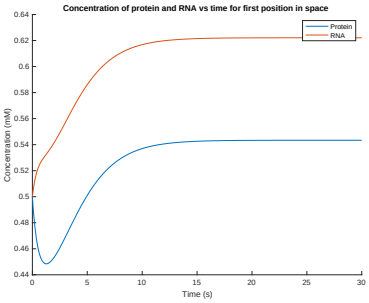
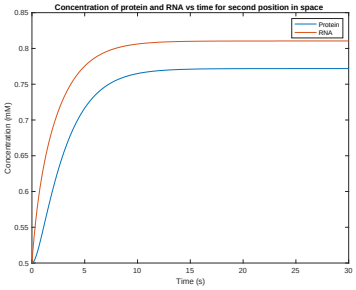
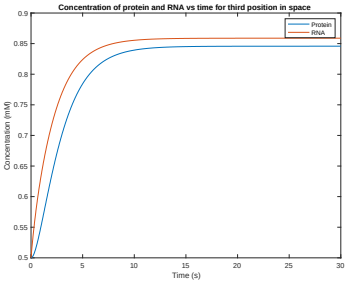
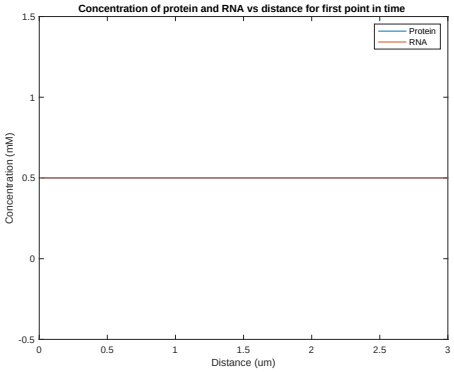
Part A: 1.

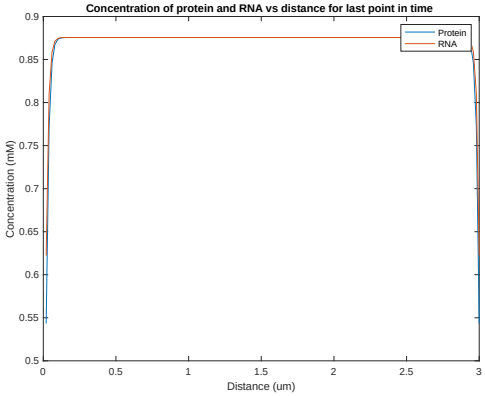






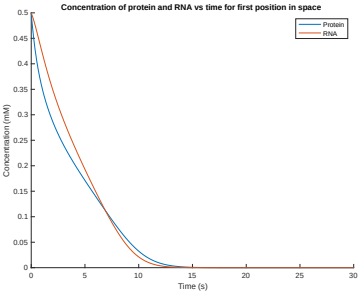
Figures 1-3 Plots of concentration of RNA and protein vs time of the first, second, and third positions in space of the Finite Difference / Forward Euler model of an autoregulatory gene. Initial conditions of 0.5mM of protein and RNA everywhere.

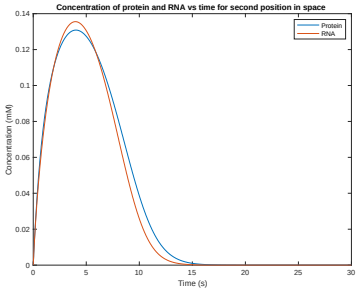


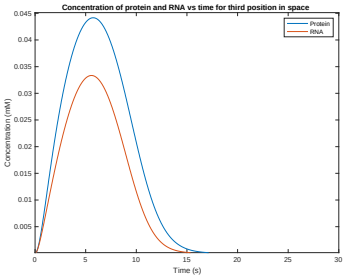


Figures 3-4 Plots of concentration of protein and RNA vs distance of one dimensional autoregulatory gene model. Initial conditions of 0.5mM of protein and RNA everywhere.

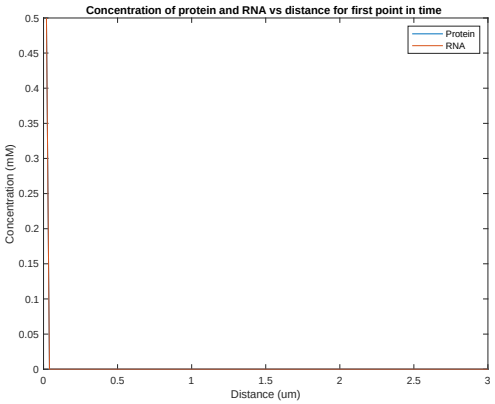
2.

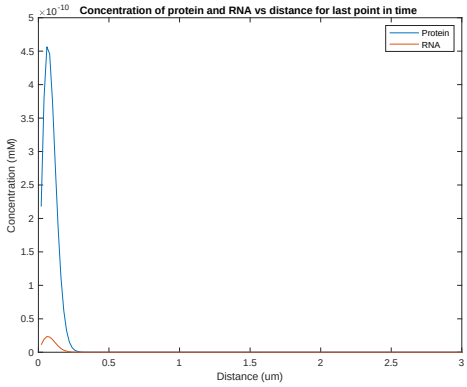






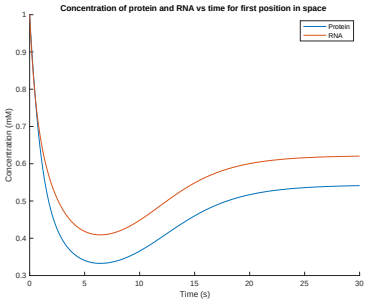
Figures 5-7 Plots of concentration of protein and RNA vs time for first, second and third positions in space with initial condition of 0.5mM of protein and RNA at first position only.

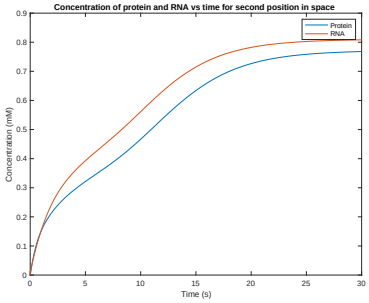


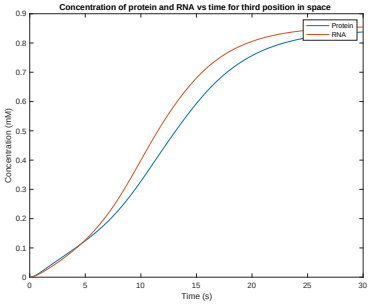


Figures 8-9 Plots of concentration of protein and RNA vs distance with initial conditions of 0.5 mM protein and RNA at position one only, zero everywhere else.

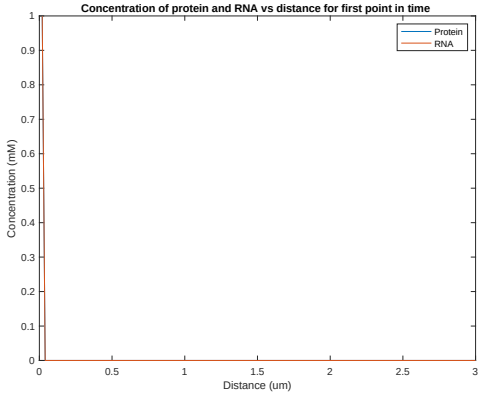
3.

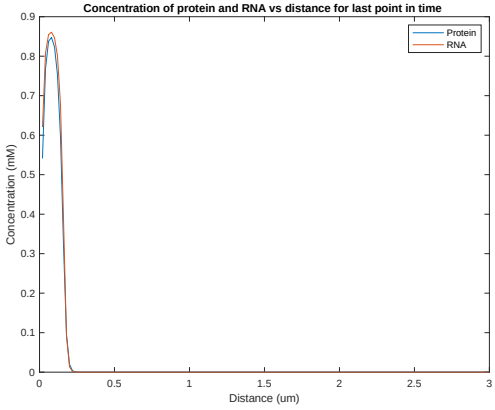






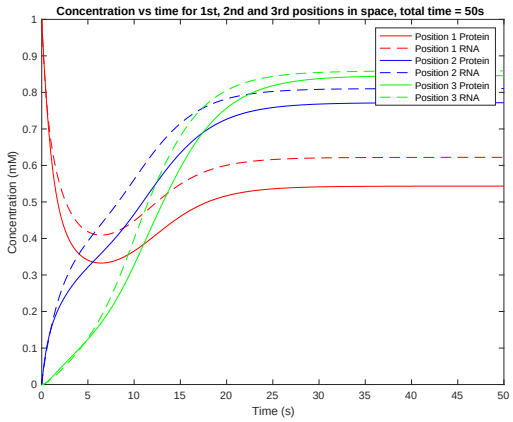
Figures 10-12 Plots of concentration of protein and RNA vs time for first, second and third positions in space with initial condition of 1.0 mM of protein and RNA at first position only.

