

22S-CSB150-EEB159 Lab3

LISA WANG

TOTAL POINTS

90 / 100

QUESTION 1

1 Ex.1 40 / 50

- 0 pts Correct
- 15 pts Simulate Eqs for different initial conditions
 - 5 pts Describe what happened
 - 5 pts Correctly indicate mRNA and protein trend
 - 5 pts Correctly state that all dynamics converge to equilibrium point
- ✓ - 10 pts *Correctly overlay dynamics onto a vector field. See TA in office hours for an explanation of what this plot should look like.*
- 3 pts Plot related issues
- 2 pts mRNA decreases initially in case 2

should be equal to ` $-b$ `

- 5 pts Need to talk more about what your plots imply
- 15 pts need to plot
- 50 pts attempt problem

QUESTION 2

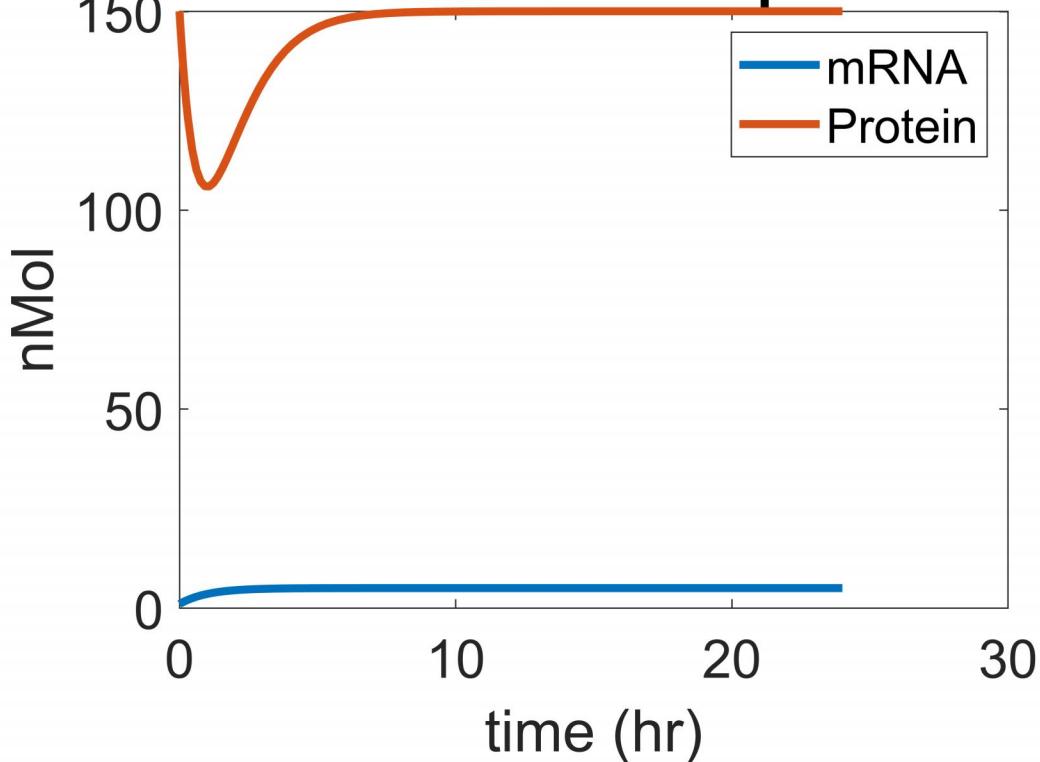
2 Ex.2 50 / 50

- ✓ - 0 pts *Correct*
- 10 pts Correctly characterize the shape of the return - should be exponential/logistic
 - 10 pts Correctly predict what it should be from the linearized system of equations and verify the quantitative rate of return.
- 30 pts Correctly estimating the fixed point and rate of return for 3 different parameter sets.
- 3 pts Plot aesthetics
- 5 pts Plot in log space and see that slope

