Homework Cover Sheet

Student Name: David Hwang
SBU ID: 116049238
Homework # (Unit): module 1

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 10 2024

Part A

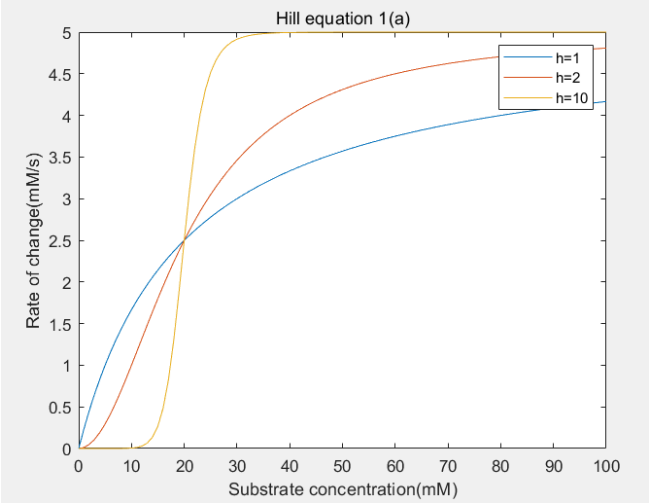
1.

Let K(½) = K

(a)

```
Vmax = 5;
K = 20;
S1 = []; S2=[]; S3=[];
V1 = []; V2=[]; V3=[];
% h = 1
h = 1;
for (i=0:100)
   S1(i+1) = i;
   V1(i+1) = (Vmax*(S1(i+1)^h))/(K^h + S1(i+1)^h);
end
plot(S1,V1)
% h = 2
h = 2;
for (i=0:100)
   S2(i+1) = i;
   V2(i+1) = (Vmax*(S2(i+1)^h))/(K^h + S2(i+1)^h);
end
hold on
plot(S2,V2)
% h = 10
h = 10;
for (i=0:100)
   S3(i+1) = i;
   V3(i+1) = (Vmax*(S3(i+1)^h))/(K^h + S3(i+1)^h);
end
plot(S3,V3)
hold off
```

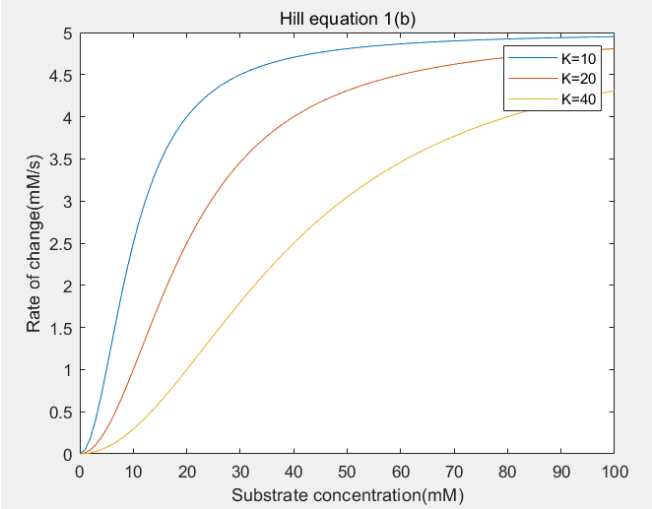
```
xlabel('Substrate concentration(mM)')
ylabel('Rate of change(mM/s)')
legend('h=1','h=2','h=10')
title('Hill equation 1(a)')
```



(b)

```
Vmax = 5;
h = 2;
S1 = []; S2=[]; S3=[];
V1 = []; V2=[]; V3=[];
%K =10
K = 10;
for (i=0:100)
   S1(i+1) = i;
   V1(i+1) = (Vmax*(S1(i+1)^h))/(K^h + S1(i+1)^h);
end
plot(S1,V1)
%K =20
K = 20;
for (i=0:100)
   S2(i+1) = i;
   V2(i+1) = (Vmax*(S2(i+1)^h))/(K^h + S2(i+1)^h);
end
hold on
plot(S2,V2)
%K =40
K = 40;
for (i=0:100)
   S3(i+1) = i;
   V3(i+1) = (Vmax*(S3(i+1)^h))/(K^h + S3(i+1)^h);
end
plot(S3,V3)
hold off
xlabel('Substrate concentration(mM)')
```