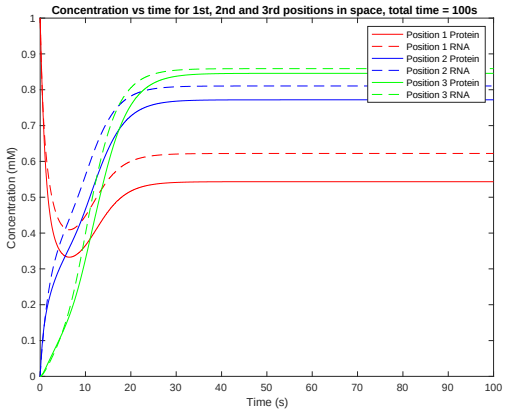


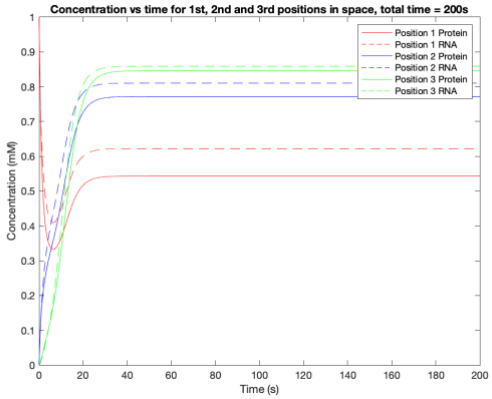


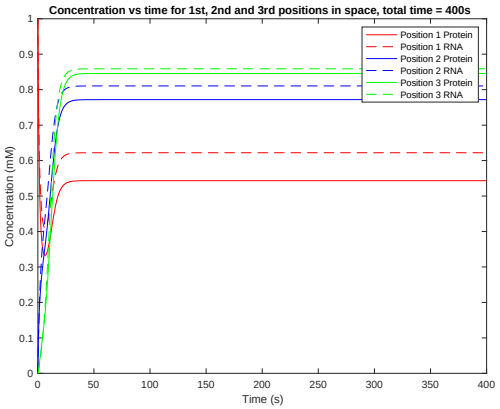
Figures 13-14 Plots of concentration of protein and RNA vs distance with initial conditions of 1.0 mM protein and RNA at position one only, zero everywhere else.

3.

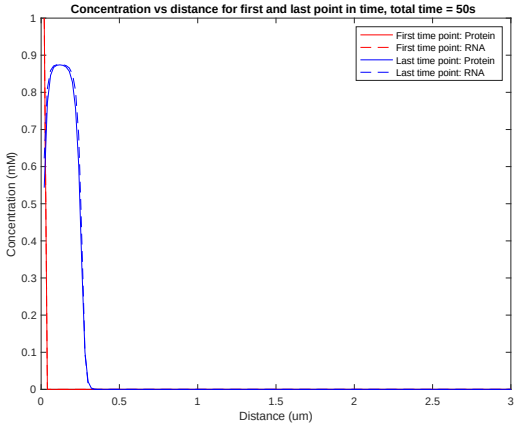


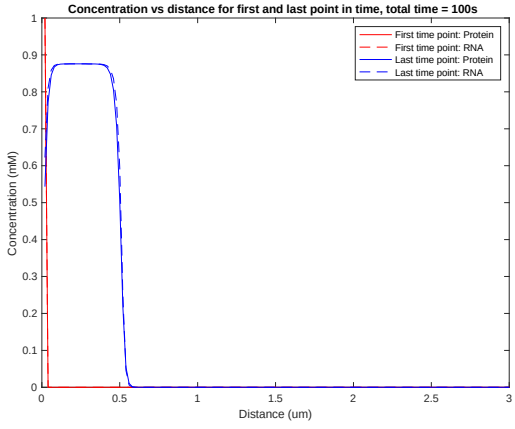


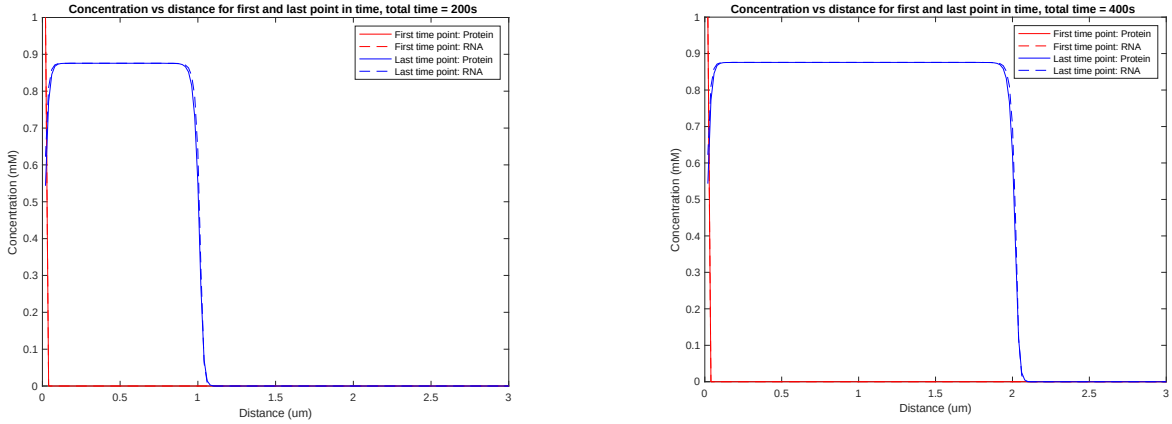




Figures 15-18 Plots of concentration vs time of protein and RNA for three different positions in space. Each plot has a different total time of simulation.



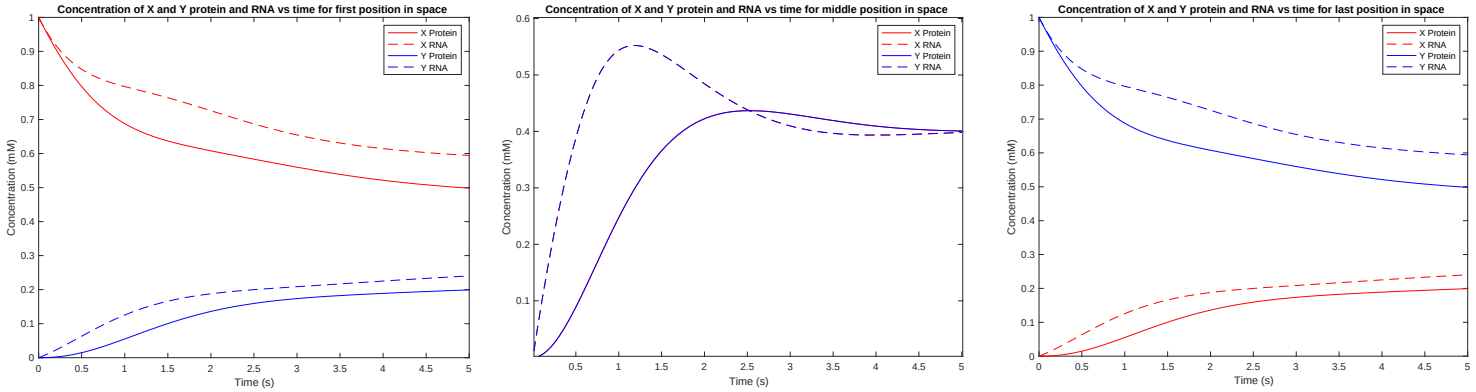




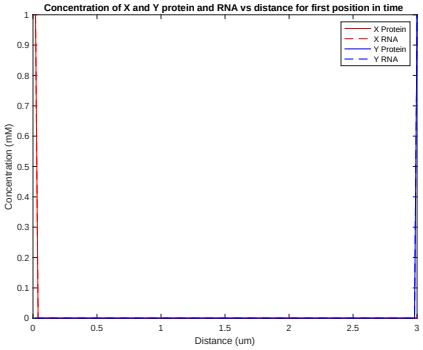
Figures 19-22 Plots of concentration vs distance of protein and RNA for first and last points in time. Each plot has a different total time of simulation.

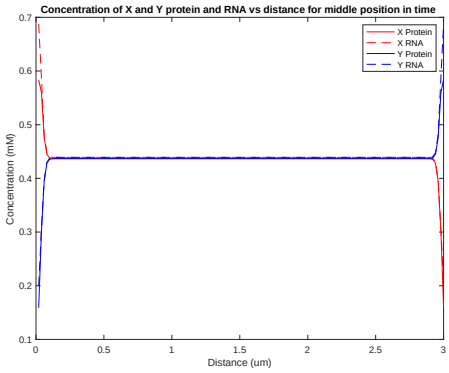
5. These results show that a steady state is reached at just under 0.9mM of protein and RNA. The steady state is initially reached only in the position closest to the point where the concentration starts high, and as the simulation is allowed to run for longer, the steady state moves outward and fills the distance (figures 19-22). The steady state is smaller near the edge because of the absorbing boundary conditions where the concentration is set to zero at the boundary, this pulls the concentration near the edge down because it is "diffusing" out the edge (this is seen in figures 15-18). The threshold of concentration of protein and RNA to bring the system to a steady state is somewhere between 0.5mM and 1.0mM because at 0.5mM the system goes to zero (figures 5-9) but at 1.0mM the system goes to a non-zero steady state (figures 10-12, just under 0.9mM).

