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Unit 1: Introduction to modeling cellular physiology

Project 1 Report

Part A: Understanding the Hill equation

1. Plotting the Hill equation with varying h, $K_{1/2}$, and V_{max}. (d) is the text under each of the three plots.

   (a) Hill equation with h=1, 2, and 10.

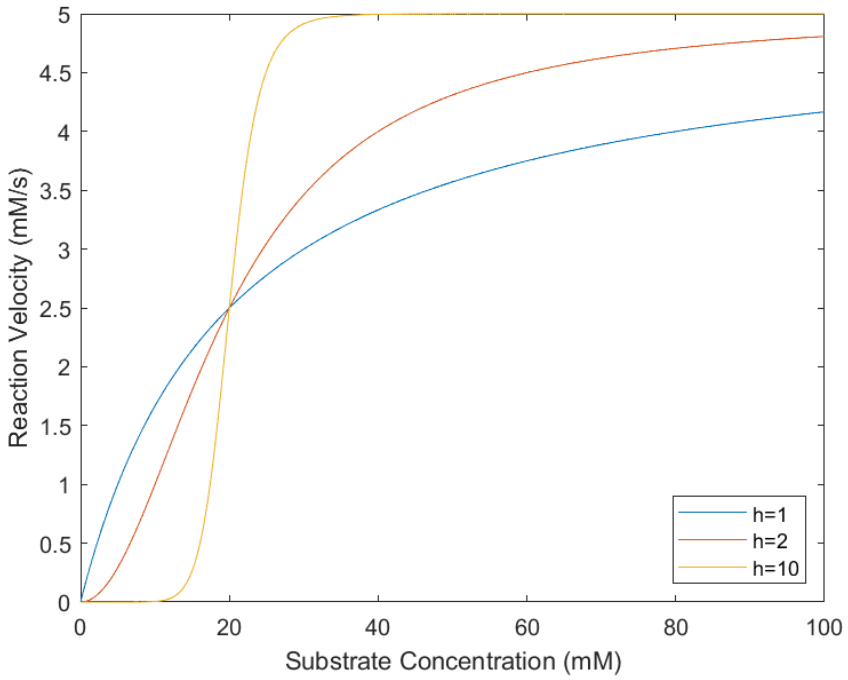


Figure 1: The Hill equation was plotted as reaction velocity in mM/s as a function of substrate concentration in mM. $K_{1/2}$ was 20.0mM and V_{max} was 5.0mM/s. Three different values for the Hill coefficient, h, were plotted.

The Hill coefficient, h, is a measure of binding cooperativity. Cooperativity occurs if the binding of one substrate to an enzyme can influence the binding of substrate molecules at other sites on the enzyme. A Hill coefficient of h=1 indicates noncooperative, or independent, binding. In such a case, an enzyme's affinity for a substrate does not change depending on whether other substrates are bound. A Hill coefficient of greater than 1, such as 2 or 10, indicates positive cooperative binding. When h=2, the binding of one substrate increases the enzyme's affinity for other substrate molecules, thus facilitating the binding of other substrate molecules. The greater the Hill coefficient, the stronger this positive cooperativity. Such is the case where h=10, as the binding of a substrate in that case increases the enzyme's affinity for other substrate molecules even more so. In terms of the plot generated from this equation, a more positive Hill coefficient will make the curve more sigmoidal. At low substrate concentrations, the affinity for substrate molecules is low and therefore the reaction velocity is also low. As substrate concentration increases, the affinity increases. This is intensified as the Hill coefficient becomes more positive. For a more positive hill coefficient, the reaction velocity remains low for a larger range of substrate concentrations because the number of bound molecules needed to enhance affinity increases. However, once the affinity increases, the curve is much steeper for a large Hill coefficient. This is because affinity increases more and more with each additional bound substrate. This allows systems with the most positive Hill coefficient to reach saturation at a lower substrate concentration. As seen in Figure 1, at the same substrate concentration of 40 mM the three systems have very different reaction velocities. Compared to when h=1, the substrate binding affinity at the same concentration is much

greater when h=2, and even greater when h=10. As h becomes more positive, substrate molecules are more likely to bind and all available binding sites are more likely to become saturated. This caused the h=10 velocity to level out at the lowest substrate concentration.

As visible in Figure 1, all three curves intersect at a substrate concentration of 20.0 mM and a reaction velocity of 2.5 mM/s. At this point, substrate concentration is equal to the $K_{1/2}$ and reaction velocity is half its maximum, or $V_{max}/2$. All curves approach the same V_{max}, and the substrates in the three systems have equal affinity for the enzymes. The only variation is the degree of cooperativity given by the Hill coefficient, which determines the shape of the curve.

(b) Hill equation with $K_{1/2}$ = 10.0 mM, 20.0 mM, and 40.0 mM.

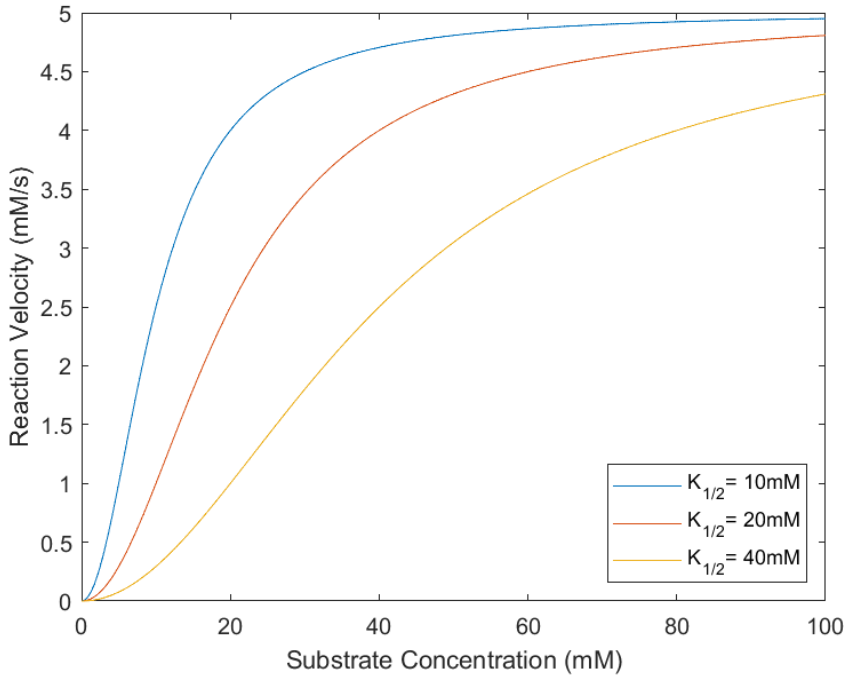


Figure 2: The Hill equation was plotted as reaction velocity in mM/s as a function of substrate concentration in mM. V_{max} was 5.0mM/s and h was 2. Three different values for the constant $K_{1/2}$ were plotted.

The constant $K_{1/2}$ is analogous to the Michaelis-Menten constant K_M, which equals the substrate concentration at which the reaction has reached half its maximum velocity V_{max}. For all three curves, V_{max} = 5.0 mM/s, so half the maximum velocity is 2.5 mM/s. As seen in Figure 2, each curve reaches this reaction velocity at a substrate concentration equal to its $K_{1/2}$ value. The K_M, and therefore the $K_{1/2}$, is a measure of the substrate's affinity for the enzyme. A smaller $K_{1/2}$ indicates a higher affinity, as seen in the curve for $K_{1/2}$ = 10mM. In that case, the velocity reaches its half-maximum at the lowest substrate concentration compared to the other curves. The likelihood of the substrate binding to the enzyme is greatest at a lower $K_{1/2}$, so less substrate molecules are required to saturate the enzyme's binding sites. The substrate's affinity for the enzyme decreases as the $K_{1/2}$ increases, since a greater substrate concentration is required for saturation. This also explains why the $K_{1/2}$ = 10mM has the steepest slope and $K_{1/2}$ = 40mM has the shallowest slope. Because substrate molecules have lower affinity for the enzyme in the latter case, saturation occurs more gradually with respect to an increasing substrate concentration. However, all three curves approach the same V_{max} value because this was held constant.

(c) Hill equation with V_{max} = 2.0 mM/s, 5.0 mM/s, and 10.0 mM/s.

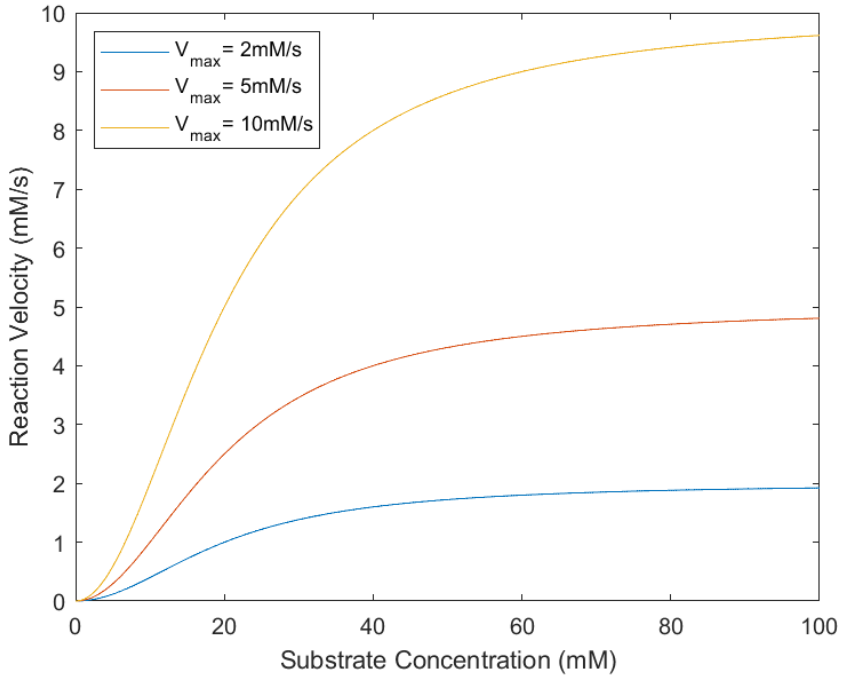


Figure 3: The Hill equation was plotted as reaction velocity in mM/s as a function of substrate concentration in mM. $K_{1/2}$ was 20.0mM and h was 2. Three different values for the constant V_{max} were plotted.