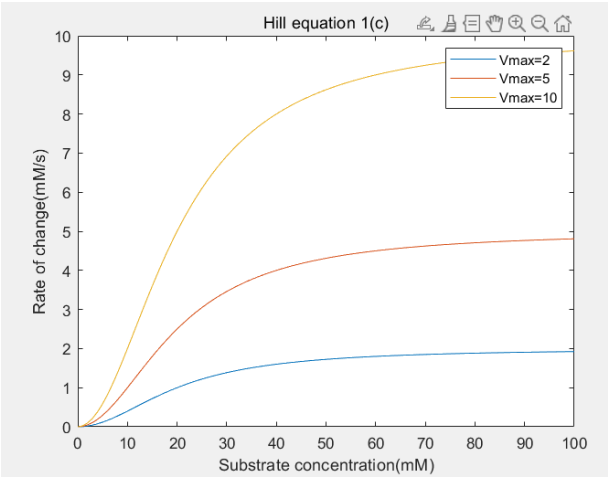
```
ylabel('Rate of change(mM/s)')
legend('K=10','K=20','K=40')
title('Hill equation 1(b)')
```



(c)

```
K = 20;
h = 2;
S1 = []; S2=[]; S3=[];
V1 = []; V2=[]; V3=[];
%Vmax=2
Vmax = 2;
for (i=0:100)
   S1(i+1) = i;
   V1(i+1) = (Vmax*(S1(i+1)^h))/(K^h + S1(i+1)^h);
end
plot(S1,V1)
%Vmax=5
Vmax =5;
for (i=0:100)
   S2(i+1) = i;
   V2(i+1) = (Vmax*(S2(i+1)^h))/(K^h + S2(i+1)^h);
end
hold on
plot(S2,V2)
%Vmax=10
Vmax = 10;
for (i=0:100)
   S3(i+1) = i;
   V3(i+1) = (Vmax*(S3(i+1)^h))/(K^h + S3(i+1)^h);
end
plot(S3,V3)
hold off
xlabel('Substrate concentration(mM)')
```

```
ylabel('Rate of change(mM/s)')
legend('Vmax=2','Vmax=5','Vmax=10')
title('Hill equation 1(c)')
```



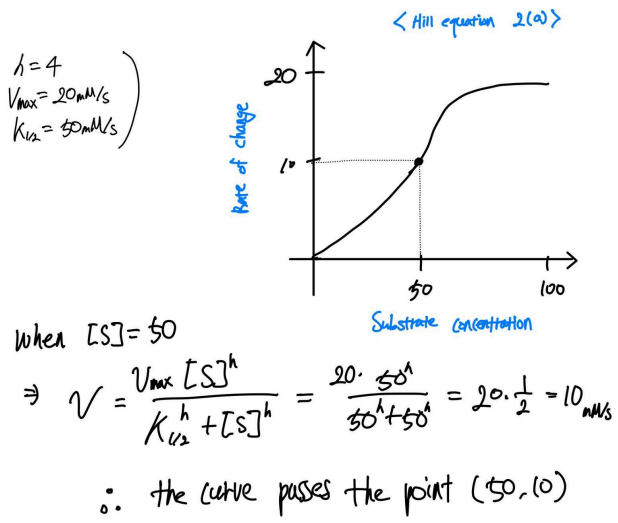
(d)

The curves have the same starting point, but because the variables are different, the curve's model and the value it converges are different.

From (a), I could see that if [S]=K(½), the rate of change has(Vmax/2). Also, as the Hill coefficient increases, the graph converges very rapidly to the 'rate of change'=Vmax line. From (b), it was confirmed that the graph slowly converges to 'rate of change'=Vmax line as the value of K(½) increases. And from (c), It was confirmed that 'rate of change'=Vmax line is the point where the curves approach

2.