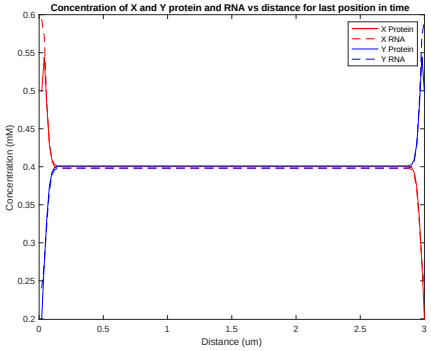
Part B 2.



Figures 23-25 Plots of concentration vs time for first, middle, and last positions in space of X and Y mutually inhibitory genes. Initial concentrations of 1.0mM for X protein and RNA at the first position and 1.0mM for Y protein and RNA at the last position. Figure 24 has both X and Y with the exact same values.

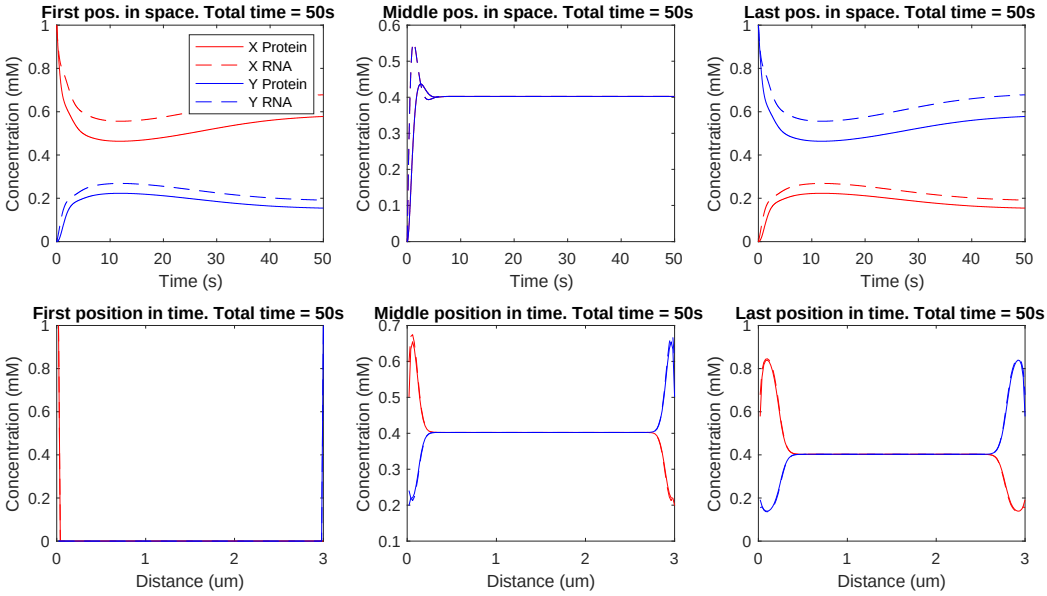


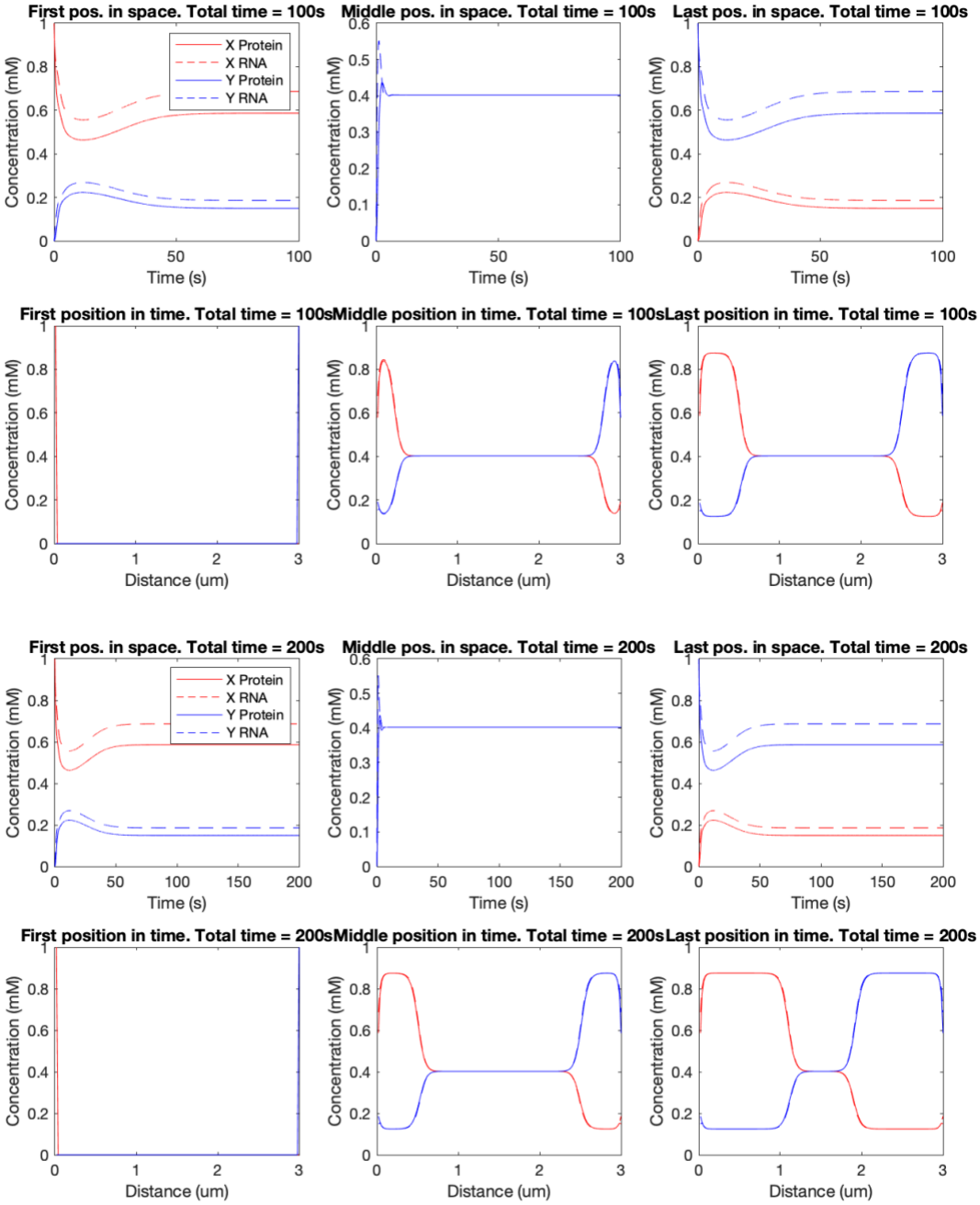


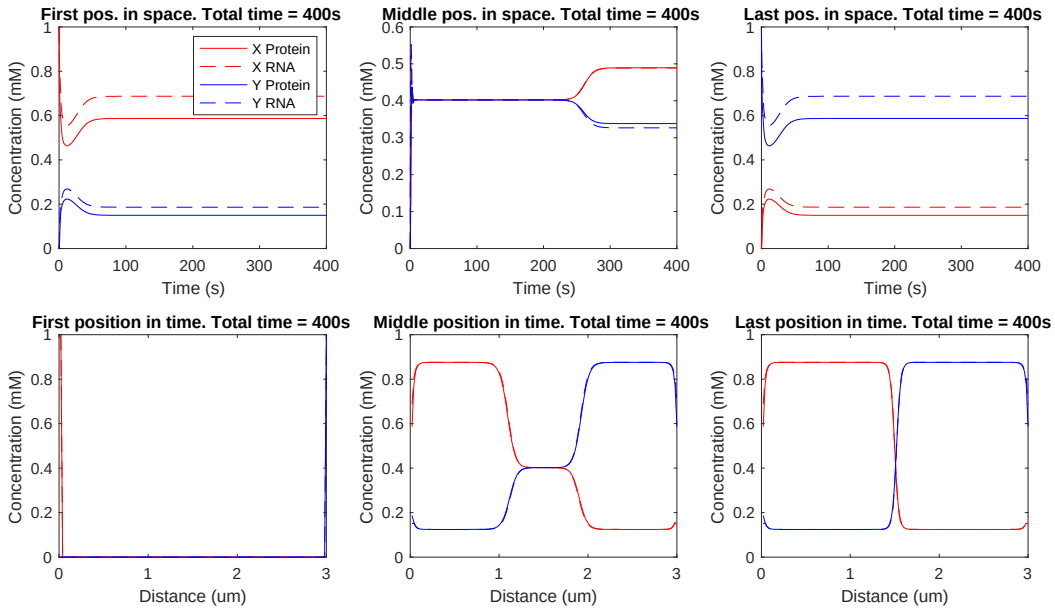


Figures 26-28 Plots of concentration vs distance for first, middle, and last points in time of X and Y mutually inhibitory genes. Initial concentrations of 1.0mM for X protein and RNA at the first position and 1.0mM for Y protein and RNA at the last position.