V_{max} is the maximal rate that is possible for a reaction. This limit is reached when all of the enzyme's available binding sites are occupied due to an excess substrate concentration. Substrate molecules are constantly binding and unbinding, but the substrate concentration is in such excess that the binding sites are being constantly reoccupied. This point where the curve levels off is known as saturation. V_{max} can be influenced by various factors, most obviously the enzyme concentration and number of binding sites on each enzyme. These influence a reaction's turnover rate from substrate to product. In Figure 3, it is clear that a greater V_{max} allows the reaction to reach a higher

rate before leveling off. Also visible in the figure, the $K_{1/2}$ for each curve was held constant at 20mM. Each curve reaches its half-maximum velocity ($V_{max}/2$) at the same substrate concentration of 20mM, despite those velocity values being varied. This indicates that the substrate's affinity for the enzyme does not vary with V_{max}. Altering V_{max} only alters the range of possible reaction velocities for the system.

2.

(a) Sketch of predicted Hill plot if h = 4, V_{max} = 20 mM/s and $K_{1/2}$ = 50 mM

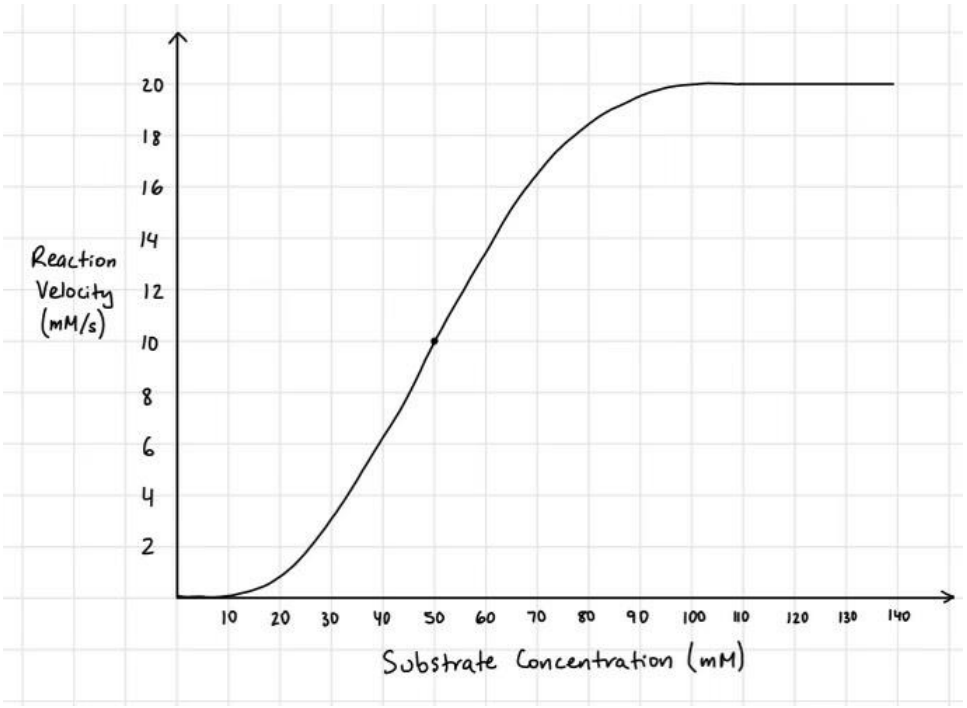


Figure 4: This curve was predicted for the case that h = 4, V_{max} = 20 mM/s and $K_{1/2}$ = 50 mM. This was based on the previous plots (Figures 1-3) and the effects of varying h, V_{max}, and $K_{1/2}$ on the formation of those curves.

Firstly, it is known that the initial substrate concentration is 0 mM and reaction velocity is 0 mM/s at this point since there are no substrate molecules for the enzyme to convert to products. The one point on the curve that can be exactly predicted is where the reaction velocity reaches $V_{max}/2$, or 10 mM/s. At this point, the substrate concentration is equal to the $K_{1/2}$ of 50 mM. This point is marked on the curve in Figure 4. It is also known that the reaction velocity will level off at a V_{max} of 20 mM/s at some point. The curve therefore extends to a substrate concentration of 140 mM to emphasize that it levels out to a perfectly horizontal line. A Hill coefficient of greater than 1 indicates positive cooperativity, which causes the curve to become more sigmoidal as in Figure 1. This is because the enzyme's affinity for substrates remains low at low substrate concentrations, resulting in a low reaction velocity until enough substrates bind the enzyme. The Hill coefficient of h=4 was predicted to have such a sigmoidal curve, but the extent of this was predicted to be more so than if h=2 but less than h=10. The curve was therefore drawn with a sigmoidal shape, ensuring that it crosses the $V_{max}/2$ point and plateaus at 20 mM/s.

(b) Hill equation with h = 4, V_{max} = 20 mM/s and $K_{1/2}$ = 50 mM.

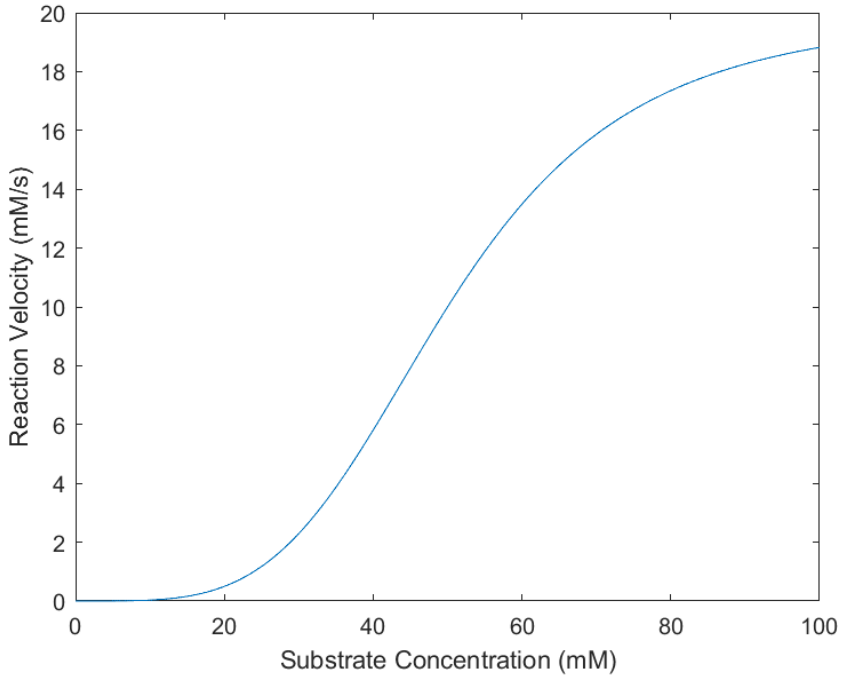


Figure 5: The Hill equation was plotted as reaction velocity in mM/s as a function of substrate concentration in mM. This curve models the case that h = 4, V_{max} = 20 mM/s and $K_{1/2}$ = 50 mM.

Few differences exist between Figures 4 and 5, as the Hill plot curve shape and specific points can be accurately predicted using the three constants involved in the Hill equation. The V_{max} gives the maximum reaction velocity and end behavior of the curve. This along with the $K_{1/2}$ give the half-maximum point, which is very useful in guiding the slope of the curve. The Hill coefficient gives the shape of the curve, in terms of its sigmoidal nature. The one observable difference is that the curve in Figure 4 was drawn to be too sigmoidal, as it reaches the V_{max} at a much lower substrate concentration than

the curve in Figure 5. The enzyme's binding cooperativity was slightly overestimated compared to a system with the given Hill coefficient of 4.

3.

(a) Hill equation with h = 4, V_{max} = 20 mM/s and $K_{1/2}$ = 50 mM. Using Forward Euler to plot substrate concentration as a function of time.

