FFR110, Computational biology 1
Problem set 2

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Problem 1

(a) To derive the time evolution of the total population size $N = I + S$, one obtain the time evolution of the total population $\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt}$. By inserting Eq. (1) from the assignment, the resulting equation becomes

$$\frac{dN}{dt} = b(I+S) - dS - \frac{S(I+S)}{K} - aSI + D\nabla^2 S + -dI - \frac{I(I+S)}{K} + aSI + D\nabla^2 I. \quad (1)$$

By using the fact that $N = I + S$ the equation above can be simplified to the following equation,

$$\frac{dN}{dt} = (b-d)N(1 - \frac{N}{K(b-d)}) + D\nabla^2 N, \quad (2)$$

which is on the the same form as the Fisher's equation.

In order to analyze the expression, we need to dedimensionalize it by setting $N = N^*(b-d)K$, $t = \frac{t^*}{(b-d)}$ and $x = x^*\sqrt{\frac{D}{(b-d)}}$ the resulting equation simplifies to,

$$\frac{dN^*}{dt^*} = N^*(1-N^*) + \frac{d^2N^*}{dx^2}. \quad (3)$$

If N^* is independent of x^*, i.e a homogenous solution, we have a dynamical system with two steady states,

$$N^* = 0, \text{unstable fixed point}$$
$$N^* = 1, \text{stable fixed point.}$$

One searches for the traveling waves connecting the steady states at large $|z|$, with the ansatz: $z = x - ct$, where we assume that $c \geq 0$:

$$-c\frac{d}{dz}u(z) = u(z)(1-u(z)) + \frac{d^2}{dz^2}u(z), \quad (4)$$

with the boundary conditions set the same as the fixed points,

$$\begin{aligned} \lim_{z\to-\infty} u(z) &= 1 \\ \lim_{z\to\infty} u(z) &= 0. \end{aligned} \quad (5)$$

To get the first order system, the help variable $\frac{du}{dz}$ is introduced, resulting in the following system,

$$\begin{aligned} \frac{du}{dz} &= v \\ \frac{dv}{dz} &= -cv - u(1-u), \end{aligned} \quad (6)$$

with the following steady states,

$$\begin{aligned} (u^*, v^*) &= (0,0) \\ (u^*, v^*) &= (1,0). \end{aligned} \quad (7)$$

By linearising, the stability matrix give rise to the following eigenvalue equation,

$$
\begin{aligned}
0 &= \det(\mathbb{J} - \lambda\mathbb{I}) = \lambda(\lambda + c) - (2u - 1) \\
\Rightarrow \lambda_{\pm} &= \frac{1}{2}(-c \pm \sqrt{c^2 + 8u - 4}) \\
(u^*, v^*) = (0,0) &: \begin{cases} \text{stable node} \\ \text{if } c > 2 \\ \text{stable spiral} \\ \text{if } c < 2 \end{cases} \\
(u^*, v^*) = (1,0) &: \text{ saddle point.} \\
&.
\end{aligned} \tag{8}
$$

Since we assume that $c \geq 0$, only the solution for the stable node $c \geq 0$ is valid, i.e $c_{min} = 2$.

To get the minimal wave speed of the travelling wave in terms of the parameters, one needs to reintroduce the dimensions following the ansatz $z = x^* - ct^*$ with dimensionless variables. By reintroducing dimensions, the resulting equation becomes

$$z = x\sqrt{\frac{D}{b-d}} - c\frac{t}{b-d} = 0. \tag{9}$$

The minimal wave speed is then obtained by,

$$\frac{x}{t} = c_{min}\sqrt{(b-d)D} = 2\sqrt{(b-d)D}. \tag{10}$$

(b) The fixed points for the spatially homogeneous model (D=0) is obtained when $\frac{dN^*}{dt^*} = N^*(1-N^*) = 0$, which is fulfilled when $N^* = 0$ (unstable fixed point) and $N^* = 1$ (stable fixed point).

The steady states can be found where,

$$N^* = I + S,$$

and thereby

$$S = k(b-d) - I,$$

for $N^* = 1$, and

$$S = -I,$$

for $N^* = 0$.

By insertion of these expressions into the equation for $\frac{dI}{dt}$, the result is

$$\frac{dI}{dt} = I(-b + a(b-d)K - aI) \tag{11}$$

and,

$$\frac{dI}{dt} = -dI - aI^2. \tag{12}$$

By setting the equations to zero, one can find the fixed points for the stable steady state to be $I^* = 0$, $S^* = (b-d)K$, $I^* = \frac{-b}{a} + (b-d)\cdot K$ and $S^* = \frac{b}{a}$. The fixed point for the unstable steady state was found to be $I^* = 0$, $S^* = 0$, as well as the negative fixed point $I^* = \frac{-d}{a}$, $S^* = \frac{d}{a}$, which is not biologically relevant.