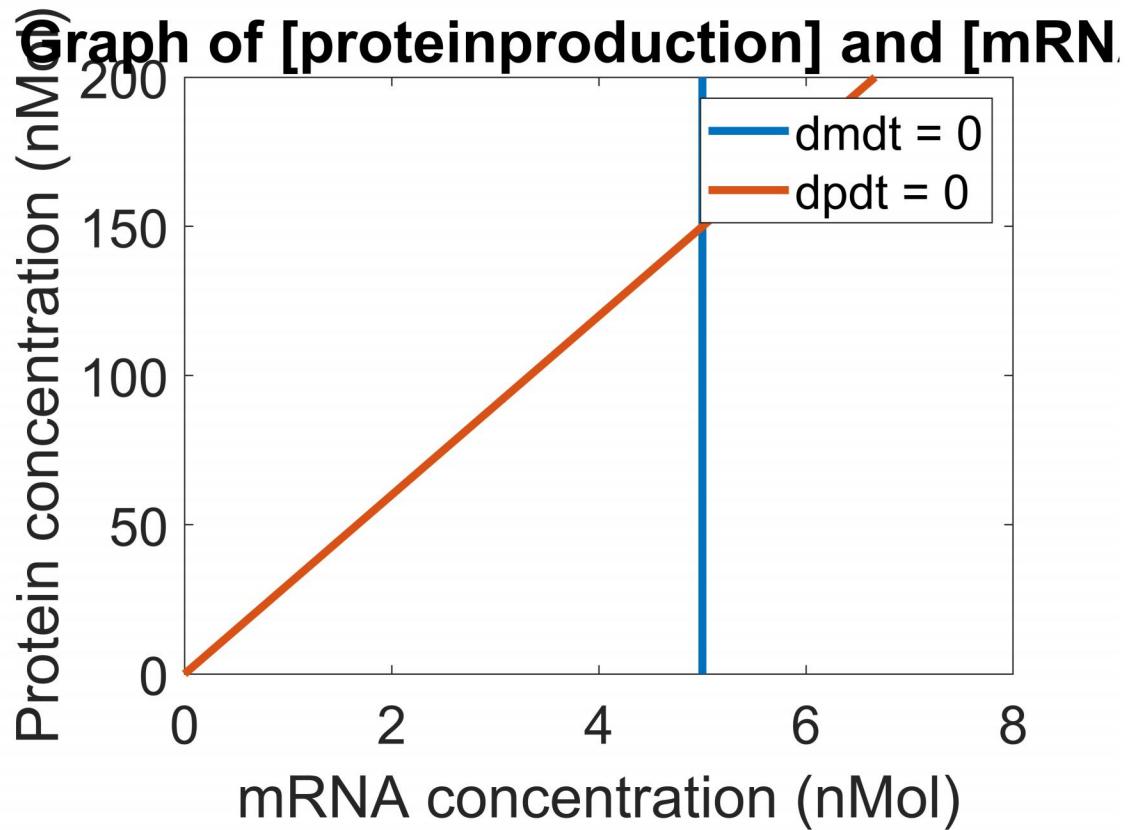
```
%Exercise 1 answers, typed:
%the protein values proliferate and this is what I expect to happen initially.
% This is because translation is happening without meeting the threshold.
%%The Protein production has decreased in this scenario,
% it has been
%%decreasing as time increased. We can see in
% all the above cases when
%%extended to a time interval of 24 hours, then
% protein values converges to a value of
%%150.
% more specifically, the IC [0 0] and [7 25] will both produce a graph
% with exponential growth
% growth in the first hour, then converge to 150 mMol
% then the [1 150] graph will decrease in the first hour but then fluctuate
% so that it also follows the 150 nMol trend to converge.
```

```
pars.a = 5; % nM/hr
pars.b = 1; % /hr
pars.r = 30; % proteins/(mRNA*hr)
x0 = [1 150]; % Initial values
t0 = 0; % Time to start
tf = 24; % Final time
[t,x] = ode45(@(t,x) proteinproduction(t,x,pars),[t0 tf],x0);
plot(t,x,'LineWidth',3)
xlabel('time (hr)', 'FontSize', 20)
ylabel('nMol', 'FontSize', 20)
title('Concentration of mRNA and protein over time');
legend('mRNA', 'Protein')
set(gca, 'FontSize', 20)
```

concentration of mRNA and protein over



```
% Define the nullclines
mnullcline = pars.a/pars.b; % A fixed value
pnullcline = @(p) pars.b.*p./pars.r; % An 'anonymous' function
% Define a vector of protein and mRNA values
pvec = 0:20:200;
mvec = 0:1:8;
% Plot the mRNA nullcline
plot(mnullcline*ones(size(pvec)),pvec,'LineWidth',3)
title('Graph of [proteinproduction] and [mRNA]');
hold on
% Overlay the protein nullcline
plot(pnullcline(pvec),pvec,'LineWidth',3)
hold off
% Add some plotting notes and modify the axes
legend('dmdt = 0', 'dpdt = 0')
xlim([min(mvec) max(mvec)])
ylim([min(pvec) max(pvec)])
xlabel('mRNA concentration (nMol)', 'FontSize', 20)
ylabel('Protein concentration (nMol)', 'FontSize', 20)
set(gca, 'FontSize', 20)
```



```

dmdt = @(m) pars.a - pars.b.*m;
dpdt = @(m,p) pars.r.*m-pars.b.*p;
[MM,PP] = meshgrid(mvec,pvec);

pars.a = 5; % nM/hr
pars.b = 1; % /hr
pars.r = 30; % proteins/(mRNA*hr)
x0 = [0 0]; % Initial values
t0 = 0; % Time to start
tf = 24; % Final time
[t,x] = ode45(@(t,x) proteinproduction(t,x,pars),[t0 tf],x0);
plot(t,x,'LineWidth',3)
xlabel('time (hr)', 'FontSize', 20)
ylabel('nMol', 'FontSize', 20)
legend('mRNA', 'Protein')
set(gca, 'FontSize', 20)
hold on

pars.a = 5; % nM/hr
pars.b = 1; % /hr
pars.r = 30; % proteins/(mRNA*hr)
x0 = [7 25]; % Initial values
t0 = 0; % Time to start