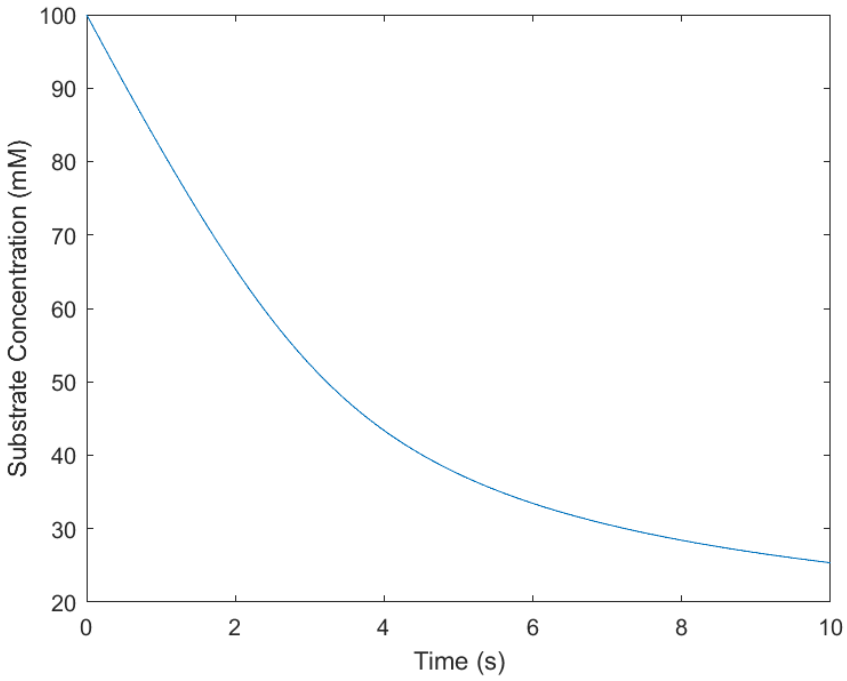


Figure 6: The Hill equation was plotted as substrate concentration in mM as a function of time in seconds. This curve models the case that h = 4, V_{max} = 20 mM/s and $K_{1/2}$ = 50 mM. The Forward Euler algorithm was used to implement the dynamics of this enzyme-catalyzed reaction.

(b) The graphs from 2(b) and 3(a) differ mainly by their axes. Although both graphs model the same reaction dynamics using the Hill equation with the same parameters,

Figure 5 gives the reaction rate as a function of the substrate concentration and Figure 6 gives the substrate concentration as a function of time. These two graphs offer two different perspectives of the reaction dynamics. However, these graphs can be interpreted together to understand the progression of the enzyme-catalyzed reaction. In Figure 6, The substrate concentration is high in the beginning, which means there is a high number of substrates bound to enzyme. Because of the positive cooperativity indicated by a Hill coefficient of 4, this enhances the enzyme's binding affinity for other substrate molecules. This is why the substrate concentration decreases very quickly in the beginning when concentration is high, then its slope decreases over time when the concentration decreases. It makes sense that the substrate concentration decreases over time, as the enzyme is converting substrate into product. According to this interpretation, Figure 5 gives the reverse of this progression. Figure 5 can be instead viewed from right to left to better align it with Figure 6. Once the reaction begins, substrate concentration decreases over time. Since the substrate concentration and the enzyme's binding affinity are highest in the beginning, the reaction velocity is also at its V_{max}. The substrate concentration decreases with the progressing reaction. Since less substrate molecules are available to bind the enzyme and be converted into product, the reaction rate also slows down until it reaches 0. Figure 6 gives us a more holistic idea of how the reaction progresses. For example, the substrate concentration decreases to $K_{1/2}$ at roughly 3.5 seconds. This shows that the reaction rate quickly decreases to half its maximum value but takes much longer to reach 0. From this, we can deduce that the reaction rate decreases over time. This is confirmed by Figure 5.

Part B: An autoregulatory gene

1. The Forward Euler approach was used to model differential equations for a simple autoregulatory gene. This gene encodes a protein that is involved in activating its own transcription. The initial concentrations of protein and RNA were varied for each plot, but the parameters μ, ω, $\chi_{protein}$, and χ_{rna} were kept consistent at 1 s^{-1} and $K_{1/2}$ at 0.33 mM.

   (a) Initial protein concentration of 0.5 mM, initial RNA concentration 0.5 mM

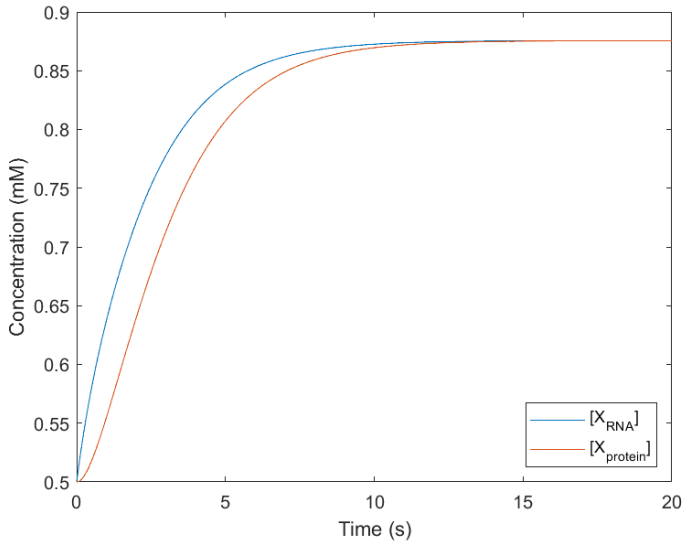


Figure 7: RNA and protein concentrations were plotted over time using the Forward Euler method. The blue line represents the RNA concentration, and the red line represents the protein concentration. Here, both concentrations were initially 0.5 mM.

(b) Initial protein concentration of 0.2 mM, initial RNA concentration 0 mM

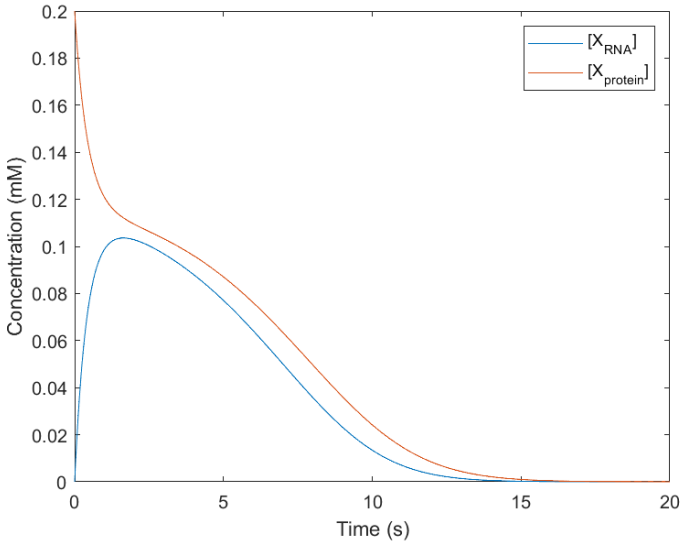


Figure 8: RNA and protein concentrations were plotted over time using the Forward Euler method. The blue line represents the RNA concentration, and the red line represents the protein concentration. Here, protein concentration was initially 0.2 mM and RNA concentration was 0 mM.

(c) Initial protein concentration of 0.5 mM, initial RNA concentration 0 mM

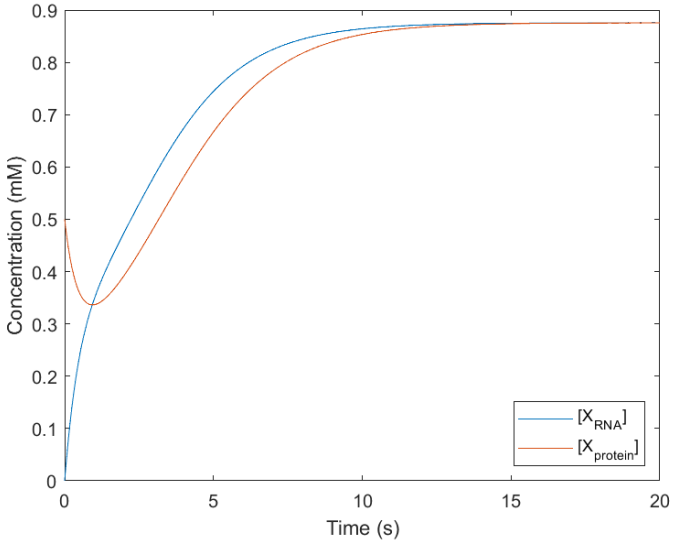


Figure 9: RNA and protein concentrations were plotted over time using the Forward Euler method. The blue line represents the RNA concentration, and the red line represents the protein concentration. Here, protein concentration was initially 0.5 mM and RNA concentration was 0 mM.

(d) Initial protein concentration of 0 mM, initial RNA concentration 0.2 mM

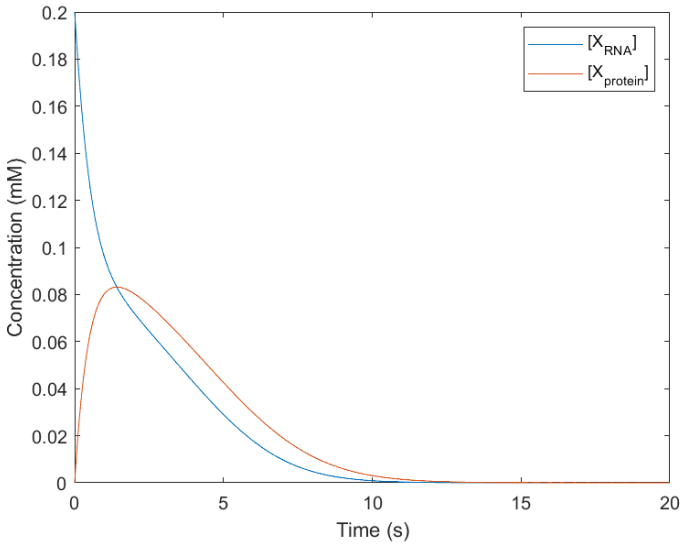


Figure 10: RNA and protein concentrations were plotted over time using the Forward Euler method. The blue line represents the RNA concentration, and the red line represents the protein concentration. Here, RNA concentration was initially 0.2 mM and protein concentration was 0 mM.