(a)

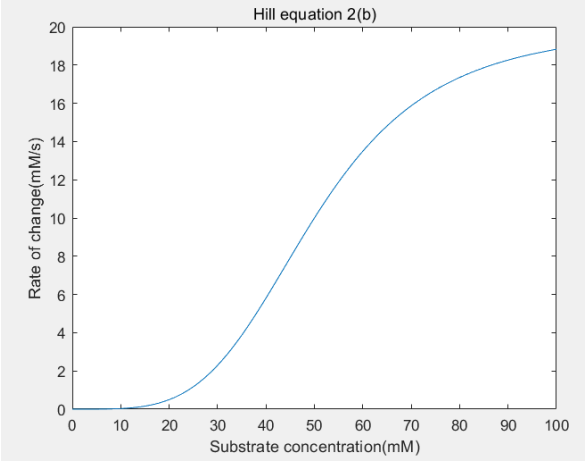


I expected when [S] is small, the rate of change increases little by little because the influence of K(½) is large and as [S] increases, the influence of K(½) becomes negligible and eventually converses to the maximum speed, Vmax.

(b)

```
K = 50; h = 4;
S1 = []; V1 = [];
Vmax = 20;
for (i=0:100)
   S1(i+1) = i;
   V1(i+1) = (Vmax*(S1(i+1)^h))/(K^h + S1(i+1)^h);
end
plot(S1,V1)
xlabel('Substrate concentration(mM)')
ylabel('Rate of change(mM/s)')
title('Hill equation 2(b)')
```

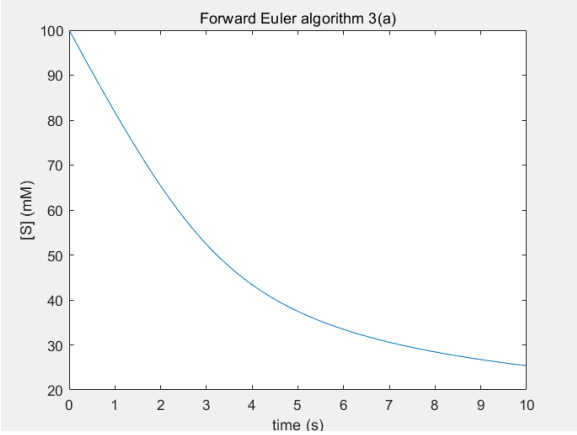
Before [S] became 50 I thought the speed would increase slowly, but due to the influence of the hill coefficient, I found that even a small increase in [S] increases the speed significantly.



3. Let K(½) = K and S =[S]

(a)

```
h=4; Vmax = 20; K=50;
totaltime = 10;
stepsize = 0.01;
numsteps = totaltime/stepsize;
% let S = [S] : the concetration of substrate
S = zeros(numsteps,1);
t = zeros(numsteps,1);
S(1)=100; t(1)=0;
for (i=1:numsteps-1)
   dS_dt = -Vmax*(S(i)^h)/(K^h + S(i)^h);
   S(i+1) = S(i) + dS_dt*stepsize;
   t(i+1) = t(i) + stepsize;
end
plot(t,S)
xlabel('time (s)')
ylabel('[S] (mM)')
title('Forward Euler algorithm 3(a)')
```



(b)

2(b) represents the change in V according to [S] through hill equation, and 3(a) is different because it is a graph that predicts how [S] changes according to the change in time for 10 seconds from the initial point using that V we got in 2(b).

However, Since they both use the same Hill equation with the same parameters, we can see that depending on the V value at the specific value of [S] in 2(a)graph, the rate of change of the value of [S] in 3(a)graph becomes large or small.