```

```

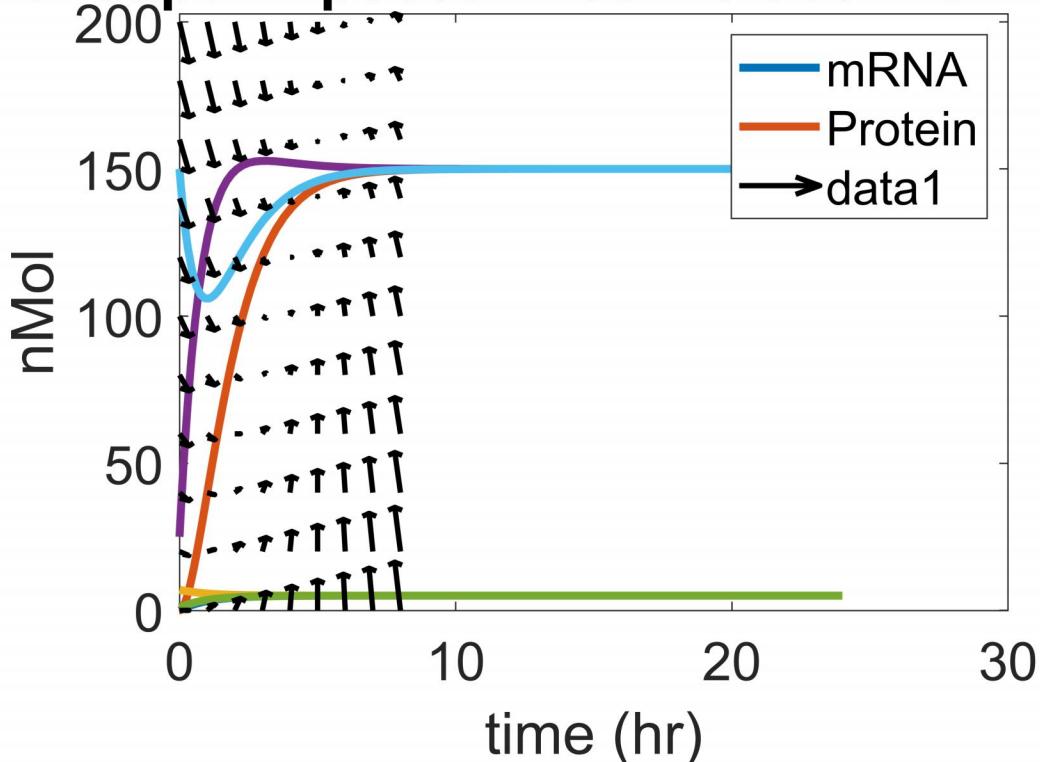
tf = 24; % Final time
[t,x] = ode45(@(t,x) proteinproduction(t,x,pars),[t0 tf],x0);
plot(t,x,'LineWidth',3)
xlabel('time (hr)', 'FontSize',20)
ylabel('nMol', 'FontSize',20)
legend('mRNA', 'Protein')
set(gca,'FontSize',20)
hold on

pars.a = 5; % nM/hr
pars.b = 1; % /hr
pars.r = 30; % proteins/(mRNA*hr)
x0 = [1 150]; % Initial values
t0 = 0; % Time to start
tf = 24; % Final time
[t,x] = ode45(@(t,x) proteinproduction(t,x,pars),[t0 tf],x0);
plot(t,x,'LineWidth',3)
title('Graph of superimposed initial values with vector fields');
xlabel('time (hr)', 'FontSize',20)
ylabel('nMol', 'FontSize',20)
legend('mRNA', 'Protein')
set(gca,'FontSize',20)
hold on

quiver(MM,PP,dmdt(MM),dpdt(MM), 'k', 'MaxHeadSize', .015, 'LineWidth',2);
hold off

```

| of superimposed initial values with vec



```

pars.a = 5; % nM/hr
pars.b = 1; % /hr
pars.r = 30; % proteins/(mRNA*hr)

pstar = pars.r*pars.a/pars.b^2;
mstar = pars.a/pars.b;

pperturb = pstar.*.01;
mperturb = mstar.*.01;
x0 = [mstar+mperturb pstar+pperturb];
t0 = 0;
tf = 5;
[t,x] = ode45(@proteinproduction,[t0 tf],x0,[],pars);
plot(t,x(:,2),'LineWidth',3)
title('Concentration of protein with altered perturbations');
hold on
xlabel('time (hr)', 'FontSize', 20)
ylabel('Concentration (nMol)', 'FontSize', 20)
legend('Protein')
set(gca, 'FontSize', 20)

pstar = pars.r*pars.a/pars.b^2;
mstar = pars.a/pars.b;

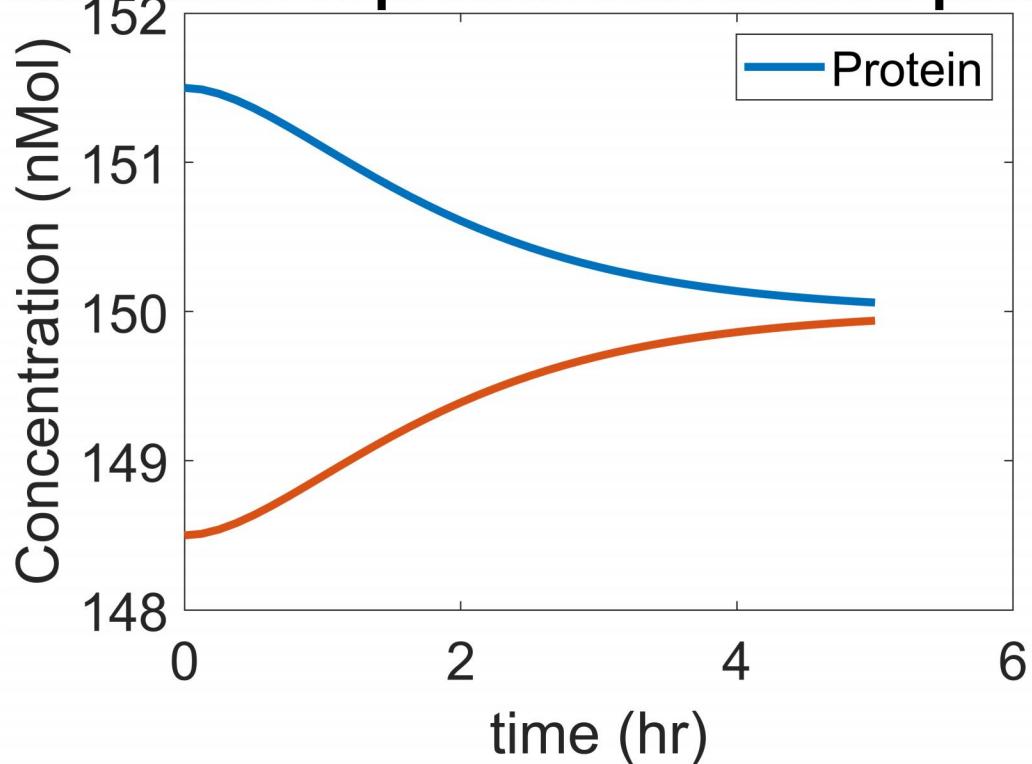
pperturb = pstar.*-.01;
mperturb = mstar.*-.01;
x0 = [mstar+mperturb pstar+pperturb];
t0 = 0;
tf = 5;
[t,x] = ode45(@proteinproduction,[t0 tf],x0,[],pars);
plot(t,x(:,2),'LineWidth',3)
hold on
xlabel('time (hr)', 'FontSize', 20)
ylabel('Concentration (nMol)', 'FontSize', 20)
legend('Protein')
set(gca, 'FontSize', 20)