In Figure 10, the initial concentration of RNA was only slightly greater than the protein concentration. This amount of RNA was not enough to maintain a protein

(e) Initial protein concentration of 0 mM, initial RNA concentration 0.5 mM

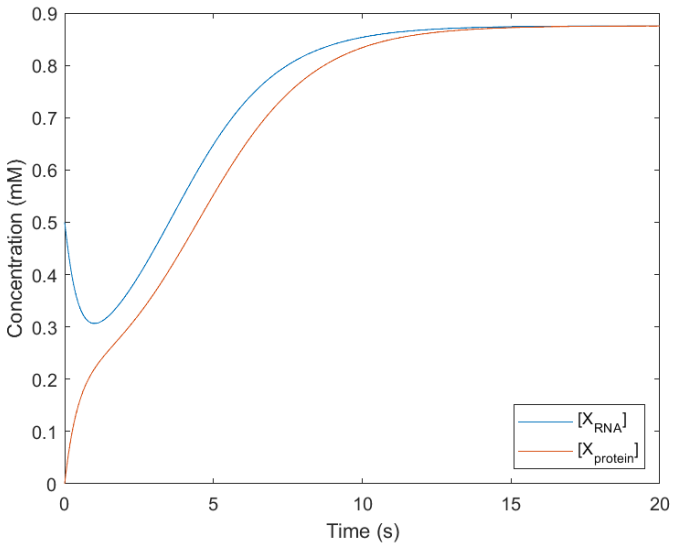


Figure 11: RNA and protein concentrations were plotted over time using the Forward Euler method. The blue line represents the RNA concentration, and the red line represents the protein concentration. Here, RNA concentration was initially 0.5 mM and protein concentration was 0 mM.

(f) The change in protein concentration over time is equal to $\omega[X_{rna}] - \chi_{protein}[X_{protein}]$. In this case where all constants (except $K_{1/2}$) are equal to 1, this shows that the change in protein concentration is equal to 0 when the concentrations of RNA and protein are equal. If the RNA concentration is increasing at this point, the protein synthesis term will surpass the degradation term in the next moment, causing the protein concentration to begin to increase. This is the behavior exhibited in Figure 9. Starting with a relatively high protein concentration (0.5mM) allowed the RNA concentration to quickly grow despite starting at 0 mM. Although this caused the protein

concentration to be depleted, the RNA concentration was high enough that it greatly increased protein synthesis and both concentrations approached the nonzero steady state. With an RNA concentration so high, RNA degradation (influenced by RNA concentration) became equal to RNA synthesis (influenced by protein concentration). At this point, protein and RNA concentrations became equal, causing protein concentration to reach its steady state. The system was then in equilibrium.

This was not the case in Figure 8, where the initial protein concentration of 0.2 mM did not promote transcription enough for the RNA concentration to surpass the protein concentration. The two plots did not intersect. Since the protein concentration remained greater than the RNA concentration, the protein was degraded faster than it could be synthesized. Without protein, RNA transcription is not favored. This causes both concentrations to approach the steady state concentration of 0.

If the RNA concentration is decreasing at the intersection of the protein and RNA plots, protein degradation will surpass protein synthesis, causing the protein concentration to decrease. Once again, decreasing protein concentration caused the decreased promotion of RNA transcription. Both concentrations approach the steady state concentration of 0. This was modeled in Figure 10, where the initial RNA concentration of 0.2 mM was quickly depleted to produce protein (initially at 0 mM), but the amount of protein translated was not enough for RNA synthesis to surpass its degradation.

As shown in Figure 11, an initial RNA concentration of 0.5 mM was initially depleted to produce protein (initially at 0 mM). However, in this case the relatively high concentration of RNA allowed enough protein to be translated to maintain an RNA

synthesis rate that was greater than the RNA degradation rate. Both concentrations continued to increase and level off at the non-zero steady state.

Lastly, in Figure 7 the protein synthesis and degradation rates were initially equal due to initial RNA and protein concentrations being equal at 0.5 mM. However, the relatively high initial concentration of protein caused RNA synthesis to be greater than RNA degradation. Since the RNA concentration was increasing past the protein concentration, protein synthesis surpassed degradation. Both concentrations continued to increase, approaching the non-zero steady state.

2. (a) and (b) resulted in Figure 12.

   Varying protein and RNA initial concentrations from 0.0 to 1.4 mM in intervals of 0.2 mM, plotting all combinations.

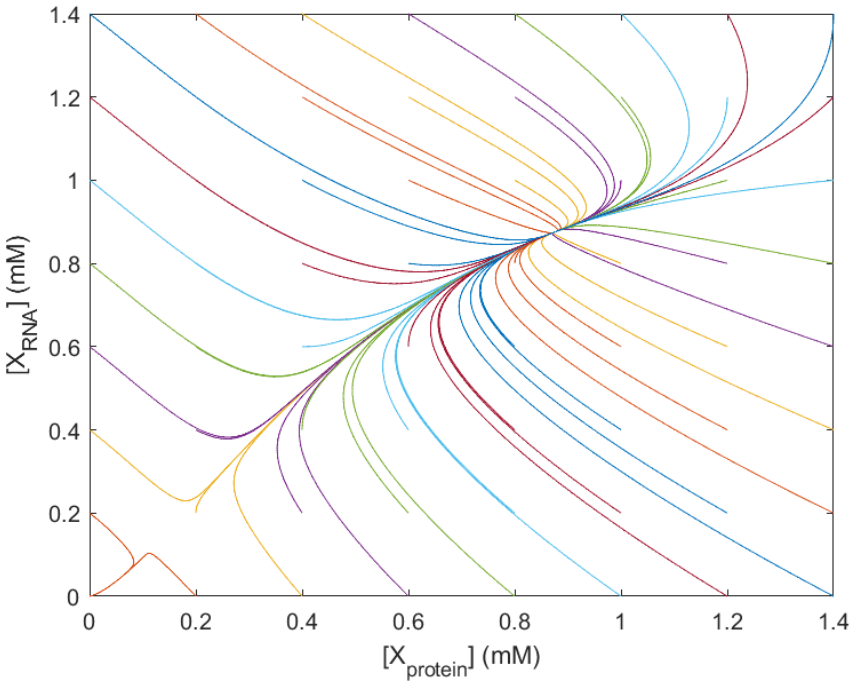


Figure 12: The Forward Euler method was implemented to model the dynamics of an autoregulatory gene. Initial RNA and protein concentrations were both varied from 0.0 to 1.4 mM in intervals of 0.2 mM. All 64 combinations were plotted as RNA concentration as a function of protein concentration.

(c) Each curve on the graph in Figure 12 represents the simulated dynamics that result from a different initial state. The beginning and end of each line represent the initial and final states of that simulation. While there are 64 different points at which initial states exist, there are only 2 different points at which final states seem to exist. This indicates that the system has two stable states. One of these stable points is at the origin, whereas the other is a non-zero stable point. The majority of the trajectories end at the non-zero equilibrium state at roughly (0.9mM, 0.9mM). All of these trajectories seem to be collecting on one curve leading to that stable stationary point. This curve is the attracting manifold of the graph. Curves with low initial protein and RNA concentrations move toward a saddle point roughly between (0.1mM, 0.1mM) and ((0.2mM, 0.2mM), then outward toward either one of the stable points. The line on which they move toward the saddle point is the repelling manifold of the graph, as all trajectories avoid this line. Only curves with the lowest initial concentrations approach the stable stationary point at the origin.

3. In Figure 12, curves where both initial states are 0mM, or one is 0mM and the other is 0.2mM have final states at the origin stable point. In these instances, protein and RNA degradation was greater than their synthesis, causing their concentrations to level off at zero. Two of these scenarios were simulated in Figure 8 and 10 above. If starting with 0.2mM protein, protein concentration begins to decrease while RNA concentration

increases somewhat. However, both are soon depleted because the degradation rate is greater than the synthesis rate. Essentially the same occurs if starting with 0.2mM RNA. All other curves where, both initial states are 0.2mM or greater, have final states at the non-zero stable point. In all of those cases, the protein and RNA synthesis rates were greater than their degradation rates, until both concentrations reached non-zero steady states. These steady states create a stable stationary point in the graph.

These results did not explore the influences of varying each of the 5 different parameters in the system of differential equations for an autoregulatory gene. These include μ, ω, $\chi_{protein}$, χ_{rna}, and $K_{1/2}$.