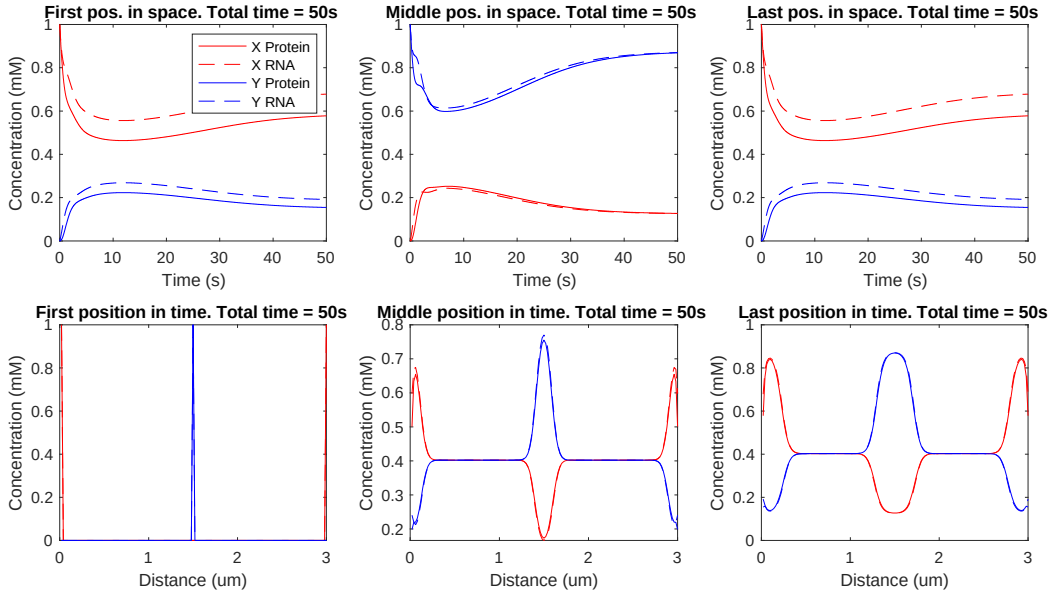
3.

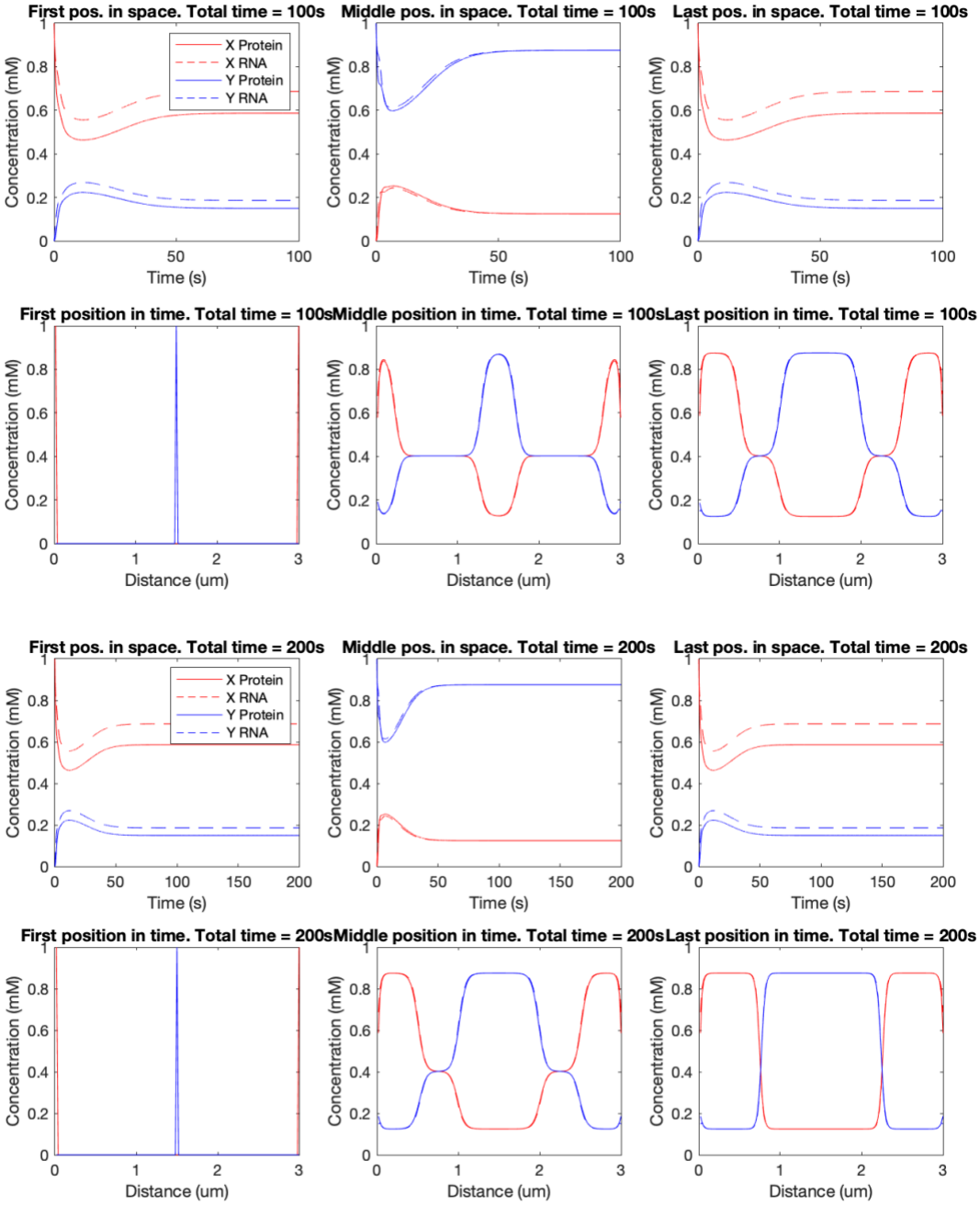


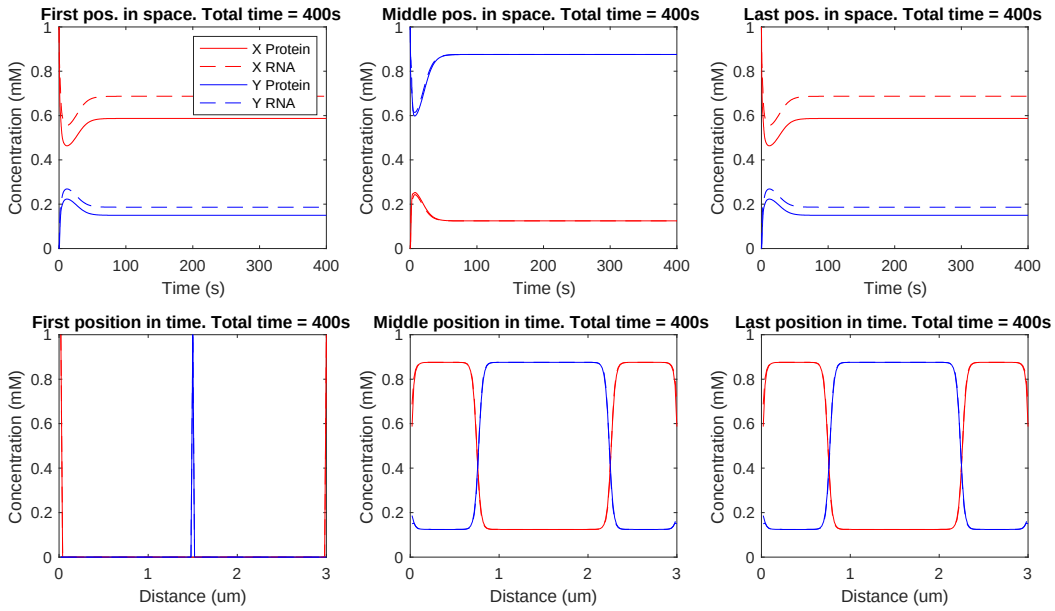

First pos. in space. Total time = 100s
Middle pos. in space. Total time = 100s
Last pos. in space. Total time = 100s
X Protein
X RNA
Y Protein
Y RNA
Concentration (mM)
Time (s)
First position in time. Total time = 100s
Middle position in time. Total time = 100s
Last position in time. Total time = 100s
Distance (um)
First pos. in space. Total time = 200s
Middle pos. in space. Total time = 200s
Last pos. in space. Total time = 200s
First position in time. Total time = 200s
Middle position in time. Total time = 200s
Last position in time. Total time = 200s



Figures 29-32 Plots of concentration vs distance and concentration vs time for first, middle, and last points in time and first middle and last points in space of X and Y mutually inhibitory genes. Varying total time conditions. Initial concentrations of 1.0mM for X protein and RNA at the first position and 1.0mM for Y protein and RNA at the last position.