Part B

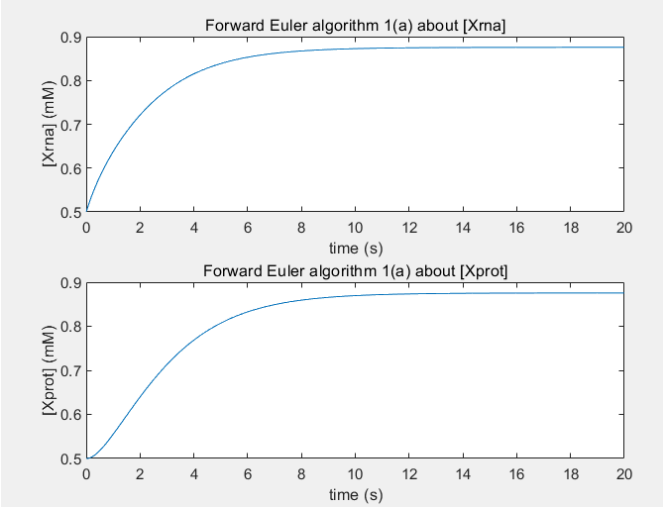
1.

Terms Xprot & Xrna in this coding mean the concentration of Xprot and Xrna

Terms CXprot & CXrna in this coding mean Xprot and Xrna in the system of ODEs

(a)

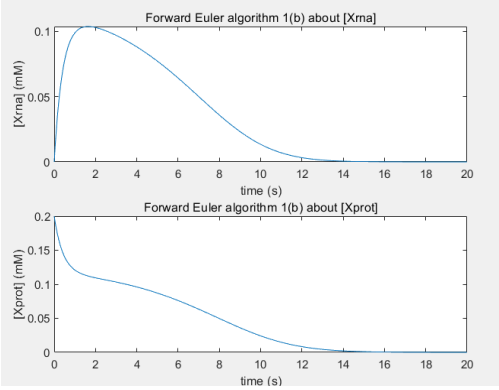
```
% Xprot means [Xprot] Xrna means [Xrna] from the ODE
% CXprot means Xprot  CXrna means Xrna from the ODE
% K = K(1/2)
w=1; u=1; CXprot=1; CXrna=1; K=0.33;
totaltime = 20;
stepsize = 0.01;
numsteps = totaltime/stepsize;
Xprot = zeros(numsteps,1);
Xrna = zeros(numsteps,1);
t = zeros(numsteps,1);
Xprot(1)=0.5; Xrna(1)=0.5; t(1)=0;
for (i=1:numsteps-1)
   dXrna_dt = u*(Xprot(i)^2)/(K^2+Xprot(i)^2)-CXrna*Xrna(i);
   dXprot_dt = w*Xrna(i) - CXprot*Xprot(i);
   Xrna(i+1) = Xrna(i) + dXrna_dt*stepsize;
   Xprot(i+1) = Xprot(i) + dXprot_dt*stepsize;
   t(i+1) = t(i) + stepsize;
end
figure(1)
subplot(2,1,1)
plot(t,Xrna)
xlabel('time (s)')
ylabel('[Xrna] (mM)')
title('Forward Euler algorithm 1(a) about [Xrna]')
subplot(2,1,2)
plot(t,Xprot)
ylabel('[Xprot] (mM)')
xlabel('time (s)')
title('Forward Euler algorithm 1(a) about [Xprot]')
```