```

1 Ex.1 40 / 50

- 0 pts Correct
 - 15 pts Simulate Eqs for different initial conditions
 - 5 pts Describe what happened
 - 5 pts Correctly indicate mRNA and protein trend
 - 5 pts Correctly state that all dynamics converge to equilibrium point
- ✓ - 10 pts *Correctly overlay dynamics onto a vector field. See TA in office hours for an explanation of what this plot should look like.*
- 3 pts Plot related issues
 - 2 pts mRNA decreases initially in case 2

centration of protein with altered pertur



exercise 2

```
% based on the graph here, the equilibrium point is 150 nMol  
% and the graphs shows  
% that after perturbation it progresses into  
% equilibrium after 5 hours.
```

```
pars.a = 5; % nM/hr  
pars.b = 1; % /hr  
pars.r = 30; % proteins/(mRNA*hr)  
  
pstar = pars.r*pars.a/pars.b^2;  
mstar = pars.a/pars.b;  
  
pperturb = pstar.*.01;  
mperturb = mstar.*.01;  
x0 = [mstar+mperturb pstar+pperturb];  
t0 = 0;  
tf = 5;  
[t,x] = ode45(@proteinproduction,[t0 tf],x0,[],pars);  
plot(t,x(:,2),'LineWidth',3)  
hold on  
xlabel('time (hr)', 'FontSize', 20)
```

```

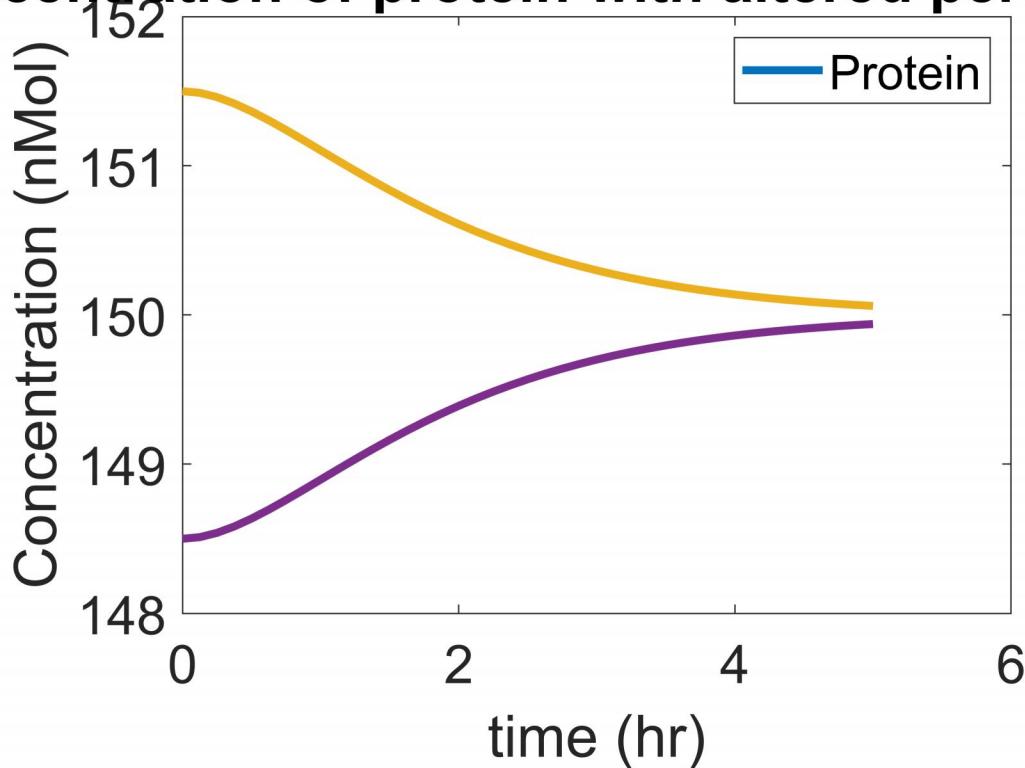
ylabel('Concentration (nMol)', 'FontSize', 20)
legend('Protein')
set(gca, 'FontSize', 20)

pstar = pars.r*pars.a/pars.b^2;
mstar = pars.a/pars.b;

pperturb = pstar.*-.01;
mperturb = mstar.*-.01;
x0 = [mstar+mperturb pstar+pperturb];
t0 = 0;
tf = 5;
[t,x] = ode45(@proteinproduction,[t0 tf],x0,[],pars);
plot(t,x(:,2), 'LineWidth', 3)
hold on
xlabel('time (hr)', 'FontSize', 20)
ylabel('Concentration (nMol)', 'FontSize', 20)
legend('Protein')
set(gca, 'FontSize', 20)

```

centration of protein with altered pertur



```

pars.a = 5; % nM/hr
pars.b = 1; % /hr
pars.r = 30; % proteins/(mRNA*hr)