The only fixed point that can be ≥ 0 for both I and S is $I^* = \frac{-b}{a} + (b-d) \cdot K$ and $S^* = \frac{b}{a}$. By setting the the stable fixed point (involving parameter K) to zero, we can find K_c. The critical value for $K > K_c$ of this fixed point is where $K_C = \frac{b}{a(b-d)}$.

The eigenvalues were obtained from the stability matrix

$$\begin{pmatrix} b - d - aI - S/K - (I+S)/K & aI - I/K \\ b - aS - S/K & -d - I/K + aS - (I+S)/K. \end{pmatrix}$$

The eigenvalues were found to be $\{-b + d, b - a \cdot b \cdot K + a \cdot d \cdot K\}$. The first eigenvalue is independent of K and thereby always negative (stable). By inserting $K > K_C$ into the second eigenvalue, one can also see that it will be ≤ 0, i.e also stable.

(c) A traveling wave was found, as visualized in figure [1]. The total population expands over the habitat as a traveling wave, i.e it has the same shape over time. From figure [2] and [3] one can see that the amount of susceptibles increase faster than the amount of infected.

To find the minimal wave speed can one fix $N_0 = 0.1$ for a given time t and then search for the corresponding x to that time t. The times were chosen to be before the population reaches a homogeneous state. Then by plotting these different times against the corresponding x, the slopes gives the minimal wave speed. The minimal wave speed was found to be $c = 1.5$. In the subtask 1a), the minimal wave speed with the given parameter values was found to be $c \approx 1.414$, which is close to the estimated value. The small difference may be due to the accuracy in the values chosen for t and x in the estimated minimal wave speed.

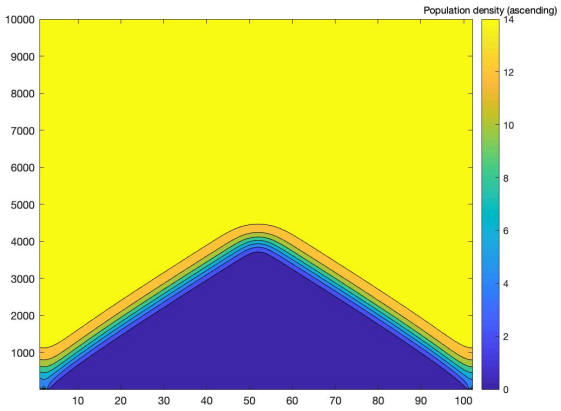

Figure 1: Heat map of the evolution of the total population N = S + I as a function of time and space, with time on the y axis and space on the x axis. The color bar shows the total population density.

(d) The fixed time t was chosen by searching for the corresponding time in figure [1] when the x coordinate is around 30.

By inserting the given parameter values in the biologically relevent fixed points from subtast 1b), i.e: $I^* = 0$, $S^* = (b-d)K$, $I^* = \frac{-b}{a} + (b-d) \cdot K$, $S^* = \frac{b}{a}$ and $I^* = 0$, $S^* = 0$, the fixed points obtained the following values: $(I^*, S^*) = (0, 0)$, $(I^*, S^*) = (0, 15)$ and $(I^*, S^*) = (5, 10)$. The fixed point in $(0, 0)$ in unstable and the other two fixed points are stable. When analysing the stability matrix by inserting the values for the fixed point

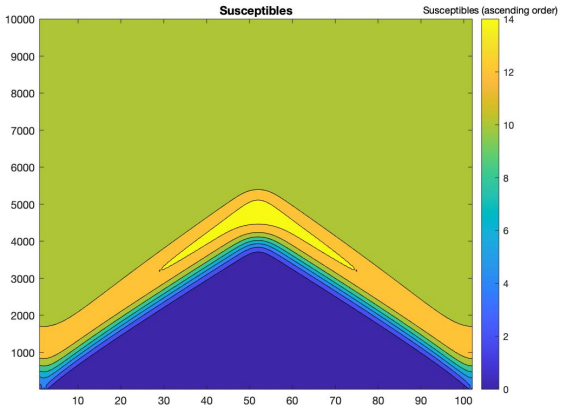

Figure 2: Heat map of the evolution of the susceptibles as a function of time and space, with time on the y axis and space on the x axis.The color bar shows the density of the susceptibles.