First pos. in space. Total time = 100s
Middle pos. in space. Total time = 100s
Last pos. in space. Total time = 100s
X Protein
X RNA
Y Protein
Y RNA
Concentration (mM)
Time (s)
First position in time. Total time = 100s
Middle position in time. Total time = 100s
Last position in time. Total time = 100s
Distance (um)
First pos. in space. Total time = 200s
Middle pos. in space. Total time = 200s
Last pos. in space. Total time = 200s
First position in time. Total time = 200s
Middle position in time. Total time = 200s
Last position in time. Total time = 200s



Figures 33-36 Plots of concentration vs distance and concentration vs time for first, middle, and last points in time and first middle and last points in space of X and Y mutually inhibitory genes. Varying total time conditions. Initial concentrations of 1.0mM for X protein and RNA at the first and last position and 1.0mM for Y protein and RNA at the middle position.

These results show that steady states begin to form in areas near where the initial concentration were set to one. This is seen in the concentration vs distance plots where as the time gets longer, the steady states expand in distance and eventually stop expanding around 200s where areas of high X and low Y are directly neighboring areas of high Y and low X. We also see that for part (3), the middle position in space plot of concentration vs time appears to only have one line because the concentrations are exactly the same for protein X and Y protein and RNA. This is a result of using mass action kinetics which is a deterministic model that always gives the same result and does not depend on randomness, like a real system would.

Appendix

Part A: 1

```
%set up time and space parameters
timestep = 0.01;
totaltime = 30;
time = (0:timestep:totaltime);
numtsteps = totaltime/timestep;
distancestep = 0.02;
totaldistance = 3;
distance = (distancestep:distancestep:totaldistance);
numdsteps = totaldistance/distancestep;

%initialize protein and RNA matrices: rows are distance, columns are time
Xrna = zeros(numdsteps, numtsteps);
```

```
Xprot = zeros(numdsteps, numtsteps);

%initial conditions
Xrna(:,1) = 0.5;
Xprot(:,1) = 0.5;

for (t=1:numtsteps)
    for (i=1:numdsteps)



        %find laplacian for each species with absorbing boundary conditions
        switch i
            case 1
                lap_rna = (Xrna(2,t) - 2*Xrna(1,t))/ distancestep^2;
                lap_prot = (Xprot(2,t) - 2*Xprot(1,t))/ distancestep^2;
            case numdsteps
                lap_rna = (Xrna(numdsteps-1,t)-2*Xrna(numdsteps,t)) /
distancestep^2;
                lap_prot = (Xprot(numdsteps-1,t)-2*Xprot(numdsteps,t)) /
distancestep^2;
            otherwise
                lap_rna = (Xrna(i+1, t) + Xrna(i-1, t) - 2*Xrna(i, t)) /
distancestep^2;
                lap_prot = (Xprot(i+1, t) + Xprot(i-1, t) - 2*Xprot(i, t)) /
distancestep^2;
        end



        %find rates for each species
        dXprot_dt = Xrna(i, t) - Xprot(i, t) + 0.0001*lap_prot;
        dXrna_dt = ( (Xprot(i,t)^2)/((0.33^2) + (Xprot(i,t)^2)) ) - Xrna(i,t)
+ 0.0001*lap_rna;

        %forward euler
        Xprot(i, t+1) = Xprot(i,t) + dXprot_dt*timestep;
        Xrna(i, t+1) = Xrna(i,t) + dXrna_dt*timestep;

    end

end
hold on
figure(1)
plot(time, Xprot(1,:), 'DisplayName', 'Protein')
plot(time, Xrna(1,:), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs time for first position in space')
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off

figure(2)
plot(time, Xprot(2,:), 'DisplayName', 'Protein')
hold on
plot(time, Xrna(2,:), 'DisplayName', 'RNA')
```

```
title('Concentration of protein and RNA vs time for second position in
space')
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off

figure(3)
plot(time, Xprot(3,:), 'DisplayName', 'Protein')
hold on
plot(time, Xrna(3,:), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs time for third position in space')
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off

figure(4)
plot(distance, Xprot(:,1), 'DisplayName', 'Protein')
hold on
plot(distance, Xrna(:,1), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs distance for first point in time')
xlabel('Distance (um)')
ylabel('Concentration (mM)')
legend()
hold off

figure(5)
plot(distance, Xprot(:,numtsteps), 'DisplayName', 'Protein')
hold on
plot(distance, Xrna(:,numtsteps), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs distance for last point in time')
xlabel('Distance (um)')
ylabel('Concentration (mM)')
hold off
legend()
```

Part A: 2

```
%set up time and space parameters
timestep = 0.01;
totaltime = 30;
time = (0:timestep:totaltime);
numtsteps = totaltime/timestep;
distancestep = 0.02;
totaldistance = 3;
distance = (distancestep:distancestep:totaldistance);
numdsteps = totaldistance/distancestep;

%initialize protein and RNA matrices: rows are distance, columns are time
Xrna = zeros(numdsteps, numtsteps);
Xprot = zeros(numdsteps, numtsteps);

%initial conditions
Xrna(1,1) = 0.5;
Xprot(1,1) = 0.5;
```

```
for (t=1:numtsteps)
    for (i=1:numdsteps)



        %find laplacian for each species with absorbing boundary conditions
        switch i
            case 1
                lap_rna = (Xrna(2,t) - 2*Xrna(1,t))/ distancestep^2;
                lap_prot = (Xprot(2,t) - 2*Xprot(1,t))/ distancestep^2;
            case numdsteps
                lap_rna = (Xrna(numdsteps-1,t)-2*Xrna(numdsteps,t)) /
distancestep^2;
                lap_prot = (Xprot(numdsteps-1,t)-2*Xprot(numdsteps,t)) /
distancestep^2;
            otherwise
                lap_rna = (Xrna(i+1, t) + Xrna(i-1, t) - 2*Xrna(i, t)) /
distancestep^2;
                lap_prot = (Xprot(i+1, t) + Xprot(i-1, t) - 2*Xprot(i, t)) /
distancestep^2;
        end


        %find rates for each species
        dXprot_dt = Xrna(i, t) - Xprot(i, t) + 0.0001*lap_prot;
        dXrna_dt = ( (Xprot(i,t)^2)/((0.33^2) + (Xprot(i,t)^2)) ) - Xrna(i,t)
+ 0.0001*lap_rna;

        %forward euler
        Xprot(i, t+1) = Xprot(i,t) + dXprot_dt*timestep;
        Xrna(i, t+1) = Xrna(i,t) + dXrna_dt*timestep;

    end

end
hold on
figure(1)
plot(time, Xprot(1,:), 'DisplayName', 'Protein')
plot(time, Xrna(1,:), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs time for first position in space')
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off

figure(2)
plot(time, Xprot(2,:), 'DisplayName', 'Protein')
hold on
plot(time, Xrna(2,:), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs time for second position in
space')
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
```

```
hold off

figure(3)
plot(time, Xprot(3,:), 'DisplayName', 'Protein')
hold on
plot(time, Xrna(3,:), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs time for third position in space')
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off

figure(4)
plot(distance, Xprot(:,1), 'DisplayName', 'Protein')
hold on
plot(distance, Xrna(:,1), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs distance for first point in time')
xlabel('Distance (um)')
ylabel('Concentration (mM)')
legend()
hold off

figure(5)
plot(distance, Xprot(:,numtsteps), 'DisplayName', 'Protein')
hold on
plot(distance, Xrna(:,numtsteps), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs distance for last point in time')
xlabel('Distance (um)')
ylabel('Concentration (mM)')
hold off
legend()
```

