Ode matlab code:

1.

```
n=11;am=10;bm=0.3;b1=0.4;b2=0.4;
km=logspace(-1,2,n);
ks=logspace(-1,3,n);
a1=linspace(0,40,n);
a2=linspace(0,40,n);
m=a1/a2;
[A1,A2]=meshgrid(km,ks);
M=zeros(size(A1));
N=zeros(size(A1))
for i=1:n
    for j=1:n
        a1=A1(i,j);a2=A2(i,j);

odefun=@(t,x)[a1-b1*x(1)-k1*x(1)*x(2)-k2*x(1)*x(3);a2-b2*x(2)-k1*x(1)*x(2)-k2*x(2)*x(3);am-b
m*x(3)-k2*x(1)*x(3)-k3*x(2)*x(3)];
        [t,y]=ode45(odefun,[0 7],[0 0 0]')
        M(i,j)=max(y(:,3))
        N(i,j)=0.5*max(y(:,3))
    end
end
subplot(2,2,1);mesh(A1,A2,M);
subplot(2,2,2);contour3(A1,A2,M);colormap
subplot(2,2,3);plot3(A1,A2,M);
subplot(2,2,4);contour(A1,A2,M);colormap
```

2.

```
am=30;bm=0.03;a1=30;a2=30;b1=0.3;b2=0.3;k1=0.79;k2=0.1;k3=0.1;

odefun1=@(t2,x2)[a1-b1*x2(1)-k1*x2(1)*x2(2)-k2*x2(1)*x2(3);a2-b2*x2(2)-k1*x2(1)
*x2(2)-k3*x2(2)*x2(3);am-bm*x2(3)-k2*x2(1)*x2(3)-k3*x2(2)*x2(3)];
                    [t2,y2]=ode45(odefun1,[0 30],[0 0 0]');
  plot(t2,y2,'linewidth',3)
  legend('s1','s2','m')
  xlabel('time')
  ylabel('molecule')
  title('a1:a2=1:1')
```

Parameter sensitivity analysis:

Local sensitivity analysis matlab code

```
am=10;bm=0.02;a1=20;a2=20;b1=0.1;b2=0.1;k1=10;k2=0.2;k3=0.2;i=1;p
=0.001*am;

odefun1=@(t2,x2)[a1-b1*x2(1)-k1*x2(1)*x2(2)-k2*x2(1)*x2(3);a2-b2*x2
(2)-k1*x2(1)*x2(2)-k3*x2(2)*x2(3);am-bm*x2(3)-k2*x2(1)*x2(3)-k3*x2(2
)*x2(3)];
                    [t2,y2]=ode45(odefun1,[0 30],[0 0 0]');
   subplot(131)
   plot(t2,y2)
   legend('s1','s2','m')
   title(a1)

amm=10+p;bmm=0.3;a11=80;a22=40;b11=0.4;b22=0.4;k11=10;k22=0.2;
k33=0.2;

odefun11=@(t22,x22)[a11-b11*x22(1)-k11*x22(1)*x22(2)-k22*x22(1)*x
22(3);a22-b22*x22(2)-k11*x22(1)*x22(2)-k33*x22(2)*x22(3);amm-bmm
*x22(3)-k22*x22(1)*x22(3)-k33*x22(2)*x22(3)];
                    [t22,y22]=ode45(odefun11,[0 30],[0 0 0]');
     z1=mean(y2);z11=mean(y22);
     z1
```

```
z11

s=(z11(:,i)-z1(:,i))/p;

s
```

Parameter sweep

```
clc
a=xlsread('data.xlsx');
x=a(:,3);y=a(:,4);z=a(:,7);
[X,Y,Z]=griddata(x,y,z,linspace(min(x),max(x))',linspace(min(y),max(y)),'v4');
[C,h]=contourf(X,Y,Z);
clabel(C,h)
figure
[C,h]=contourf(X,Y,Z,[6,6]);
figure
[C,h]=contour(X,Y,Z,[6,6]);
figure
scatter(C(1,:),C(2,:))
```