(b)

```
w=1; u=1; CXprot=1; CXrna=1; K=0.33;
totaltime = 20;
```

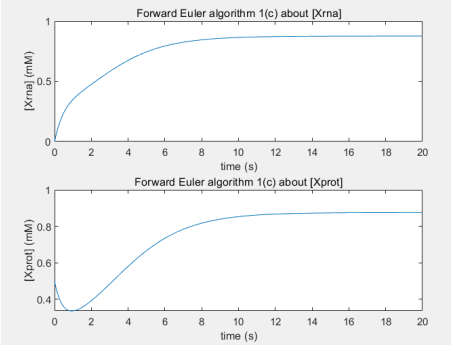
```
stepsize = 0.01;
numsteps = totaltime/stepsize;
Xprot = zeros(numsteps,1);
Xrna = zeros(numsteps,1);
t = zeros(numsteps,1);
Xprot(1)=0.2; Xrna(1)=0; t(1)=0;
for (i=1:numsteps-1)
   dXrna_dt = u*(Xprot(i)^2)/(K^2+Xprot(i)^2)-CXrna*Xrna(i);
   dXprot_dt = w*Xrna(i) - CXprot*Xprot(i);
   Xrna(i+1) = Xrna(i) + dXrna_dt*stepsize;
   Xprot(i+1) = Xprot(i) + dXprot_dt*stepsize;
   t(i+1) = t(i) + stepsize;
end
figure(1)
subplot(2,1,1)
plot(t,Xrna)
xlabel('time (s)')
ylabel('[Xrna] (mM)')
title('Forward Euler algorithm 1(b) about [Xrna]')
subplot(2,1,2)
plot(t,Xprot)
ylabel('[Xprot] (mM)')
xlabel('time (s)')
title('Forward Euler algorithm 1(b) about [Xprot]')
```



(c)

```
w=1; u=1; CXprot=1; CXrna=1; K=0.33;
totaltime = 20;
stepsize = 0.01;
numsteps = totaltime/stepsize;
Xprot = zeros(numsteps,1);
Xrna = zeros(numsteps,1);
t = zeros(numsteps,1);
Xprot(1)=0.5; Xrna(1)=0; t(1)=0;
for (i=1:numsteps-1)
   dXrna_dt = u*(Xprot(i)^2)/(K^2+Xprot(i)^2)-CXrna*Xrna(i);
   dXprot_dt = w*Xrna(i) - CXprot*Xprot(i);
   Xrna(i+1) = Xrna(i) + dXrna_dt*stepsize;
   Xprot(i+1) = Xprot(i) + dXprot_dt*stepsize;
```

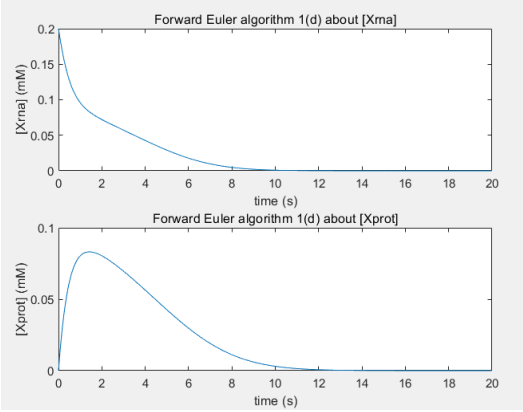
```
   t(i+1) = t(i) + stepsize;
end
figure(1)
subplot(2,1,1)
plot(t,Xrna)
xlabel('time (s)')
ylabel('[Xrna] (mM)')
title('Forward Euler algorithm 1(c) about [Xrna]')
subplot(2,1,2)
plot(t,Xprot)
ylabel('[Xprot] (mM)')
xlabel('time (s)')
title('Forward Euler algorithm 1(c) about [Xprot]')
```



(d)

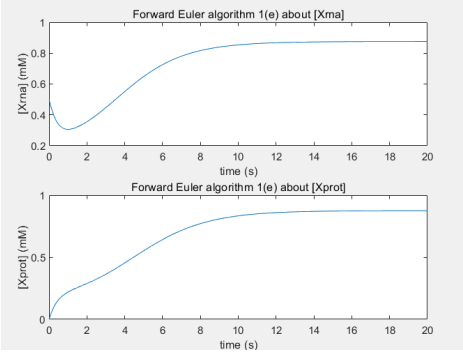
```
w=1; u=1; CXprot=1; CXrna=1; K=0.33;
totaltime = 20;
stepsize = 0.01;
numsteps = totaltime/stepsize;
Xprot = zeros(numsteps,1);
Xrna = zeros(numsteps,1);
t = zeros(numsteps,1);
Xprot(1)=0; Xrna(1)=0.2; t(1)=0;
for (i=1:numsteps-1)
   dXrna_dt = u*(Xprot(i)^2)/(K^2+Xprot(i)^2)-CXrna*Xrna(i);
   dXprot_dt = w*Xrna(i) - CXprot*Xprot(i);
   Xrna(i+1) = Xrna(i) + dXrna_dt*stepsize;
   Xprot(i+1) = Xprot(i) + dXprot_dt*stepsize;
   t(i+1) = t(i) + stepsize;
end
figure(1)
subplot(2,1,1)
plot(t,Xrna)
xlabel('time (s)')
ylabel('[Xrna] (mM)')
title('Forward Euler algorithm 1(d) about [Xrna]')
subplot(2,1,2)
plot(t,Xprot)
ylabel('[Xprot] (mM)')
```

```
xlabel('time (s)')
title('Forward Euler algorithm 1(d) about [Xprot]')
```