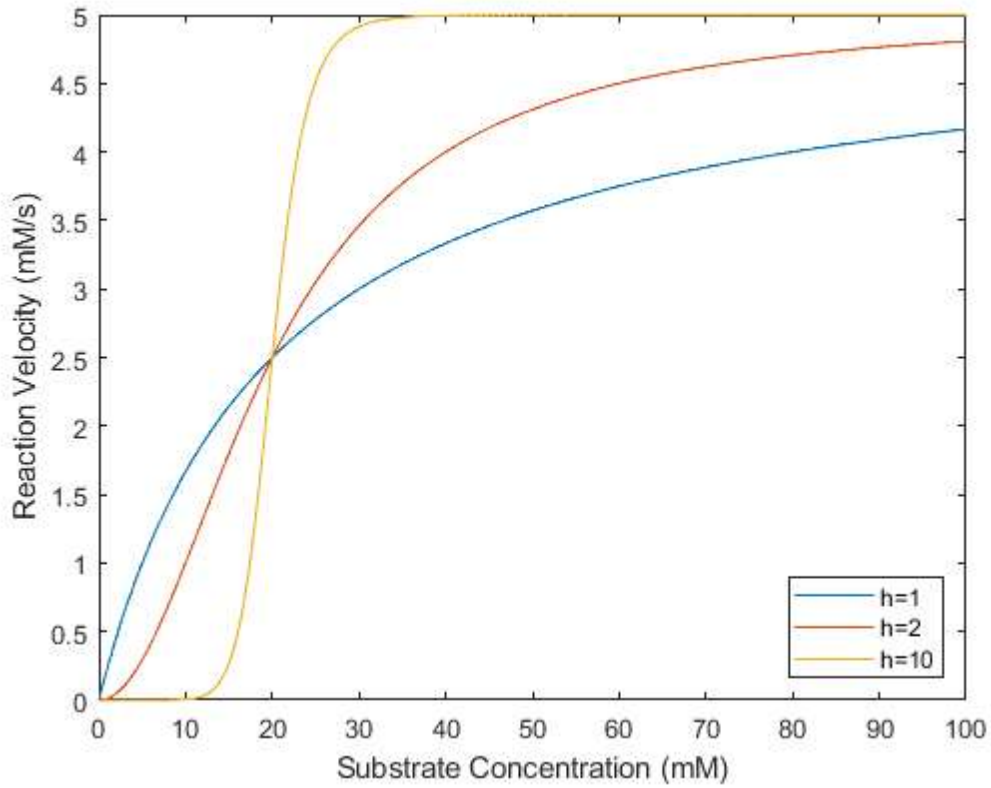
Part A: Understanding the Hill equation

Contents

1.

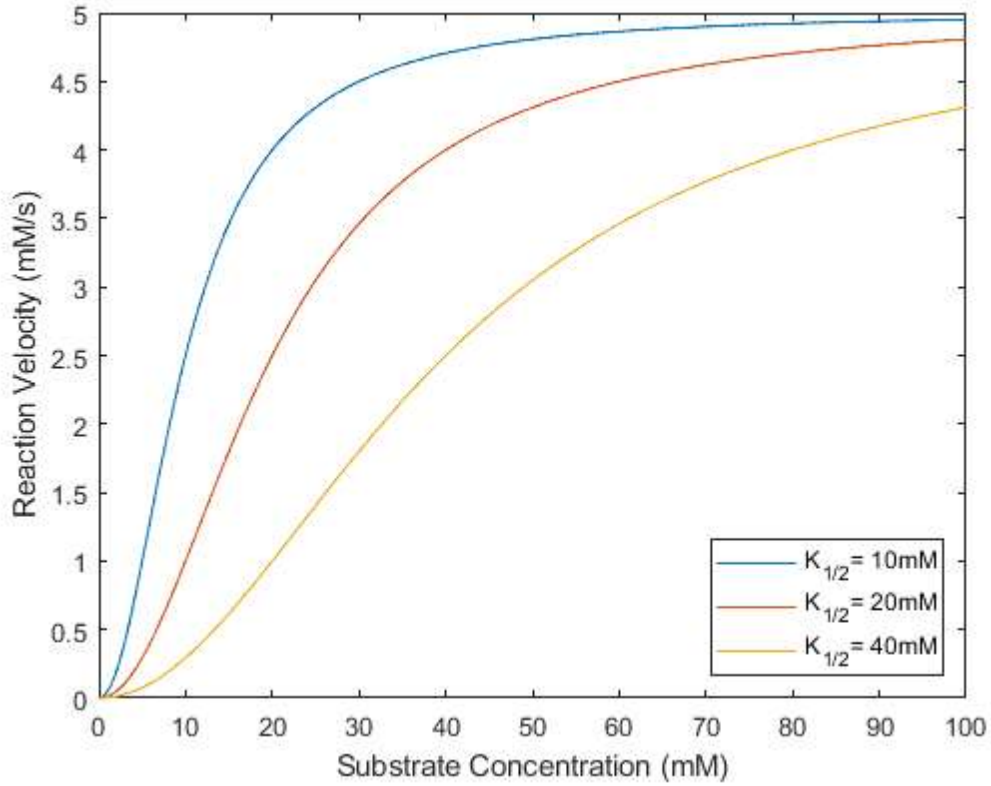
1(a)

```
fig1 = figure(1);
S = 0:0.1:100; % mM
Vmax = 5; % mM/s
K = 20.0; % mM

h1 = 1;
v1 = (Vmax.*(S.^h1))./((K.^h1) + (S.^h1));
plot(S, v1)
hold on

h2 = 2;
v2 = (Vmax.*(S.^h2))./((K.^h2) + (S.^h2));
plot(S, v2)
hold on

h3 = 10;
v3 = (Vmax.*(S.^h3))./((K.^h3) + (S.^h3));
plot(S, v3)

xlabel('Substrate Concentration (mM)')
ylabel('Reaction Velocity (mM/s)')
legend('h=1', 'h=2', 'h=10', 'Location','southeast')
hold off
```



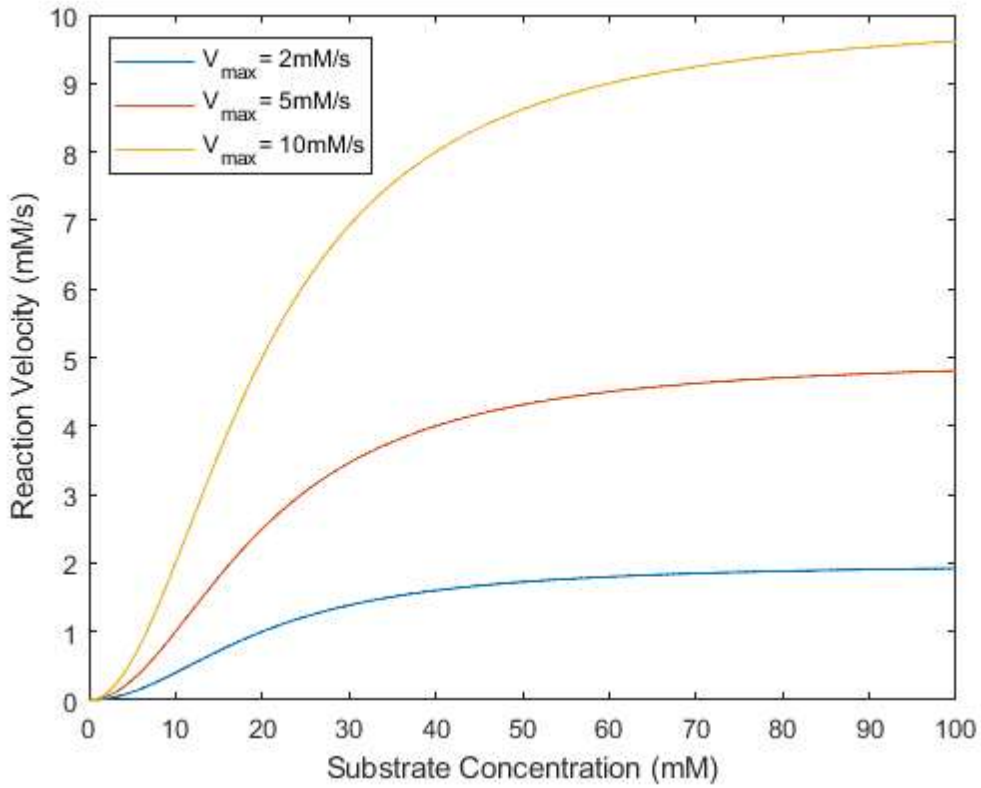
1(b)

```
fig2 = figure(2);
S = 0:0.1:100; % mM
Vmax = 5; % mM/s
h = 2;

K1 = 10.0; % mM
v1 = (Vmax.*(S.^h))./((K1.^h) + (S.^h));
plot(S, v1)
hold on

K2 = 20.0;
v2 = (Vmax.*(S.^h))./((K2.^h) + (S.^h));
plot(S, v2)
hold on

K3 = 40.0;
v3 = (Vmax.*(S.^h))./((K3.^h) + (S.^h));
plot(S, v3)

xlabel('Substrate Concentration (mM)')
ylabel('Reaction Velocity (mM/s)')
legend('K_{1/2}= 10mM', 'K_{1/2}= 20mM', 'K_{1/2}= 40mM', 'Location','southeast')
hold off
```



1(c)