Noise analysis-model:

```
function [t,x]= example

% Two-state model of gene expression


% Reaction network:

%      0 ->s1
```

```
%       0 ->s2
%       0 ->m
%       s1->0
%       s2->0
%       m->0
%       s1+m ->0
%       s2+m ->0
%       s1+s2 ->0


tspan = [0, 5500]; %simulation time seconds
x0 = [0,0,0];    %s1,s2,m
stoich_matrix    =[1 0 0;%       0 ->s1
                   0 1 0;%       0 ->s2
                   0 0 1;%       0 ->m
                   -1 0 0;%       s1->0
                   0 -1 0;%       s2->0
                   0 0 -1;%       m->0
                   -1 0 -1;%       s1+m ->0
                  % 0 -1 -1;%       s2+m ->0
                   -1 -1 0]%       s1+s2 ->0
% Rate constants
```

```
p.am = 18;p.bm = 0.12;p.km = 0.4;p.ks=3.16;p.bs = 0.3;p.as1 = 60; p.as2
= 30;
%p.?

% Run simulation
%[t,x]  =  directMethod(stoich_matrix,  @propensities_2state,  tspan,  x0,
p);
[t,x] = directMethod(stoich_matrix, @propensities_2state, tspan, x0, p);

% Plot time course
figure(gcf);
stairs(t,x);
set(gca,'XLim',tspan);
xlabel('time (s)');
ylabel('molecules');
legend({'s1','s2','m'});title('a1:a2=2:1')
end

function a = propensities_2state(x,p)
s1 = x(1);
s2 =x(2);
m =x(3);
```

```
a = [p.as1;%      0 ->s1
p.as2;%      0 ->s2
p.am;%      0 ->m
s1*p.bs;%      s1->0
s2*p.bs;%      s2->0
m*p.bm;%      m->0
p.km*s1*m;%      s1+m ->0
%p.km*s2*m;%      s2+m ->0
p.ks*s1*s2 %      s1+s2 ->0
];

End
```

2.

```
function [t,x]= example
% Two-state model of gene expression

% Reaction network:
```

```
%       0 ->s1
%       0 ->s2
%       0 ->m
%       s1->0
%       s2->0
%       m->0
%       s1+m ->0
%       s2+m ->0
%       s1+s2 ->0


tspan = [0, 3000]; %simulation time seconds
x0 = [0,0,0];     %s1,s2,m
stoich_matrix     =[1 0 0;%       0 ->s1
                    0 1 0;%       0 ->s2
                    0 0 1;%       0 ->m
                    -1 0 0;%       s1->0
                    0 -1 0;%       s2->0
                    0 0 -1;%       m->0
                    -1 0 -1;%       s1+m ->0
                    0 -1 -1;%       s2+m ->0
```

```
                                -1 -1 0]%      s1+s2 ->0

% Rate constants

p.am = 15;p.bm = 0.06;p.km = 0.158;p.ks=6.31;p.bs = 0.3;p.as1 = 60;

p.as2 = 30;

%p.?


% Run simulation

%[t,x] = directMethod(stoich_matrix, @propensities_2state, tspan, x0,

p);

[t,x] = directMethod(stoich_matrix, @propensities_2state, tspan, x0, p);


% Plot time course

figure(gcf);

stairs(t,x);

set(gca,'XLim',tspan);

xlabel('time (s)');

ylabel('molecules');

legend({'s1','s2','m'});title('a1:a2=2:1')

end


function a = propensities_2state(x,p)

s1 = x(1);
```

```
s2 =x(2);

m =x(3);


a = [p.as1;%      0 ->s1

p.as2;%      0 ->s2

p.am;%      0 ->m

s1*p.bs;%      s1->0

s2*p.bs;%      s2->0

m*p.bm;%      m->0

p.km*s1*m;%      s1+m ->0

p.km*s2*m;%      s2+m ->0

p.ks*s1*s2%      s1+s2 ->0

];


End


b=xlsread('comparatorp0.5.xlsx');
a=0:200;
c=hist(b(:,3),a);
d=c/1000000
figure
bar(a,d)
xlabel('mRNA');ylabel('pdf') ;axis([0,200,0,0.04]);
title('as1:as2=1:2')
```