(e)

```
w=1; u=1; CXprot=1; CXrna=1; K=0.33;
totaltime = 20;
stepsize = 0.01;
numsteps = totaltime/stepsize;
Xprot = zeros(numsteps,1);
Xrna = zeros(numsteps,1);
t = zeros(numsteps,1);
Xprot(1)=0; Xrna(1)=0.5; t(1)=0;
for (i=1:numsteps-1)
   dXrna_dt = u*(Xprot(i)^2)/(K^2+Xprot(i)^2)-CXrna*Xrna(i);
   dXprot_dt = w*Xrna(i) - CXprot*Xprot(i);
   Xrna(i+1) = Xrna(i) + dXrna_dt*stepsize;
   Xprot(i+1) = Xprot(i) + dXprot_dt*stepsize;
   t(i+1) = t(i) + stepsize;
end
figure(1)
subplot(2,1,1)
plot(t,Xrna)
xlabel('time (s)')
ylabel('[Xrna] (mM)')
title('Forward Euler algorithm 1(e) about [Xrna]')
subplot(2,1,2)
plot(t,Xprot)
ylabel('[Xprot] (mM)')
xlabel('time (s)')
title('Forward Euler algorithm 1(e) about [Xprot]')
```



(f)

I found that the result values([Xprot]&[Xrna]) vary greatly depending on the initial value even if they are within the same condition of the system of ODEs and parameters.

2.

(a)

```
w=1; u=1; CXprot=1; CXrna=1; K=0.33;
totaltime = 20;
stepsize = 0.01;
numsteps = totaltime/stepsize;
Xprot = zeros(numsteps,1);
Xrna = zeros(numsteps,1);
t = zeros(numsteps,1);
for (i=0:0.2:1.4)
   Xrna(1)=i;
   for (j=0:0.2:1.4)
       Xprot(1)=j;
       t(1)=0;
       for (i=1:numsteps-1)
           dXrna_dt = u*(Xprot(i)^2)/(K^2+Xprot(i)^2)-CXrna*Xrna(i);
           dXprot_dt = w*Xrna(i) - CXprot*Xprot(i);
           Xrna(i+1) = Xrna(i) + dXrna_dt*stepsize;
           Xprot(i+1) = Xprot(i) + dXprot_dt*stepsize;
           t(i+1) = t(i) + stepsize;
       end
   end
end
```