Part A: 3

```
%set up time and space parameters
timestep = 0.01;
totaltime = 30;
time = (0:timestep:totaltime);
numtsteps = totaltime/timestep;
distancestep = 0.02;
totaldistance = 3;
distance = (distancestep:distancestep:totaldistance);
numdsteps = totaldistance/distancestep;

%initialize protein and RNA matrices: rows are distance, columns are time
Xrna = zeros(numdsteps, numtsteps);
Xprot = zeros(numdsteps, numtsteps);

%initial conditions
Xrna(1,1) = 1;
Xprot(1,1) = 1;

for (t=1:numtsteps)
    for (i=1:numdsteps)
```

```
        %find laplacian for each species with absorbing boundary conditions
        switch i
            case 1
                lap_rna = (Xrna(2,t) - 2*Xrna(1,t))/ distancestep^2;
                lap_prot = (Xprot(2,t) - 2*Xprot(1,t))/ distancestep^2;
            case numdsteps
                lap_rna = (Xrna(numdsteps-1,t)-2*Xrna(numdsteps,t)) /
distancestep^2;
                lap_prot = (Xprot(numdsteps-1,t)-2*Xprot(numdsteps,t)) /
distancestep^2;
            otherwise
                lap_rna = (Xrna(i+1, t) + Xrna(i-1, t) - 2*Xrna(i, t)) /
distancestep^2;
                lap_prot = (Xprot(i+1, t) + Xprot(i-1, t) - 2*Xprot(i, t)) /
distancestep^2;
        end


        %find rates for each species
        dXprot_dt = Xrna(i, t) - Xprot(i, t) + 0.0001*lap_prot;
        dXrna_dt = ( (Xprot(i,t)^2)/((0.33^2) + (Xprot(i,t)^2)) ) - Xrna(i,t)
+ 0.0001*lap_rna;

        %forward euler
        Xprot(i, t+1) = Xprot(i,t) + dXprot_dt*timestep;
        Xrna(i, t+1) = Xrna(i,t) + dXrna_dt*timestep;

    end

end
hold on
figure(1)
plot(time, Xprot(1,:), 'DisplayName', 'Protein')
plot(time, Xrna(1,:), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs time for first position in space')
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off

figure(2)
plot(time, Xprot(2,:), 'DisplayName', 'Protein')
hold on
plot(time, Xrna(2,:), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs time for second position in
space')
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off

figure(3)
plot(time, Xprot(3,:), 'DisplayName', 'Protein')
hold on
```

```
plot(time, Xrna(3,:), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs time for third position in space')
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off

figure(4)
plot(distance, Xprot(:,1), 'DisplayName', 'Protein')
hold on
plot(distance, Xrna(:,1), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs distance for first point in time')
xlabel('Distance (um)')
ylabel('Concentration (mM)')
legend()
hold off

figure(5)
plot(distance, Xprot(:,numtsteps), 'DisplayName', 'Protein')
hold on
plot(distance, Xrna(:,numtsteps), 'DisplayName', 'RNA')
title('Concentration of protein and RNA vs distance for last point in time')
xlabel('Distance (um)')
ylabel('Concentration (mM)')
hold off
legend()
```

Part A: 4

```
%set up time and space parameters
timestep = 0.01;
times = [50, 100, 200, 400];
fig=1;

for (k=1:4)
totaltime=times(k);
time = (0:timestep:totaltime);
numtsteps = totaltime/timestep;
distancestep = 0.02;
totaldistance = 3;
distance = (distancestep:distancestep:totaldistance);
numdsteps = totaldistance/distancestep;

%initialize protein and RNA matrices: rows are distance, columns are time
Xrna = zeros(numdsteps, numtsteps);
Xprot = zeros(numdsteps, numtsteps);

%initial conditions
Xrna(1,1) = 1;
Xprot(1,1) = 1;

for (t=1:numtsteps)
    for (i=1:numdsteps)
```

```
        %find laplacian for each species with absorbing boundary conditions
        switch i
            case 1
                lap_rna = (Xrna(2,t) - 2*Xrna(1,t))/ distancestep^2;
                lap_prot = (Xprot(2,t) - 2*Xprot(1,t))/ distancestep^2;
            case numdsteps
                lap_rna = (Xrna(numdsteps-1,t)-2*Xrna(numdsteps,t)) /
distancestep^2;
                lap_prot = (Xprot(numdsteps-1,t)-2*Xprot(numdsteps,t)) /
distancestep^2;
            otherwise
                lap_rna = (Xrna(i+1, t) + Xrna(i-1, t) - 2*Xrna(i, t)) /
distancestep^2;
                lap_prot = (Xprot(i+1, t) + Xprot(i-1, t) - 2*Xprot(i, t)) /
distancestep^2;
        end


        %find rates for each species
        dXprot_dt = Xrna(i, t) - Xprot(i, t) + 0.0001*lap_prot;
        dXrna_dt = ( (Xprot(i,t)^2)/((0.33^2) + (Xprot(i,t)^2)) ) - Xrna(i,t)
+ 0.0001*lap_rna;

        %forward euler
        Xprot(i, t+1) = Xprot(i,t) + dXprot_dt*timestep;
        Xrna(i, t+1) = Xrna(i,t) + dXrna_dt*timestep;

    end

end
```

```
figure(fig)
plot(time, Xprot(1,:), 'r', 'DisplayName', 'Position 1 Protein')
hold on
plot(time, Xrna(1,:),'r','LineStyle','--','DisplayName', 'Position 1 RNA')

plot(time, Xprot(2,:), 'b','DisplayName', 'Position 2 Protein')
plot(time, Xrna(2,:), 'b','LineStyle','--','DisplayName', 'Position 2 RNA')

plot(time, Xprot(3,:), 'g','DisplayName', 'Position 3 Protein')
plot(time, Xrna(3,:), 'g','LineStyle','--', 'DisplayName', 'Position 3 RNA')
title(sprintf('Concentration vs time for 1st, 2nd and 3rd positions in space,
total time = %ds', totaltime))
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off

fig = fig + 1;
figure(fig)
```

```
plot(distance, Xprot(:,1), 'r','DisplayName', 'First time point: Protein')
hold on
plot(distance, Xrna(:,1),'r','LineStyle','--', 'DisplayName', 'First time
point: RNA')

plot(distance, Xprot(:,numtsteps), 'b','DisplayName', 'Last time point:
Protein')
plot(distance, Xrna(:,numtsteps), 'b','LineStyle','--', 'DisplayName', 'Last
time point: RNA')
title(sprintf('Concentration vs distance for first and last point in time,
total time = %ds' ,totaltime))
xlabel('Distance (um)')
ylabel('Concentration (mM)')
hold off
legend()

fig = fig + 1;

end
```

Part B: 2

```
%set up time and space parameters
timestep = 0.01;
totaltime=5;
time = (0:timestep:totaltime);
numtsteps = totaltime/timestep;
distancestep = 0.02;
totaldistance = 3;
distance = (distancestep:distancestep:totaldistance);
numdsteps = totaldistance/distancestep;

%initialize protein and RNA matrices: rows are distance, columns are time
Xrna = zeros(numdsteps, numtsteps);
Xprot = zeros(numdsteps, numtsteps);
Yrna = zeros(numdsteps, numtsteps);
Yprot = zeros(numdsteps, numtsteps);

%initial conditions
Xrna(1,1) = 1;
Xprot(1,1) = 1;
Yrna(numdsteps,1) = 1;
Yprot(numdsteps, 1) = 1;



for (t=1:numtsteps)
    for (i=1:numdsteps)



        %find laplacian for each species with absorbing boundary conditions
        switch i
            case 1
                lap_Xrna = (Xrna(2,t) - 2*Xrna(1,t))/ distancestep^2;
```

```
                lap_Xprot = (Xprot(2,t) - 2*Xprot(1,t))/ distancestep^2;
                lap_Yrna = (Yrna(2,t) - 2*Yrna(1,t))/ distancestep^2;
                lap_Yprot = (Yprot(2,t) - 2*Yprot(1,t))/ distancestep^2;
            case numdsteps
                lap_Xrna = (Xrna(numdsteps-1,t)-2*Xrna(numdsteps,t)) /
distancestep^2;
                lap_Xprot = (Xprot(numdsteps-1,t)-2*Xprot(numdsteps,t)) /
distancestep^2;
                lap_Yrna = (Yrna(numdsteps-1,t)-2*Yrna(numdsteps,t)) /
distancestep^2;
                lap_Yprot = (Yprot(numdsteps-1,t)-2*Yprot(numdsteps,t)) /
distancestep^2;
            otherwise
                lap_Xrna = (Xrna(i+1, t) + Xrna(i-1, t) - 2*Xrna(i, t)) /
distancestep^2;
                lap_Xprot = (Xprot(i+1, t) + Xprot(i-1, t) - 2*Xprot(i, t)) /
distancestep^2;
                lap_Yrna = (Yrna(i+1, t) + Yrna(i-1, t) - 2*Yrna(i, t)) /
distancestep^2;
                lap_Yprot = (Yprot(i+1, t) + Yprot(i-1, t) - 2*Yprot(i, t)) /
distancestep^2;
        end


        %find rates for each species
        dXprot_dt = Xrna(i, t) - Xprot(i, t) + 0.0001*lap_Xprot;
        dXrna_dt = (1 - ( (Yprot(i,t)^2)/((0.33^2) + (Yprot(i,t)^2)) )) -
Xrna(i,t) + 0.0001*lap_Xrna;
        dYprot_dt = Yrna(i, t) - Yprot(i, t) + 0.0001*lap_Yprot;
        dYrna_dt = (1 - ( (Xprot(i,t)^2)/((0.33^2) + (Xprot(i,t)^2)) )) -
Yrna(i,t) + 0.0001*lap_Yrna;

        %forward euler
        Xprot(i, t+1) = Xprot(i,t) + dXprot_dt*timestep;
        Xrna(i, t+1) = Xrna(i,t) + dXrna_dt*timestep;
        Yprot(i, t+1) = Yprot(i,t) + dYprot_dt*timestep;
        Yrna(i, t+1) = Yrna(i,t) + dYrna_dt*timestep;

    end

end


figure(1)
plot(time, Xprot(1,:), 'red','DisplayName', 'X Protein')
hold on
plot(time, Xrna(1,:),'red','LineStyle','--', 'DisplayName', 'X RNA')
plot(time, Yprot(1,:),'b', 'DisplayName','Y Protein')
plot(time, Yrna(1,:),'b','LineStyle','--','DisplayName','Y RNA')
title('Concentration of X and Y protein and RNA vs time for first position in
space')
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off
```

```
figure(2)
plot(time, Xprot((numdsteps/2),:), 'red','DisplayName', 'X Protein')
hold on
plot(time, Xrna((numdsteps/2),:),'red','LineStyle','--', 'DisplayName', 'X
RNA')
plot(time, Yprot((numdsteps/2),:),'b', 'DisplayName','Y Protein')
plot(time, Yrna((numdsteps/2),:),'b','LineStyle','--','DisplayName','Y RNA')
title('Concentration of X and Y protein and RNA vs time for middle position
in space')
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off

figure(3)
plot(time, Xprot(numdsteps,:), 'red','DisplayName', 'X Protein')
hold on
plot(time, Xrna(numdsteps,:),'red','LineStyle','--', 'DisplayName', 'X RNA')
plot(time, Yprot(numdsteps,:),'b', 'DisplayName','Y Protein')
plot(time, Yrna(numdsteps,:),'b','LineStyle','--','DisplayName','Y RNA')
title('Concentration of X and Y protein and RNA vs time for last position in
space')
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off

figure(4)
plot(distance,Xprot(:,1),'red','DisplayName', 'X Protein')
hold on
plot(distance, Xrna(:,1),'red','LineStyle','--', 'DisplayName', 'X RNA')
plot(distance, Yprot(:,1),'b', 'DisplayName','Y Protein')
plot(distance, Yrna(:,1),'b','LineStyle','--','DisplayName','Y RNA')
title('Concentration of X and Y protein and RNA vs distance for first
position in time')
xlabel('Distance (um)')
ylabel('Concentration (mM)')
legend()
hold off

figure(5)
plot(distance,Xprot(:,(numtsteps/2)),'red','DisplayName', 'X Protein')
hold on
plot(distance, Xrna(:,(numtsteps/2)),'red','LineStyle','--', 'DisplayName',
'X RNA')
plot(distance, Yprot(:,(numtsteps/2)),'b', 'DisplayName','Y Protein')
plot(distance, Yrna(:,(numtsteps/2)),'b','LineStyle','--','DisplayName','Y
RNA')
title('Concentration of X and Y protein and RNA vs distance for middle
position in time')
xlabel('Distance (um)')
ylabel('Concentration (mM)')
legend()
hold off
```

```
figure(6)
plot(distance,Xprot(:,numtsteps),'red','DisplayName', 'X Protein')
hold on
plot(distance, Xrna(:,numtsteps),'red','LineStyle','--', 'DisplayName', 'X
RNA')
plot(distance, Yprot(:,numtsteps),'b', 'DisplayName','Y Protein')
plot(distance, Yrna(:,numtsteps),'b','LineStyle','--','DisplayName','Y RNA')
title('Concentration of X and Y protein and RNA vs distance for last position
in time')
xlabel('Distance (um)')
ylabel('Concentration (mM)')
legend()
hold off
```

