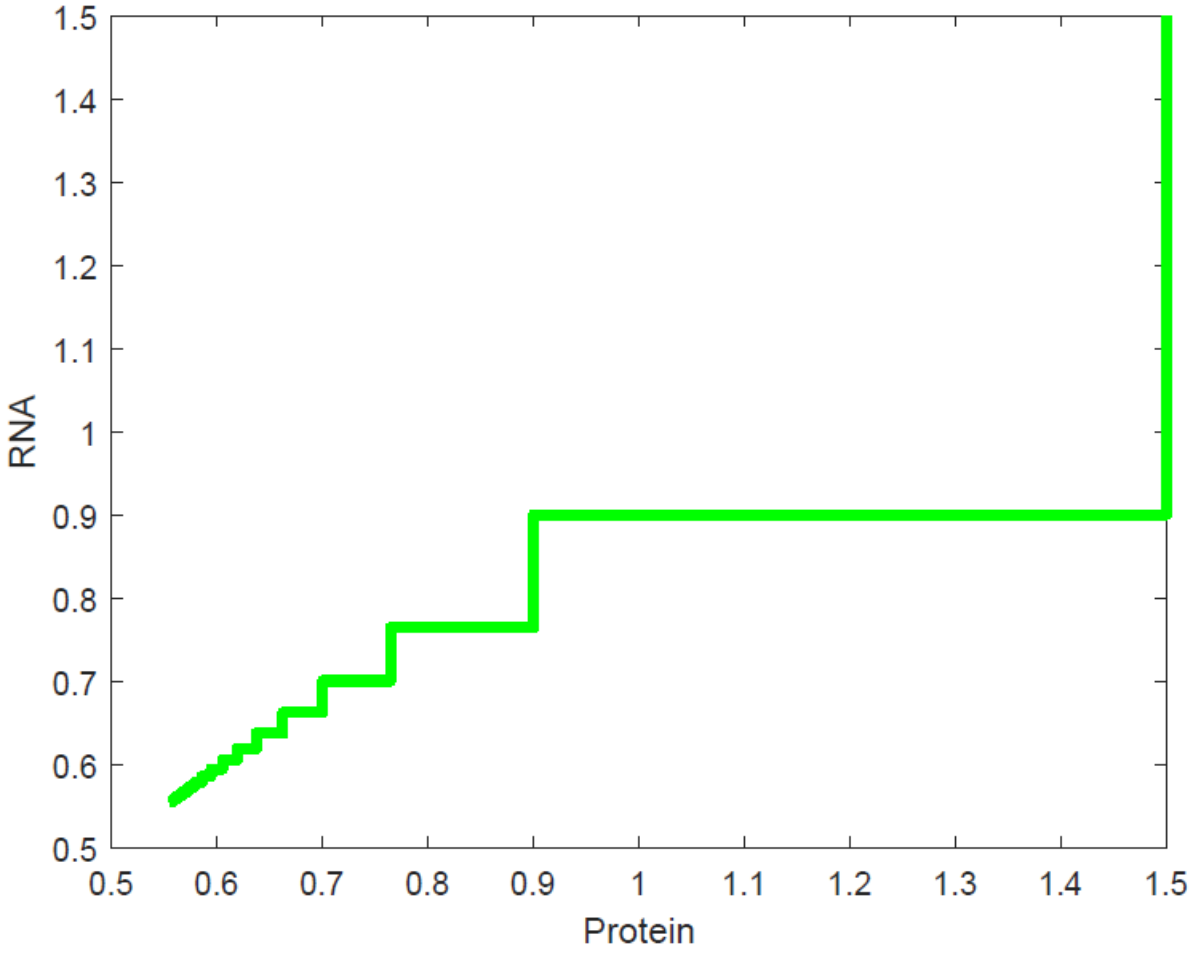


Protein vs RNA at a starting concentration of 1.5 each



The above graph shows the slope field using the provided graphs from MATLAB coding. It is not drawn to scale, but signifies the fact that the stationary point is stable at 0.

4. There are some noteworthy features about the graphs that were produced. To start, the graphs showed a relatively large negative slope using a starting concentration of 1.5, as opposed to the small negative slope at approximately .5. Furthermore, the slope then became more negative, though not significantly, when under a concentration of .5. This may signify the face that there is autoregulation, using negative feedback, to maintain homeostasis in the production of proteins via the central dogma of biology. When there is too much protein or RNA. The system quickly dissociates them. When there is relatively little, it dissociates them at a much slower pace. However, the equations were made extremely artificial by the fact that all constants were made to be a value of 1, aside from the dissociation constant. Hence, these results should not be taken to signify what happens in an actual biological environment. Additionally, it should be noted that there are stationary points aside from 0, even when all the other constants are made to be 1. After playing around with the dissociation constant, I found that a value of .25 for the dissociation constant allows another stable stationary point, demonstrated in the graph below.



This shows that there are numerous stationary points, stable or otherwise, given proper values to all relevant constants.