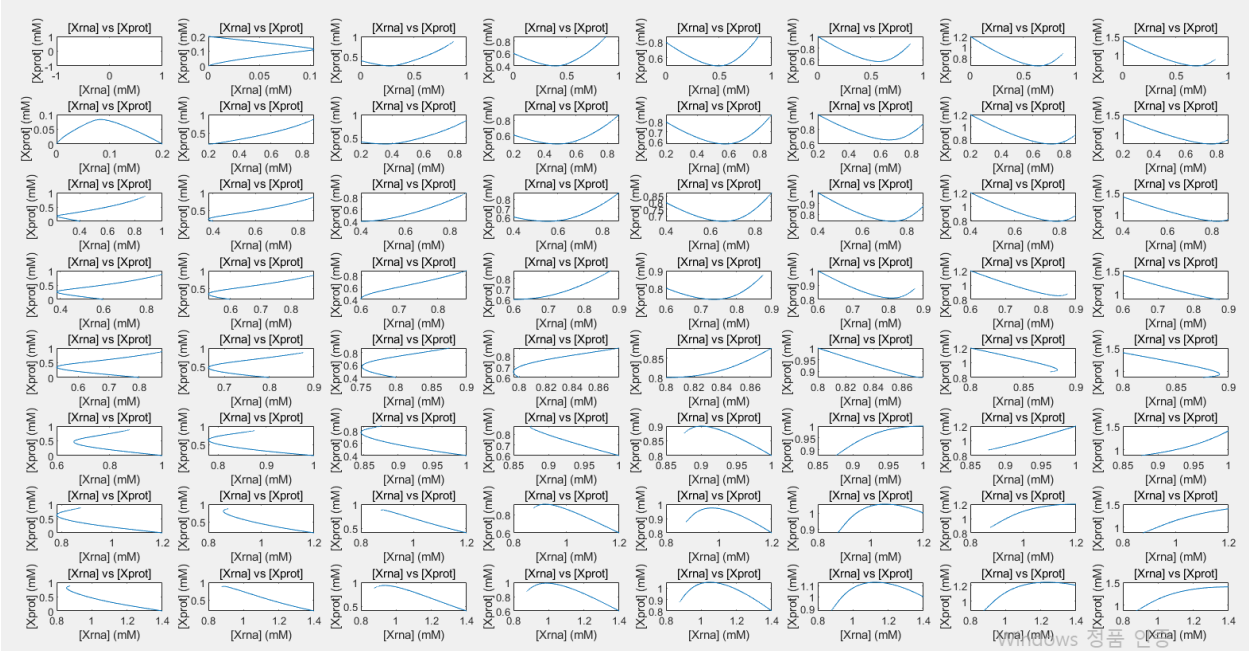
(b)

```
w=1; u=1; CXprot=1; CXrna=1; K=0.33;
totaltime = 20;
stepsize = 0.01;
numsteps = totaltime/stepsize;
Xprot = zeros(numsteps,1);
Xrna = zeros(numsteps,1);
t = zeros(numsteps,1);
n=0;
for (i=0:0.2:1.4)
   Xrna(1)=i;
```

```
    for (j=0:0.2:1.4)
        Xprot(1)=j;
        t(1)=0; n=n+1;
        for (i=1:numsteps-1)
            dXrna_dt = u*(Xprot(i)^2)/(K^2+Xprot(i)^2)-CXrna*Xrna(i);
            dXprot_dt = w*Xrna(i) - CXprot*Xprot(i);
            Xrna(i+1) = Xrna(i) + dXrna_dt*stepsize;
            Xprot(i+1) = Xprot(i) + dXprot_dt*stepsize;
            t(i+1) = t(i) + stepsize;
        end
        subplot(8,8,n)
        plot(Xrna,Xprot)
        xlabel('[Xrna] (mM)')
        ylabel('[Xprot] (mM)')
        title('[Xrna] vs [Xprot]')
    end
end
```

direction→: Initial value of [Xprot]+0.2

Direction↓: Initial value of [Xrna]+0.2



(c)

Each line has a different initial value. The lines indicate where the values of [Xprot] and [Xrna] go, depending on the initial value. Since it is not a graph about time, it is necessary to analyze it by thinking that lines start from the initial value of each graph. In particular, it can be seen that when the initial values of [Xprot] and [Xrna] are less than 1, the end values tend to increase, and when the initial values of [Xprot] and [Xrna] are greater than 1, the end values tend to decrease.

3.
This system is a model for a simple autoregulatory gene. During this process of making a protein, transcription and translation were represented as a system of ODEs. From graph 2(b), I came to know that if [Xprot] or [Xrna] is excessive, it will be reduced through this system, and if too little, it will be increased. This is consistent with the fact that the gradation rate in ODEs is proportional to [Xprot] and [Xrna]. Through this, I found that biologically, when we are in a strange situation, auto-regulatory genes tend to converge back to stable states.