Part B: 3

```
%set up time and space parameters
timestep = 0.01;
times = [50,100,200,400];
fig = 1;

for (k=1:4)
totaltime=times(k);
time = (0:timestep:totaltime);
numtsteps = totaltime/timestep;
distancestep = 0.02;
totaldistance = 3;
distance = (distancestep:distancestep:totaldistance);
numdsteps = totaldistance/distancestep;

%initialize protein and RNA matrices: rows are distance, columns are time
Xrna = zeros(numdsteps, numtsteps);
Xprot = zeros(numdsteps, numtsteps);
Yrna = zeros(numdsteps, numtsteps);
Yprot = zeros(numdsteps, numtsteps);

%initial conditions
Xrna(1,1) = 1;
Xprot(1,1) = 1;
Yrna(numdsteps,1) = 1;
Yprot(numdsteps, 1) = 1;



for (t=1:numtsteps)
    for (i=1:numdsteps)



        %find laplacian for each species with absorbing boundary conditions
        switch i
            case 1
                lap_Xrna = (Xrna(2,t) - 2*Xrna(1,t))/ distancestep^2;
```

```
                lap_Xprot = (Xprot(2,t) - 2*Xprot(1,t))/ distancestep^2;
                lap_Yrna = (Yrna(2,t) - 2*Yrna(1,t))/ distancestep^2;
                lap_Yprot = (Yprot(2,t) - 2*Yprot(1,t))/ distancestep^2;
            case numdsteps
                lap_Xrna = (Xrna(numdsteps-1,t)-2*Xrna(numdsteps,t)) /
distancestep^2;
                lap_Xprot = (Xprot(numdsteps-1,t)-2*Xprot(numdsteps,t)) /
distancestep^2;
                lap_Yrna = (Yrna(numdsteps-1,t)-2*Yrna(numdsteps,t)) /
distancestep^2;
                lap_Yprot = (Yprot(numdsteps-1,t)-2*Yprot(numdsteps,t)) /
distancestep^2;
            otherwise
                lap_Xrna = (Xrna(i+1, t) + Xrna(i-1, t) - 2*Xrna(i, t)) /
distancestep^2;
                lap_Xprot = (Xprot(i+1, t) + Xprot(i-1, t) - 2*Xprot(i, t)) /
distancestep^2;
                lap_Yrna = (Yrna(i+1, t) + Yrna(i-1, t) - 2*Yrna(i, t)) /
distancestep^2;
                lap_Yprot = (Yprot(i+1, t) + Yprot(i-1, t) - 2*Yprot(i, t)) /
distancestep^2;
        end


        %find rates for each species
        dXprot_dt = Xrna(i, t) - Xprot(i, t) + 0.0001*lap_Xprot;
        dXrna_dt = (1 - ( (Yprot(i,t)^2)/((0.33^2) + (Yprot(i,t)^2)) )) -
Xrna(i,t) + 0.0001*lap_Xrna;
        dYprot_dt = Yrna(i, t) - Yprot(i, t) + 0.0001*lap_Yprot;
        dYrna_dt = (1 - ( (Xprot(i,t)^2)/((0.33^2) + (Xprot(i,t)^2)) )) -
Yrna(i,t) + 0.0001*lap_Yrna;

        %forward euler
        Xprot(i, t+1) = Xprot(i,t) + dXprot_dt*timestep;
        Xrna(i, t+1) = Xrna(i,t) + dXrna_dt*timestep;
        Yprot(i, t+1) = Yprot(i,t) + dYprot_dt*timestep;
        Yrna(i, t+1) = Yrna(i,t) + dYrna_dt*timestep;

    end

end

sp=1;
figure(fig)
subplot(2,3,sp)
plot(time, Xprot(1,:), 'red','DisplayName', 'X Protein')
hold on
plot(time, Xrna(1,:),'red','LineStyle','--', 'DisplayName', 'X RNA')
plot(time, Yprot(1,:),'b', 'DisplayName','Y Protein')
plot(time, Yrna(1,:),'b','LineStyle','--','DisplayName','Y RNA')
title(sprintf('First pos. in space. Total time = %ds', totaltime))
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off
```

```
sp = sp+1;
subplot(2,3,sp)
plot(time, Xprot((numdsteps/2),:), 'red','DisplayName', 'X Protein')
hold on
plot(time, Xrna((numdsteps/2),:),'red','LineStyle','--', 'DisplayName', 'X
RNA')
plot(time, Yprot((numdsteps/2),:),'b', 'DisplayName','Y Protein')
plot(time, Yrna((numdsteps/2),:),'b','LineStyle','--','DisplayName','Y RNA')
title(sprintf('Middle pos. in space. Total time = %ds', totaltime))
xlabel('Time (s)')
ylabel('Concentration (mM)')
hold off

sp = sp+1;
subplot(2,3,sp)
plot(time, Xprot(numdsteps,:), 'red','DisplayName', 'X Protein')
hold on
plot(time, Xrna(numdsteps,:),'red','LineStyle','--', 'DisplayName', 'X RNA')
plot(time, Yprot(numdsteps,:),'b', 'DisplayName','Y Protein')
plot(time, Yrna(numdsteps,:),'b','LineStyle','--','DisplayName','Y RNA')
title(sprintf('Last pos. in space. Total time = %ds', totaltime))
xlabel('Time (s)')
ylabel('Concentration (mM)')
hold off

sp = sp+1;
subplot(2,3,sp)
plot(distance,Xprot(:,1),'red','DisplayName', 'X Protein')
hold on
plot(distance, Xrna(:,1),'red','LineStyle','--', 'DisplayName', 'X RNA')
plot(distance, Yprot(:,1),'b', 'DisplayName','Y Protein')
plot(distance, Yrna(:,1),'b','LineStyle','--','DisplayName','Y RNA')
title(sprintf('First position in time. Total time = %ds', totaltime))
xlabel('Distance (um)')
ylabel('Concentration (mM)')
hold off

sp = sp+1;
subplot(2,3,sp)
plot(distance,Xprot(:,(numtsteps/2)),'red','DisplayName', 'X Protein')
hold on
plot(distance, Xrna(:,(numtsteps/2)),'red','LineStyle','--', 'DisplayName',
'X RNA')
plot(distance, Yprot(:,(numtsteps/2)),'b', 'DisplayName','Y Protein')
plot(distance, Yrna(:,(numtsteps/2)),'b','LineStyle','--','DisplayName','Y
RNA')
title(sprintf('Middle position in time. Total time = %ds', totaltime))
xlabel('Distance (um)')
ylabel('Concentration (mM)')
hold off

sp = sp+1;
subplot(2,3,sp)
plot(distance,Xprot(:,numtsteps),'red','DisplayName', 'X Protein')
hold on
```

```
plot(distance, Xrna(:,numtsteps),'red','LineStyle','--', 'DisplayName', 'X
RNA')
plot(distance, Yprot(:,numtsteps),'b', 'DisplayName','Y Protein')
plot(distance, Yrna(:,numtsteps),'b','LineStyle','--','DisplayName','Y RNA')
title(sprintf('Last position in time. Total time = %ds', totaltime))
xlabel('Distance (um)')
ylabel('Concentration (mM)')
hold off

fig = fig + 1;

end
```