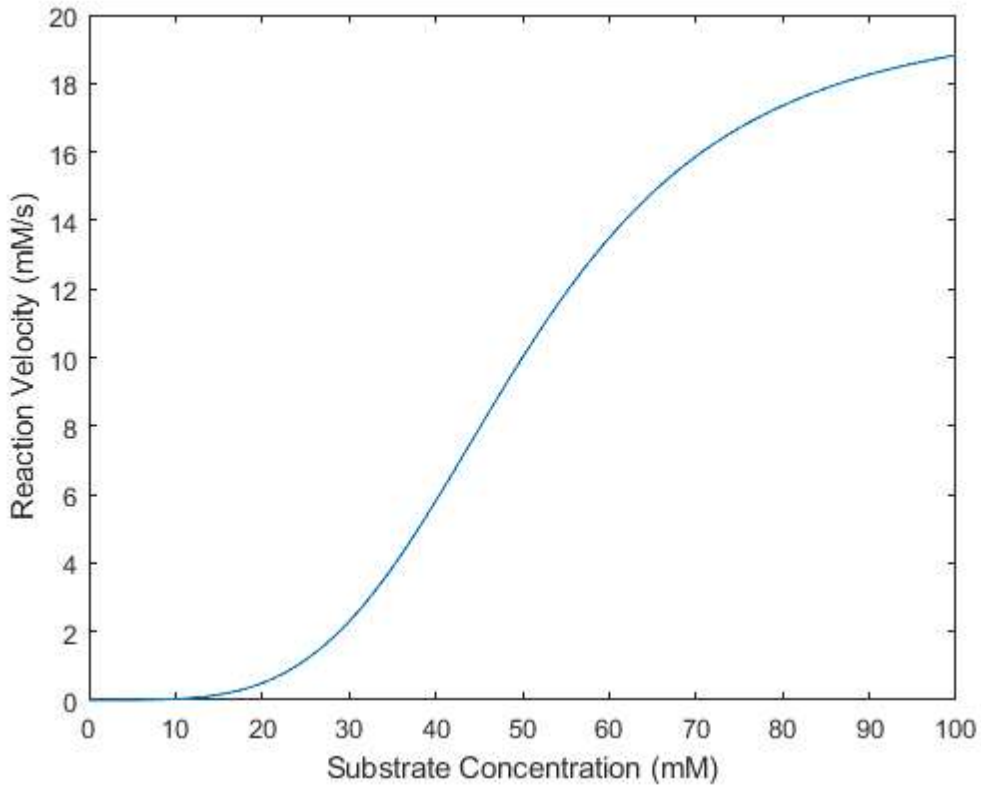
```
fig3 = figure(3);
S = 0:0.1:100; % mM
K = 20.0; % mM
h = 2;

Vmax1 = 2; % mM/s
v1 = (Vmax1.*(S.^h))./((K.^h) + (S.^h));
plot(S, v1)
hold on

Vmax2 = 5; % mM/s
v2 = (Vmax2.*(S.^h))./((K.^h) + (S.^h));
plot(S, v2)
hold on

Vmax3 = 10; % mM/s
v3 = (Vmax3.*(S.^h))./((K.^h) + (S.^h));
plot(S, v3)

xlabel('Substrate Concentration (mM)')
ylabel('Reaction Velocity (mM/s)')
legend('V_{max}= 2mM/s', 'V_{max}= 5mM/s', 'V_{max}= 10mM/s', 'Location','northwest')
hold off
```



2.

2(b)

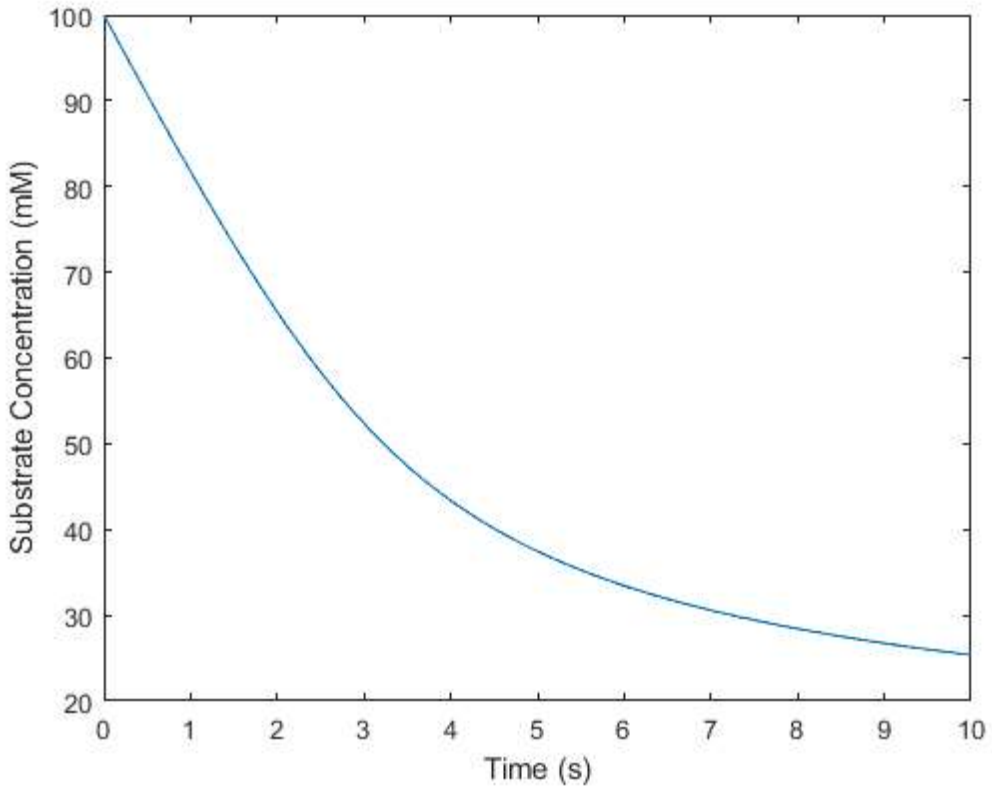
```
clear
fig4 = figure(4);
S = 0:0.1:100; % mM
Vmax = 20; % mM/s
K = 50; % mM
h = 4;
v = (Vmax.*(S.^h))./((K.^h) + (S.^h));
plot(S, v)
xlabel('Substrate Concentration (mM)')
ylabel('Reaction Velocity (mM/s)')
```



3.

3(a)

```
clear
fig5 = figure(5);
Vmax = 20; % mM/s
K = 50; % mM
h = 4;

deltaT = 0.01; % s
maxT = 10; % s
numiterations = maxT/deltaT;
t = 0:deltaT:maxT;
S0 = 100; % initial concentration (mM)
S = zeros(size(t));
S(1) = S0;
for i = 1:numiterations
    dSdt = -(Vmax*(S(i)^h))/((K^h) + (S(i)^h));
    S(i+1) = S(i) + dSdt*deltaT;
end
plot(t, S)
xlabel('Time (s)')
ylabel('Substrate Concentration (mM)')
```



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Part B: An autoregulatory gene