```

```

pstar = pars.r*pars.a/pars.b^2;
mstar = pars.a/pars.b;

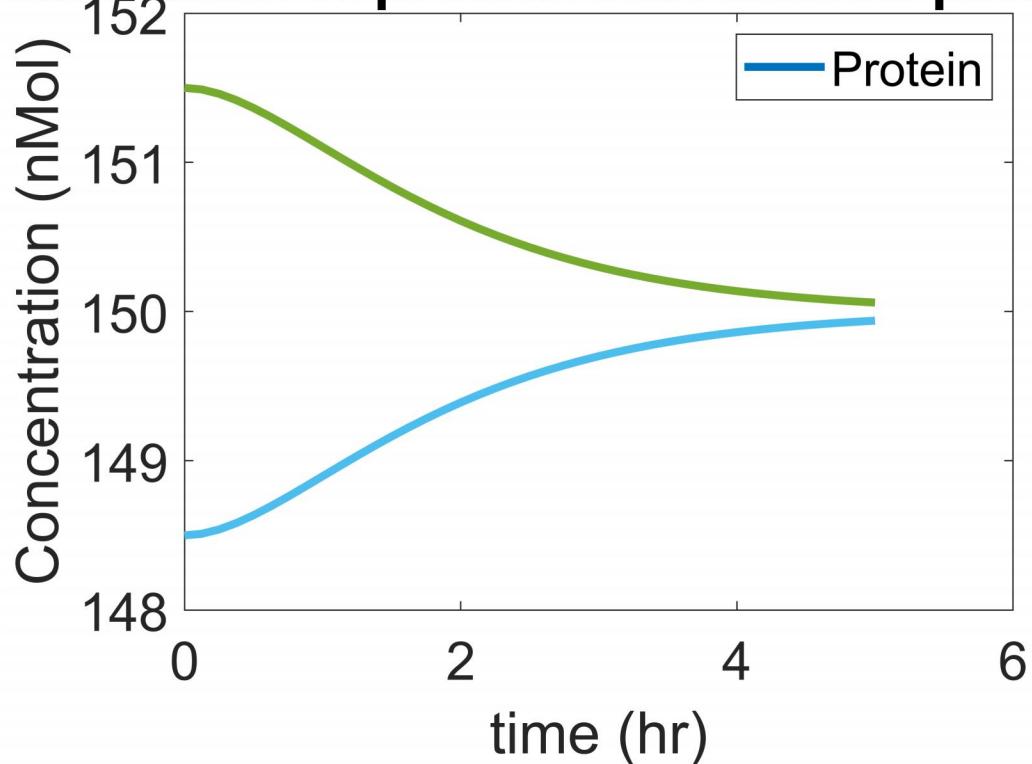
pperturb = pstar.*.01;
mperturb = mstar.*.01;
x0 = [mstar+mperturb pstar+pperturb];
t0 = 0;
tf = 5;
[t,x] = ode45(@proteinproduction,[t0 tf],x0,[],pars);
plot(t,x(:,2),'LineWidth',3)
hold on
xlabel('time (hr)', 'FontSize', 20)
ylabel('Concentration (nMol)', 'FontSize', 20)
legend('Protein')
set(gca, 'FontSize', 20)

pstar = pars.r*pars.a/pars.b^2;
mstar = pars.a/pars.b;

pperturb = pstar.*-.01;
mperturb = mstar.*-.01;
x0 = [mstar+mperturb pstar+pperturb];
t0 = 0;
tf = 5;
[t,x] = ode45(@proteinproduction,[t0 tf],x0,[],pars);
plot(t,x(:,2),'LineWidth',3)
xlabel('time (hr)', 'FontSize', 20)
ylabel('Concentration (nMol)', 'FontSize', 20)
legend('Protein')
set(gca, 'FontSize', 20)

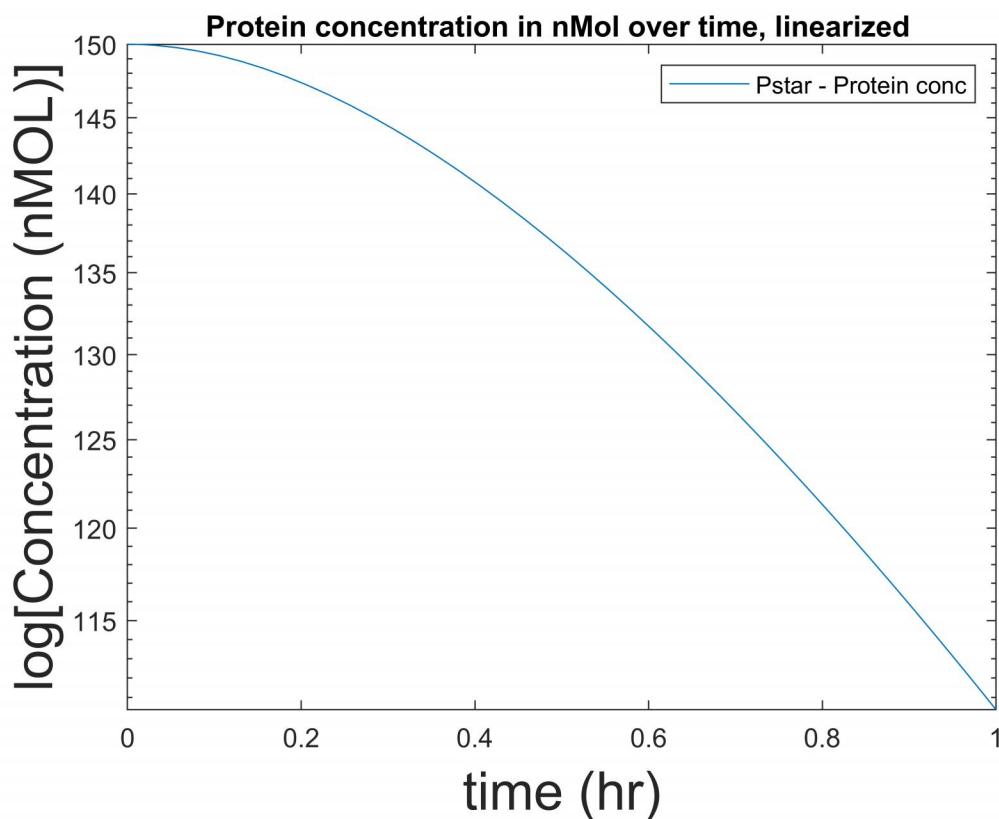
```