Part B: 4

```
%set up time and space parameters
timestep = 0.01;
times = [50,100,200,400];
fig = 1;

for (k=1:4)
totaltime=times(k);
time = (0:timestep:totaltime);
numtsteps = totaltime/timestep;
distancestep = 0.02;
totaldistance = 3;
distance = (distancestep:distancestep:totaldistance);
numdsteps = totaldistance/distancestep;

%initialize protein and RNA matrices: rows are distance, columns are time
Xrna = zeros(numdsteps, numtsteps);
Xprot = zeros(numdsteps, numtsteps);
Yrna = zeros(numdsteps, numtsteps);
Yprot = zeros(numdsteps, numtsteps);

%initial conditions
Xrna(1,1) = 1;
Xprot(1,1) = 1;
Xrna(numdsteps,1) = 1;
Xprot(numdsteps,1) = 1;
Yrna(numdsteps/2,1) = 1;
Yprot(numdsteps/2, 1) = 1;



for (t=1:numtsteps)
    for (i=1:numdsteps)



        %find laplacian for each species with absorbing boundary conditions
        switch i
            case 1
                lap_Xrna = (Xrna(2,t) - 2*Xrna(1,t))/ distancestep^2;
```

```
                lap_Xprot = (Xprot(2,t) - 2*Xprot(1,t))/ distancestep^2;
                lap_Yrna = (Yrna(2,t) - 2*Yrna(1,t))/ distancestep^2;
                lap_Yprot = (Yprot(2,t) - 2*Yprot(1,t))/ distancestep^2;
            case numdsteps
                lap_Xrna = (Xrna(numdsteps-1,t)-2*Xrna(numdsteps,t)) /
distancestep^2;
                lap_Xprot = (Xprot(numdsteps-1,t)-2*Xprot(numdsteps,t)) /
distancestep^2;
                lap_Yrna = (Yrna(numdsteps-1,t)-2*Yrna(numdsteps,t)) /
distancestep^2;
                lap_Yprot = (Yprot(numdsteps-1,t)-2*Yprot(numdsteps,t)) /
distancestep^2;
            otherwise
                lap_Xrna = (Xrna(i+1, t) + Xrna(i-1, t) - 2*Xrna(i, t)) /
distancestep^2;
                lap_Xprot = (Xprot(i+1, t) + Xprot(i-1, t) - 2*Xprot(i, t)) /
distancestep^2;
                lap_Yrna = (Yrna(i+1, t) + Yrna(i-1, t) - 2*Yrna(i, t)) /
distancestep^2;
                lap_Yprot = (Yprot(i+1, t) + Yprot(i-1, t) - 2*Yprot(i, t)) /
distancestep^2;
        end


        %find rates for each species
        dXprot_dt = Xrna(i, t) - Xprot(i, t) + 0.0001*lap_Xprot;
        dXrna_dt = (1 - ( (Yprot(i,t)^2)/((0.33^2) + (Yprot(i,t)^2)) )) -
Xrna(i,t) + 0.0001*lap_Xrna;
        dYprot_dt = Yrna(i, t) - Yprot(i, t) + 0.0001*lap_Yprot;
        dYrna_dt = (1 - ( (Xprot(i,t)^2)/((0.33^2) + (Xprot(i,t)^2)) )) -
Yrna(i,t) + 0.0001*lap_Yrna;

        %forward euler
        Xprot(i, t+1) = Xprot(i,t) + dXprot_dt*timestep;
        Xrna(i, t+1) = Xrna(i,t) + dXrna_dt*timestep;
        Yprot(i, t+1) = Yprot(i,t) + dYprot_dt*timestep;
        Yrna(i, t+1) = Yrna(i,t) + dYrna_dt*timestep;

    end

end

sp=1;
figure(fig)
subplot(2,3,sp)
plot(time, Xprot(1,:), 'red','DisplayName', 'X Protein')
hold on
plot(time, Xrna(1,:),'red','LineStyle','--', 'DisplayName', 'X RNA')
plot(time, Yprot(1,:),'b', 'DisplayName','Y Protein')
plot(time, Yrna(1,:),'b','LineStyle','--','DisplayName','Y RNA')
title(sprintf('First pos. in space. Total time = %ds', totaltime))
xlabel('Time (s)')
ylabel('Concentration (mM)')
legend()
hold off
```

```
sp = sp+1;
subplot(2,3,sp)
plot(time, Xprot((numdsteps/2),:), 'red','DisplayName', 'X Protein')
hold on
plot(time, Xrna((numdsteps/2),:),'red','LineStyle','--', 'DisplayName', 'X
RNA')
plot(time, Yprot((numdsteps/2),:),'b', 'DisplayName','Y Protein')
plot(time, Yrna((numdsteps/2),:),'b','LineStyle','--','DisplayName','Y RNA')
title(sprintf('Middle pos. in space. Total time = %ds', totaltime))
xlabel('Time (s)')
ylabel('Concentration (mM)')
hold off

sp = sp+1;
subplot(2,3,sp)
plot(time, Xprot(numdsteps,:), 'red','DisplayName', 'X Protein')
hold on
plot(time, Xrna(numdsteps,:),'red','LineStyle','--', 'DisplayName', 'X RNA')
plot(time, Yprot(numdsteps,:),'b', 'DisplayName','Y Protein')
plot(time, Yrna(numdsteps,:),'b','LineStyle','--','DisplayName','Y RNA')
title(sprintf('Last pos. in space. Total time = %ds', totaltime))
xlabel('Time (s)')
ylabel('Concentration (mM)')
hold off

sp = sp+1;
subplot(2,3,sp)
plot(distance,Xprot(:,1),'red','DisplayName', 'X Protein')
hold on
plot(distance, Xrna(:,1),'red','LineStyle','--', 'DisplayName', 'X RNA')
plot(distance, Yprot(:,1),'b', 'DisplayName','Y Protein')
plot(distance, Yrna(:,1),'b','LineStyle','--','DisplayName','Y RNA')
title(sprintf('First position in time. Total time = %ds', totaltime))
xlabel('Distance (um)')
ylabel('Concentration (mM)')
hold off

sp = sp+1;
subplot(2,3,sp)
plot(distance,Xprot(:,(numtsteps/2)),'red','DisplayName', 'X Protein')
hold on
plot(distance, Xrna(:,(numtsteps/2)),'red','LineStyle','--', 'DisplayName',
'X RNA')
plot(distance, Yprot(:,(numtsteps/2)),'b', 'DisplayName','Y Protein')
plot(distance, Yrna(:,(numtsteps/2)),'b','LineStyle','--','DisplayName','Y
RNA')
title(sprintf('Middle position in time. Total time = %ds', totaltime))
xlabel('Distance (um)')
ylabel('Concentration (mM)')
hold off

sp = sp+1;
subplot(2,3,sp)
plot(distance,Xprot(:,numtsteps),'red','DisplayName', 'X Protein')
hold on
```

```
plot(distance, Xrna(:,numtsteps),'red','LineStyle','--', 'DisplayName', 'X
RNA')
plot(distance, Yprot(:,numtsteps),'b', 'DisplayName','Y Protein')
plot(distance, Yrna(:,numtsteps),'b','LineStyle','--','DisplayName','Y RNA')
title(sprintf('Last position in time. Total time = %ds', totaltime))
xlabel('Distance (um)')
ylabel('Concentration (mM)')
hold off

fig = fig + 1;

end
```

I worked on this project completely on my own and did not discuss my answers or code with anyone in the class. I used help from lecture slides, lectures and mathworks.com for MATLAB implementation.