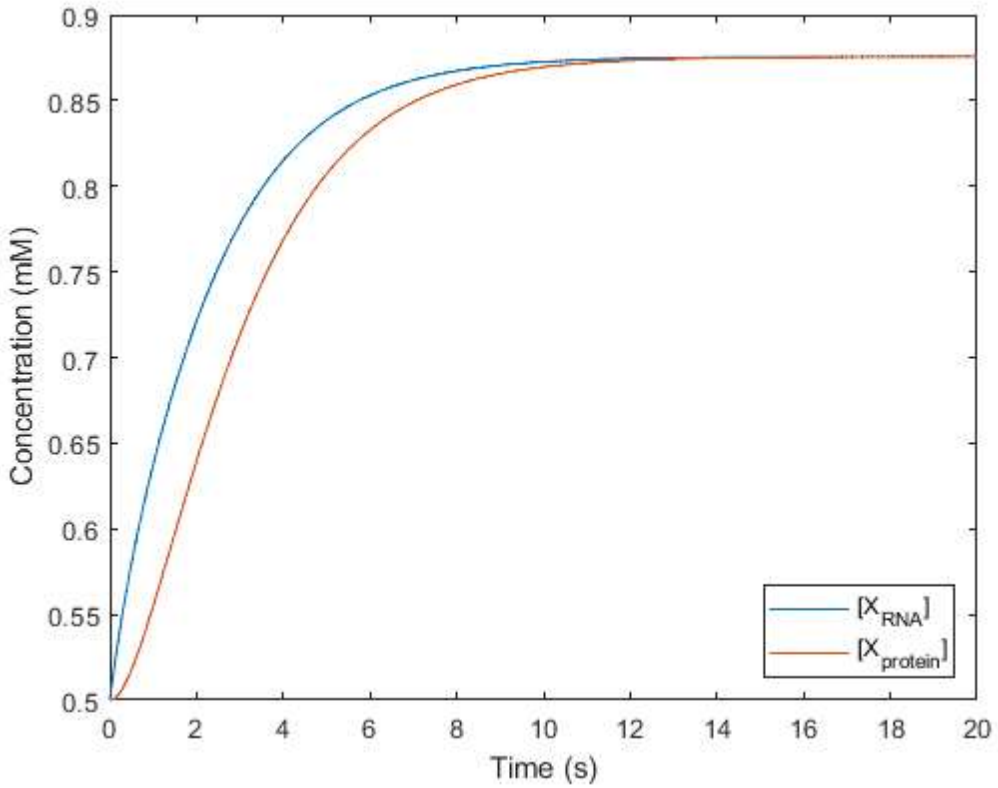
Contents

1.

```
clear

u = 1; % 1/s
w = 1; % 1/s
Xp = 1; % 1/s
Xr = 1; % 1/s
K = 0.33; % mM

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

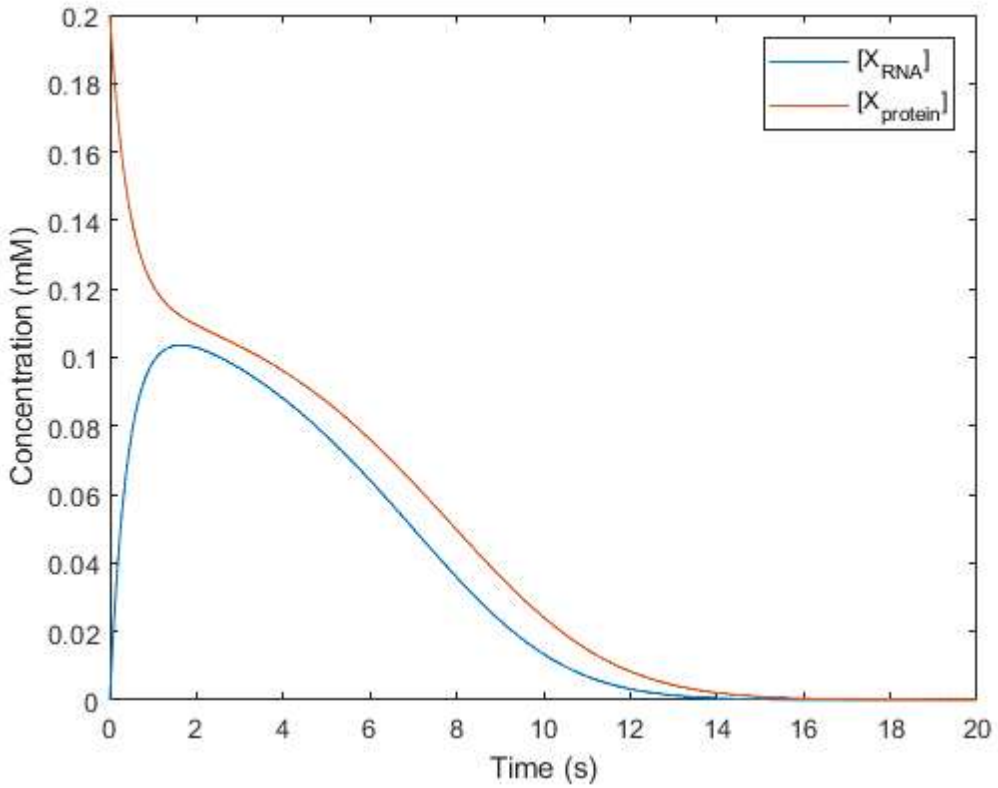
1(a)

```
fig6 = figure(6);
Xrna_0 = 0.5; % initial concentration (mM)
Xprot_0 = 0.5; % initial concentration (mM)
Xrna = zeros(size(t));
Xprot = zeros(size(t));
Xrna(1) = Xrna_0;
Xprot(1) = Xprot_0;

for i = 1:numiterations
    dXrnadt = ((u*(Xprot(i)^2)) / ((K^2)+(Xprot(i)^2))) - (Xr*Xrna(i));
    dXprotdt = (w*Xrna(i)) - (Xp*Xprot(i));
    Xrna(i+1) = Xrna(i) + dXrnadt*deltaT;
    Xprot(i+1) = Xprot(i) + dXprotdt*deltaT;
end
plot(t, Xrna)
hold on
plot(t, Xprot)
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend('[X_{RNA}]', '[X_{protein}]', 'Location', 'southeast')
hold off
```



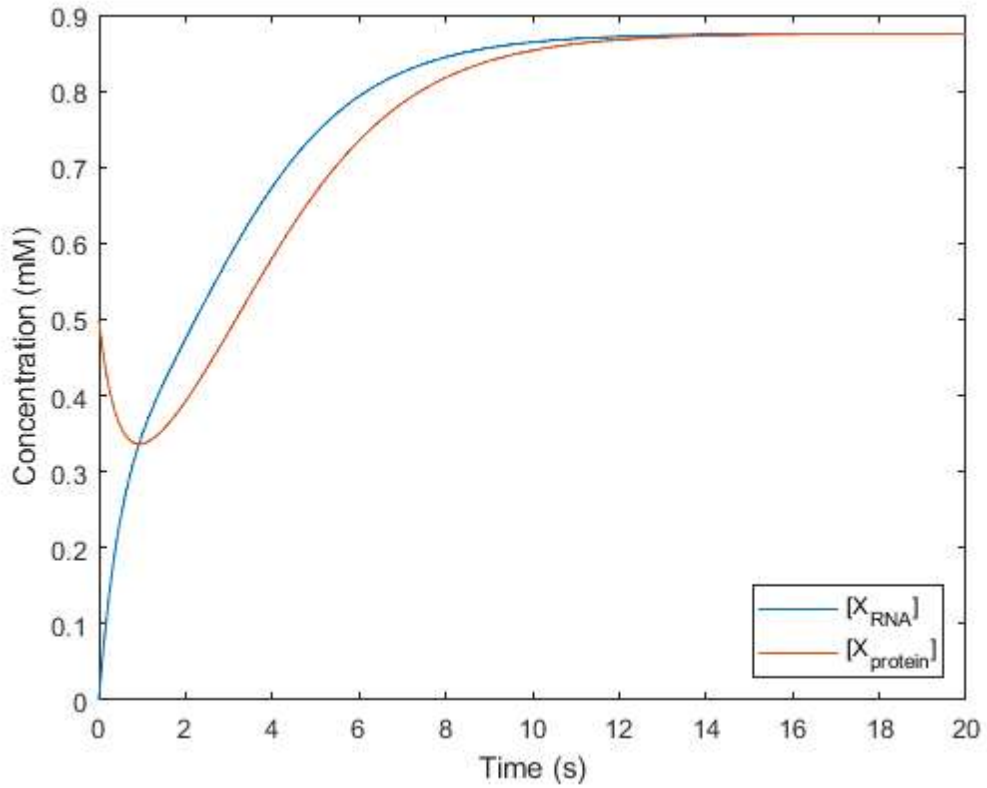
1(b)

```
fig7 = figure(7);
Xrna_0 = 0; % initial concentration (mM)
Xprot_0 = 0.2; % initial concentration (mM)
Xrna = zeros(size(t));
Xprot = zeros(size(t));
Xrna(1) = Xrna_0;
Xprot(1) = Xprot_0;

for i = 1:numiterations
    dXrnadt = ((u*(Xprot(i)^2)) / ((K^2)+(Xprot(i)^2))) - (Xr*Xrna(i));
    dXprotdt = (w*Xrna(i)) - (Xp*Xprot(i));
    Xrna(i+1) = Xrna(i) + dXrnadt*deltaT;
    Xprot(i+1) = Xprot(i) + dXprotdt*deltaT;
end
plot(t, Xrna)
hold on
plot(t, Xprot)
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend('[X_{RNA}]', '[X_{protein}]')
hold off
```



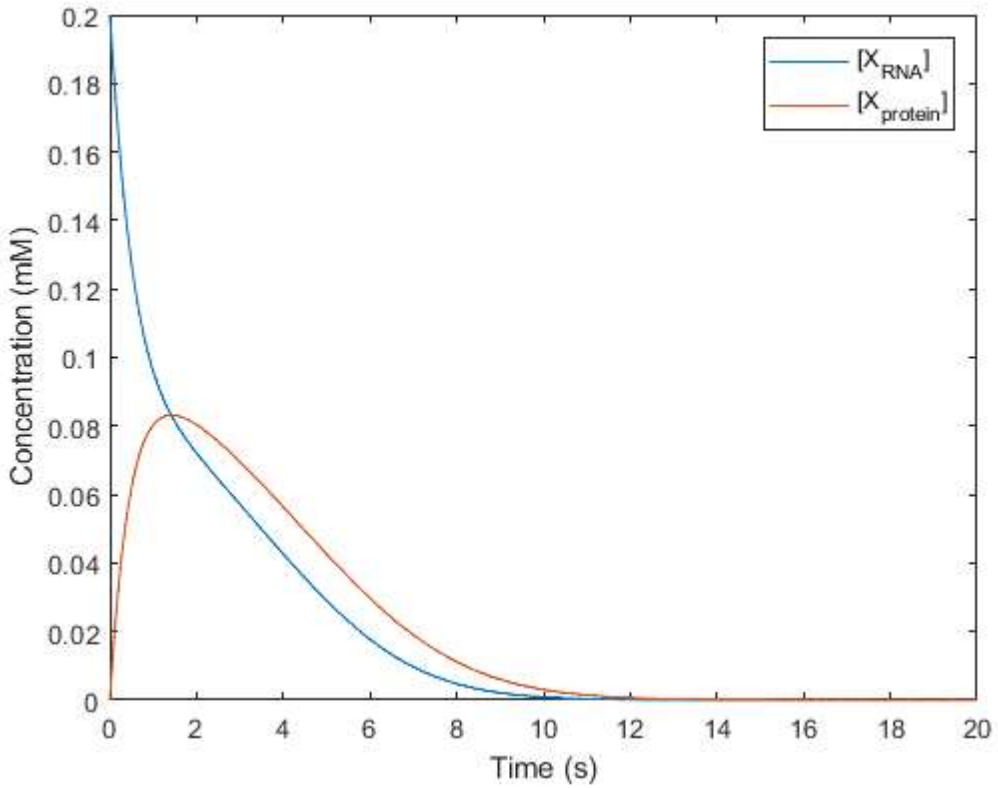
1(c)