centration of protein with altered perturk

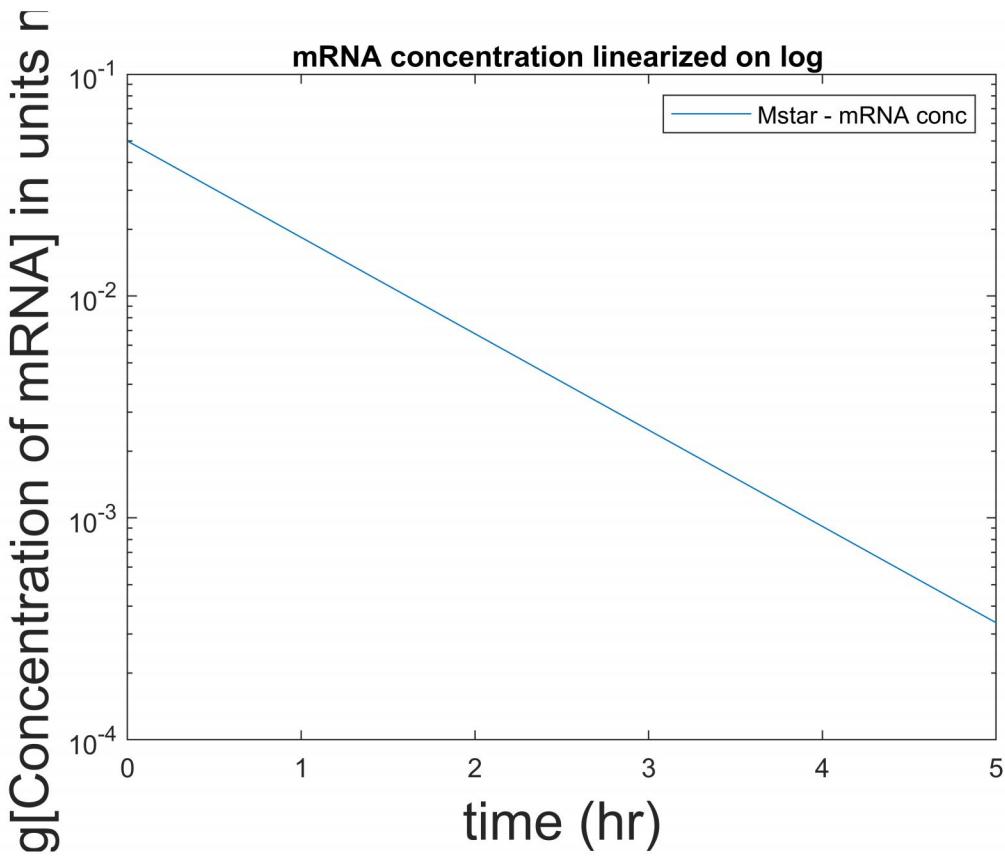


```
% protein concentration
semilogy(t,abs(x(:,2)-pstar))
hold off
xlabel('time (hr)', 'FontSize', 20)
ylabel('log[Concentration (nMOL)]', 'FontSize', 20)
title('Protein concentration in nMol over time, linearized ')
legend('Pstar - Protein conc')

legend("Pstar - Protein conc")
```



```
semilogy(t,abs(x(:,1)-mstar))
hold off
xlabel('time (hr)', 'FontSize', 20)
ylabel('log[Concentration of mRNA] in units nMol', 'FontSize', 20)
title('mRNA concentration linearized on log ')
legend('Mstar - mRNA conc')
```



now linearizing the logarithmic curves

the theoretical rate of return is an exponential curve by e^{-bt} , where once linearized

```
%becomes a plot of log vs. t, and its slope will be negative b
%since the graph of protein concentration is not yet fully linearized, we
%can estimate that it is approximately having a slope of -b.
% the rate of return on these three conditions are estimate to be:
```

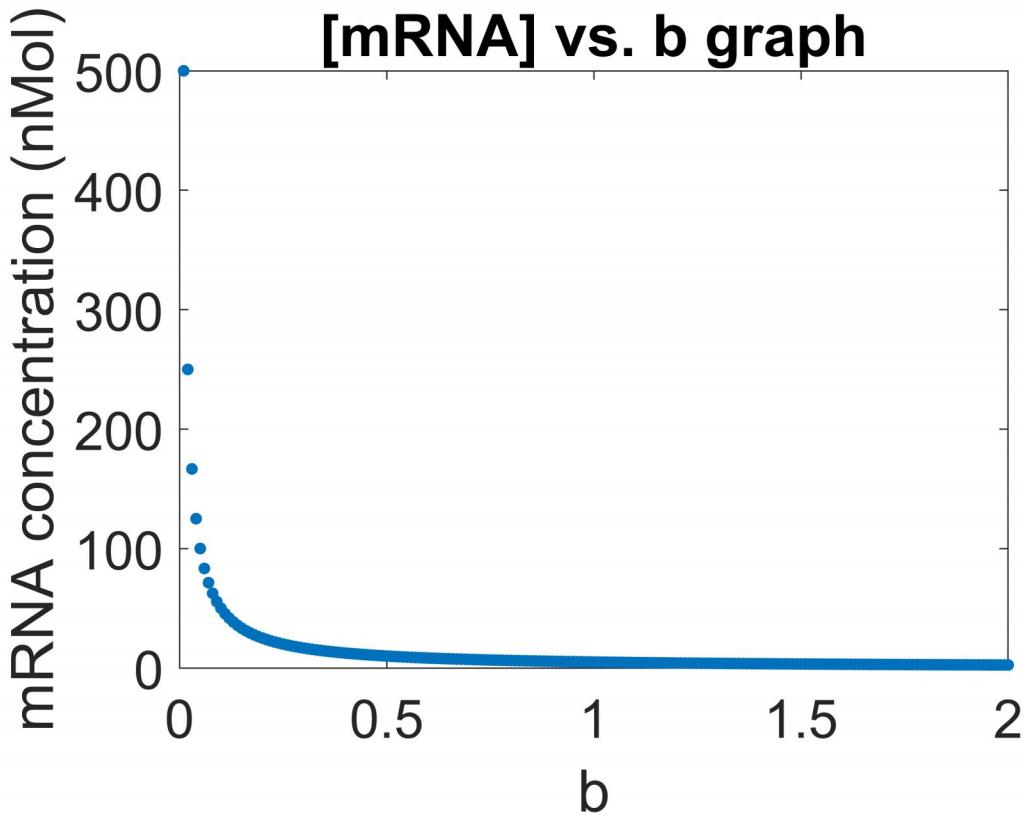
section 4

```
bvec = .01:.01:2;
mstarvec = zeros(1,length(bvec));
pstarvec = zeros(1,length(bvec));
for jj = 1:length(bvec)
pars.b = bvec(jj);
pstarvec(jj) = pars.r*pars.a/pars.b^2;
mstarvec(jj) = pars.a/pars.b;
end
figure(1)
plot(bvec,mstarvec,'.', 'MarkerSize',15)
title(' [mRNA] vs. b graph');
xlabel('b', 'FontSize',20)
```

```

ylabel('mRNA concentration (nMol)', 'FontSize', 20)
set(gca, 'FontSize', 20)

