

Attractive field model

Attractive pit (before PAN added)

```
%% input
x0 = 0;
y0 = 0;
x = -5:0.1:5;
y = -5:0.1:5;
sigmax = 1;
sigmay = 1;
A = 5000;
u = lld_gaussfun3(x0,y0,x,y,sigmax,sigmay,A);
Amax=0.63;
Km0=0.25;

%% find and redefine the concentration with
attractive intensity

for i=1:10201;
    u(i)=(Amax*u(i))/(Km0+u(i));
end;

%% mesh

mesh(x,y,u);
```

attractive pit (after PAN added)

```
%% input
x0 = 0;
y0 = 0;
x = -5:0.1:5;
y = -5:0.1:5;
sigmax = 1;
sigmay = 1;
A = 5000;
```

```

u = lld_gaussfun3(x0,y0,x,y,sigmax,sigmay,A);
Amax=0.63;
Km0=0.25;
Cmax=-0.80;
Km1=1500;

%% find and redefine the concentration with
attractive intensity

for i=1:10201;

u(i)=(Amax*u(i))/(Km0+u(i))+(Cmax*10*u(i))/(Km1
+10*u(i));
end;

%% mesh
mesh(x,y,u);

```

Sensor expression model

ODE of sensor expression

```

function
a=ode(~,y,k1,k2,k3,k4,k5,k6,k7,k8,k9,k10,k11,k1
2)
a=[
    %DNA
    k2*y(3)-k1*y(1)*y(2)+k4*y(5)-
k3*y(4)*y(1)+k10*y(9)-k9*y(8)*y(1);
    %RNAP
    k2*y(3)-k1*y(1)*y(2)+k6*y(6)-
k5*y(5)*y(2)+k12*y(10)-k11*y(9)*y(2);
    %DNA_RNAP
    k1*y(1)*y(2)-k2*y(3);
    %NahR
    k4*y(5)-k3*y(4)*y(1)+k8*y(8)-k7*y(7)*y(4);
    %NahR_DNA

```

```

k3*y(4)*y(1)-k4*y(5)+k6*y(6)-k5*y(5)*y(2);
%NahR_DNA_RNAP
k5*y(2)*y(5)-k6*y(6);
%PAN
k8*y(8)-k7*y(7)*y(4)
%PAN_NahR
k7*y(7)*y(4)-k8*y(8)+k10*y(9)-k9*y(8)*y(1)
%PAN_NahR_DNA
k9*y(1)*y(8)-k10*y(9)+k12*y(10)-
k11*y(9)*y(2)
%PAN_NahR_DNA_RNAP
k11*y(9)*y(2)-k12*y(10)
];
End

```

Main function of sensor expression

```

%% main process
%DNA+RNAP -- DNA_RNAP (k1,k2)

%NahR+DNA -- NahR_DNA (k3,k4)
%NahR_DNA+RNAP -- NahR_DNA_RNAP (k5,k6)

%PAN+NahR -- PAN_NahR(k7,k8)
%PAN_NahR+DNA -- PAN_NahR_DNA(k9,k10)
%PAN_NahR_DNA+RNAP --
PAN_NahR_DNA_RNAP(k11,k12) (μÈÓÚk5,k6)

%% input

DNA=300;
RNAP=700;
DNA_RNAP=0;
NahR=300;
NahR_DNA=0;
NahR_DNA_RNAP=0;
PAN=200;
PAN_NahR=0;

```

```

PAN_NahR_DNA=0;
PAN_NahR_DNA_RNAP=0;

%% k constant

k1=2;
k2=7000;
k3=2;
k4=7000;
k5=2;
k6=1000;
k7=2;
k8=200;
k9=2;
k10=4;
k11=2;
k12=1000;

min=-1;
max=5;
point=50;
x_plot=logspace(min,max,point);
colidx=[3,6,10];
colcnt=length(colidx);
index=0;
legends=['DNA-RNAP', 'NahR-DNA-RNAP', 'PAN-NahR-
DNA-RNAP'];
colors = ['b', 'r', 'g'];
y_PAN=zeros(point,colcnt);

%% calculation
for PAN=x_plot;
    index=index+1;
    tspan=[0,800];

y0=[DNA;RNAP;DNA_RNAP;NahR;NahR_DNA;NahR_DNA_RN
AP;PAN;PAN_NahR;PAN_NahR_DNA;PAN_NahR_DNA_RNAP]
;

```

```

[t, y]=ode15s (@ (t, y) ode3 (t, y, k1, k2, k3, k4, k5, k6, k
7, k8, k9, k10, k11, k12) , tspan, y0) ;

    last=length (y) ;
    y_PAN (index, :)=y (last, colidx) ;
end
%% sum
sum_yPAN=sum (y_PAN, 2) ;
%% plot
subplot (colcnt+2, 1, 1) ;
semilogx (x_plot, y_PAN) ;
hold on ;
legend (legends) ;

for i=1:colcnt ;
    subplot (colcnt+2, 1, i+1) ;
    semilogx (x_plot, y_PAN (:, i), colors (i)) ;
    hold on ;
    legend (legends (i)) ;
end
%% plot sum
subplot (colcnt+2, 1, colcnt+2) ;
semilogx (x_plot, sum_yPAN) ;
hold on ;
legend ('sum of all') ;

```