```
fig8 = figure(8);
Xrna_0 = 0; % initial concentration (mM)
Xprot_0 = 0.5; % initial concentration (mM)
Xrna = zeros(size(t));
Xprot = zeros(size(t));
Xrna(1) = Xrna_0;
Xprot(1) = Xprot_0;

for i = 1:numiterations
    dXrnadt = ((u*(Xprot(i)^2)) / ((K^2)+(Xprot(i)^2))) - (Xr*Xrna(i));
    dXprotdt = (w*Xrna(i)) - (Xp*Xprot(i));
    Xrna(i+1) = Xrna(i) + dXrnadt*deltaT;
    Xprot(i+1) = Xprot(i) + dXprotdt*deltaT;
end
plot(t, Xrna)
hold on
plot(t, Xprot)
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend('[X_{RNA}]', '[X_{protein}]', 'Location', 'southeast')
hold off
```



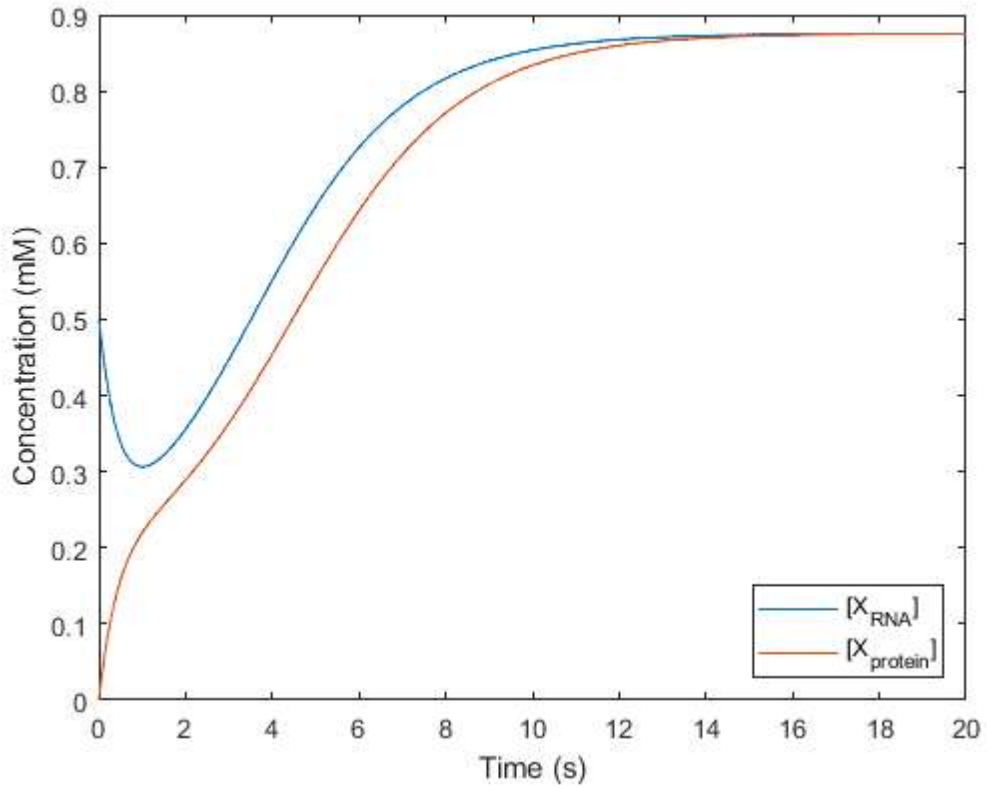
1(d)

```
fig9 = figure(9);
Xrna_0 = 0.2; % initial concentration (mM)
Xprot_0 = 0; % initial concentration (mM)
Xrna = zeros(size(t));
Xprot = zeros(size(t));
Xrna(1) = Xrna_0;
Xprot(1) = Xprot_0;

for i = 1:numiterations
    dXrnadt = ((u*(Xprot(i)^2)) / ((K^2)+(Xprot(i)^2))) - (Xr*Xrna(i));
    dXprotdt = (w*Xrna(i)) - (Xp*Xprot(i));
    Xrna(i+1) = Xrna(i) + dXrnadt*deltaT;
    Xprot(i+1) = Xprot(i) + dXprotdt*deltaT;
end
plot(t, Xrna)
hold on
plot(t, Xprot)
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend('[X_{RNA}]', '[X_{protein}]')
hold off
```



1(e)

```
fig10 = figure(10);
Xrna_0 = 0.5; % initial concentration (mM)
Xprot_0 = 0; % initial concentration (mM)
Xrna = zeros(size(t));
Xprot = zeros(size(t));
Xrna(1) = Xrna_0;
Xprot(1) = Xprot_0;

for i = 1:numiterations
    dXrnadt = ((u*(Xprot(i)^2)) / ((K^2)+(Xprot(i)^2))) - (Xr*Xrna(i));
    dXprotdt = (w*Xrna(i)) - (Xp*Xprot(i));
    Xrna(i+1) = Xrna(i) + dXrnadt*deltaT;
    Xprot(i+1) = Xprot(i) + dXprotdt*deltaT;
end
plot(t, Xrna)
hold on
plot(t, Xprot)
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend('[X_{RNA}]', '[X_{protein}]', 'Location', 'southeast')
hold off
```

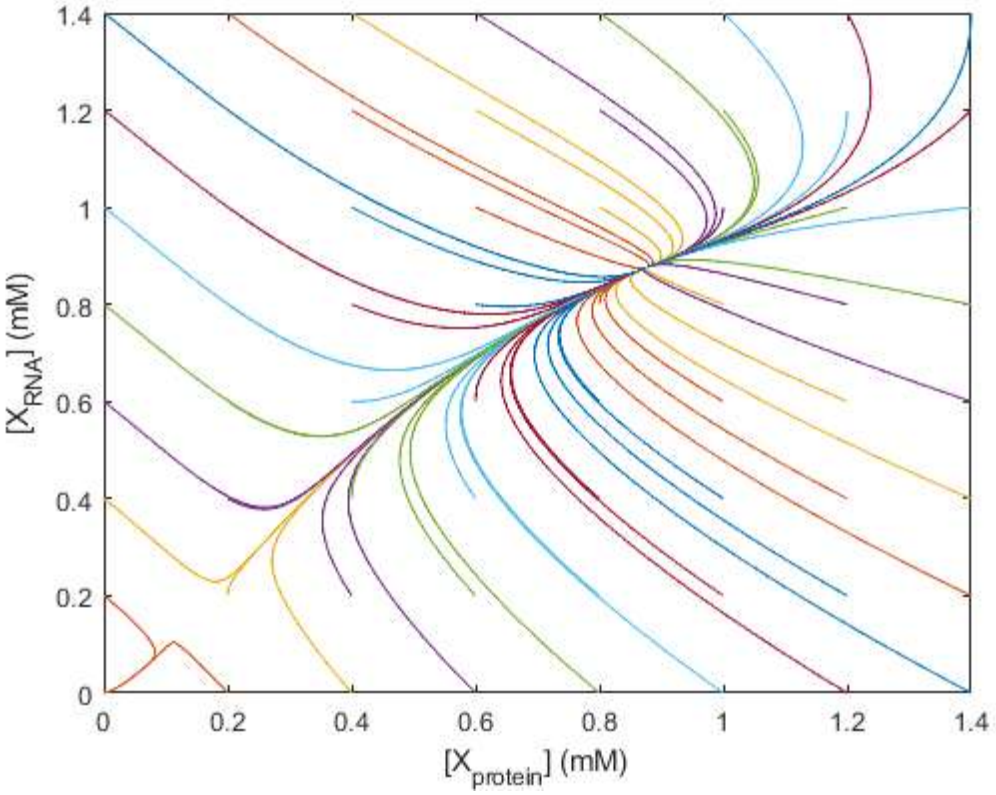


2.

2(a-b)

```
clear
close all
u = 1; % 1/s
w = 1; % 1/s
Xp = 1; % 1/s
Xr = 1; % 1/s
K = 0.33; % mM
deltaT = 0.01; % s
maxT = 20; % s
numiterations = maxT/deltaT;
t = 0:deltaT:maxT;

fig11 = figure(11);
for Xrna_0 = 0:0.2:1.4 % initial concentration (mM)
    for Xprot_0 = 0:0.2:1.4 % initial concentration (mM)
        Xrna = zeros(size(t));
        Xprot = zeros(size(t));
        Xrna(1) = Xrna_0;
        Xprot(1) = Xprot_0;
        for i = 1:numiterations
            dXrnadt = ((u*(Xprot(i)^2)) / ((K^2)+(Xprot(i)^2))) - (Xr*Xrna(i));
            dXprotdt = (w*Xrna(i)) - (Xp*Xprot(i));
            Xrna(i+1) = Xrna(i) + dXrnadt*deltaT;
            Xprot(i+1) = Xprot(i) + dXprotdt*deltaT;
        end
        plot(Xprot, Xrna)
        hold on
    end
end
```

```
xlabel('[X_{protein}] (mM)')
ylabel('[X_{RNA}] (mM)')
hold off
```



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