```



```

%%Section 5
pars.a = 5;
pars.b = 1;
pars.r = 30;
x0 = [0 0];
t0 = 0;
tf = 1;
[t,x] = ode45(@proteinproduction,[t0 tf],x0,[],pars);
tmp=plot(t,x)

```

```

tmp =
2x1 Line array:

```

```

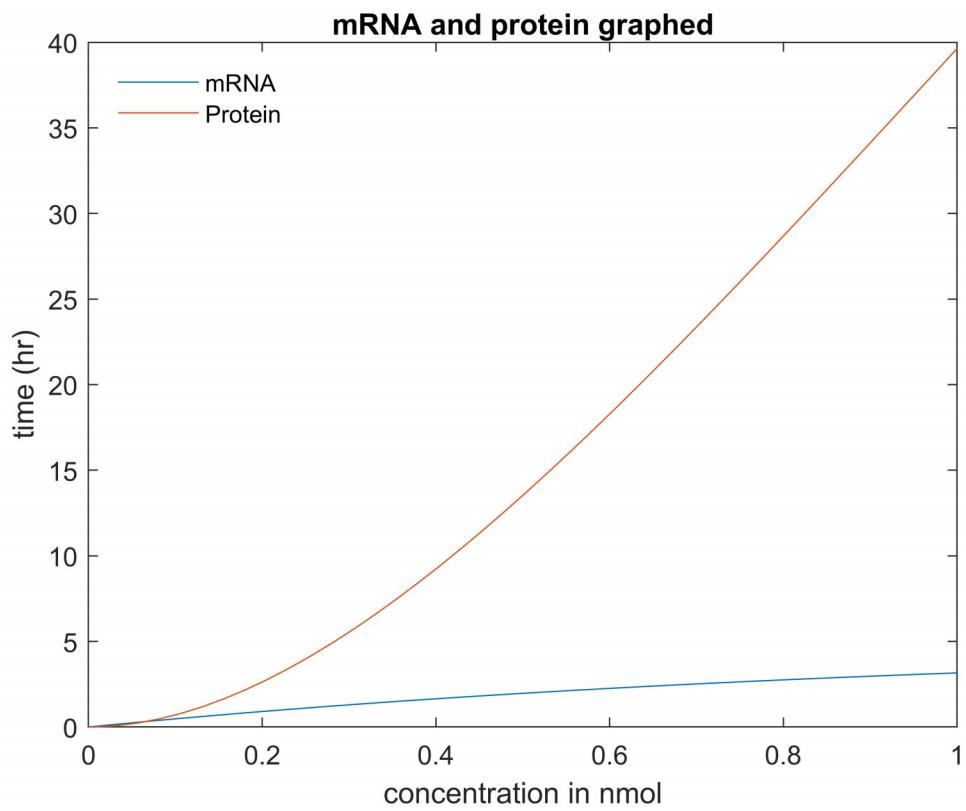
Line
Line

```

```

title('mRNA and protein graphed');
xlabel('concentration in nmol');
ylabel('time (hr)');
tmpl=legend('mRNA','Protein');
set(tmpl,'Location','NorthWest');
legend('boxoff');

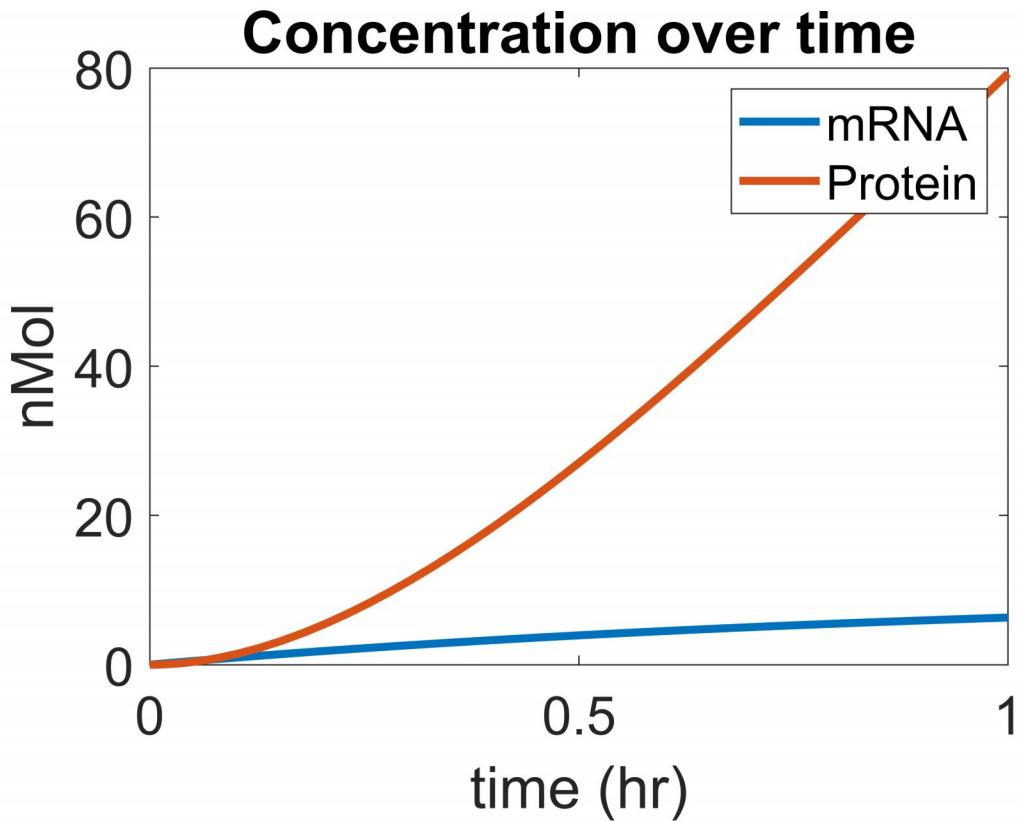
```



```

pars.a = 10; % nM/hr
pars.b = 1; % /hr
pars.r = 30; % proteins/(mRNA*hr)
x0 = [0 0]; % Initial values
t0 = 0; % Time to start
tf = 1; % Final time
[t,x] = ode45(@(t,x) proteinproduction(t,x,pars),[t0 tf],x0);
plot(t,x,'LineWidth',3)
title('Concentration over time');
xlabel('time (hr)', 'FontSize', 20)
ylabel('nMol', 'FontSize', 20)
legend('mRNA', 'Protein')
set(gca, 'FontSize', 20)

```



```

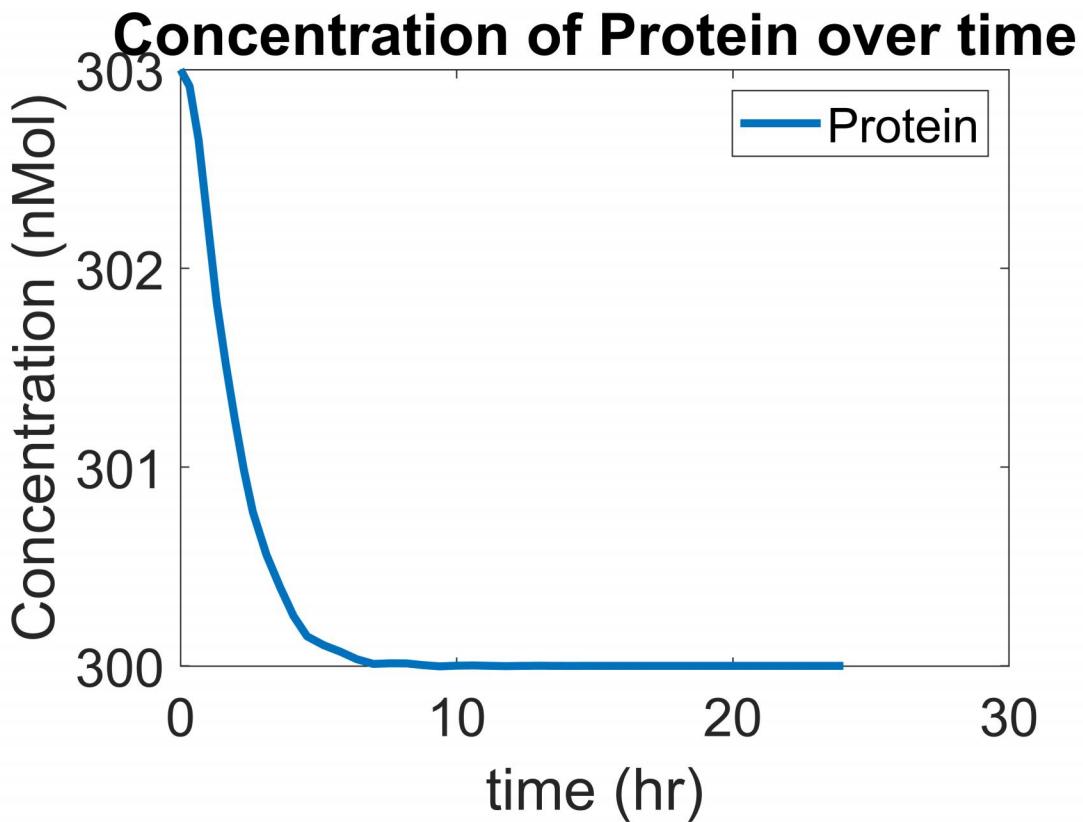
%%
pstardot = pars.r*pars.a/pars.b^2;
mstar = pars.a/pars.b;
pperturb = pstardot.*.01;
mperturb = mstar.*.01;
x0 = [mstar+mperturb pstardot+pperturb];
t0 = 0;
tf = 24;
[t,x] = ode45(@proteinproduction,[t0 tf],x0,[],pars);
plot(t,x(:,2),'LineWidth',3)
title('Concentration of Protein over time');

```

```

xlabel('time (hr)', 'FontSize', 20)
ylabel('Concentration (nMol)', 'FontSize', 20)
legend('Protein')
set(gca, 'FontSize', 20)

```



by testing ($a=5, b=1, r =30$), the fixed point is 150

by testing ($a=5, b=0.5, r=30$), the fixed point is 600

by testing ($a= 10, b=1, r =30$), the fixed point is 300

the rate of return is going to be $y = e^{-t}$, $y = e^{(-0.5t)}$, and $y = e^{-t}$, respectively.

2 Ex.2 50 / 50

✓ - 0 pts Correct

- 10 pts Correctly characterize the shape of the return - should be exponential/logistic
- 10 pts Correctly predict what it should be from the linearized system of equations and verify the quantitative rate of return.
- 30 pts Correctly estimating the fixed point and rate of return for 3 different parameter sets.
- 3 pts Plot aesthetics
- 5 pts Plot in log space and see that slope should be equal to `-b`
- 5 pts Need to talk more about what your plots imply
- 15 pts need to plot
- 50 pts attempt problem