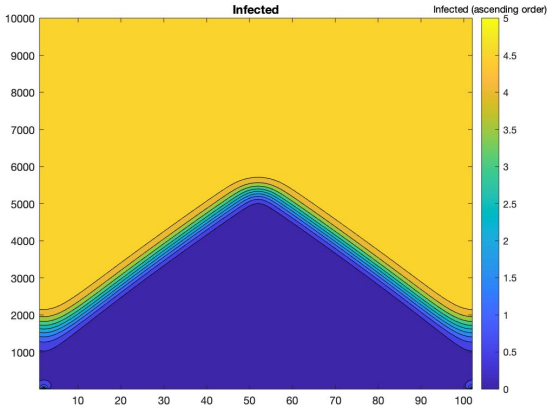

Figure 3: Heat map of the evolution of the infected as a function of time and space, with time on the y axis and space on the x axis. The color bar shows the density of the infected.

with the given parameter values, one can understand the significance of the biologically relevant fixed points. The fixed point in (0,0) and in (0,15) has one negative and one positive eigenvalue, i.e they are saddle points. The fixed point in (5,10) has two negative eigenvalues, i.e it is a stable fixed point. This correspond to the result presented in figure [4]. The figure in combination with the result from the stability matrix shows that the trajectory approaches the stable fixed point in (5,10) by first being repelled from the saddle point in (0.0) towards the saddle point in (0.15), and then repelled again, in which the flow approaches the stable fixed point in (5.10).

As seen in figure [5] the wave front of the susceptibles comes first, since it has a higher value on the y-axis. One can also see from the figure that when there are no susceptibles, the infected will be eliminated as well, which is a realistic result since the infected need susceptibles in order to increase. It is also possible to analyse figure [4] by observing that the susceptibles increase as long as the infected are 0. When the infected starts to increase one can see that the susceptibles start to decrease, which is a reasonable result.

As one can see from figure [5] the dynamics of the susceptibles and the infected fluctuates over the patch size, i.e it doesn't a constant increase or decrease. This shows that the wave profiles aren't monotonous!

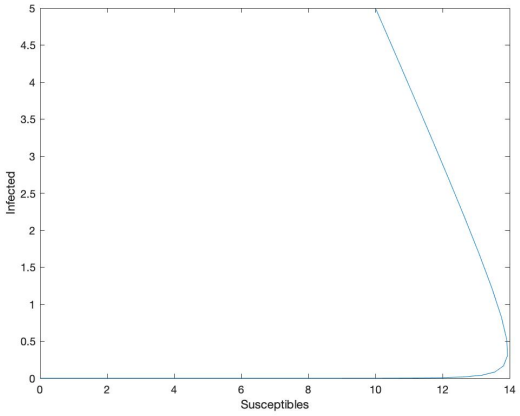

Figure 4: Plot showing the trajectories $(S(x), I(x))$ in the S-I space.

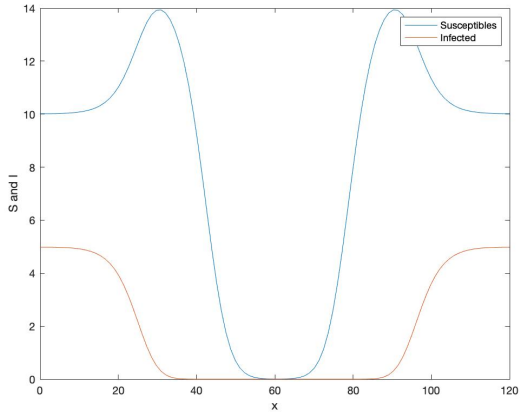

Figure 5: Plot showing the corresponding wave profiles $S(x)$ and $I(x)$ against x.

Problem 2

(a) The infection sustain ad infinitum in the model where

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \frac{\alpha}{S+I}SI - \beta I \tag{13}$$

contains a linearly stable steady state $I^* > 0$. By eliminating S from the equation by setting $N = S + I$, one gets the following equation,

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \alpha(1 - \frac{I}{N})I - \beta I. \tag{14}$$

Where the fixed points can be found to be $I^* = 0$ and $I^* = N(1 - \frac{\beta}{\alpha})$. Since $\frac{\beta}{\alpha} = \frac{1}{r_0}$ and the disease is endemic when $r_0 > 1$, the infection will sustain ad infinitum when $\frac{\alpha}{\beta} > 1$.

(b) The master equation for the probability ρ_n to observe n infected at time t in a finite population consisting of N individuals, is found as follows

$$\frac{d\rho_n}{dt} = \alpha(n+1)(1 - \frac{n+1}{N})\rho_{n+1} + \beta(n-1)\rho_{n-1} - (\alpha n(1 - \frac{n}{N}) + \beta n)\rho_n$$

. Setting $I = \frac{n}{N}$ and in the limit $N \to \infty$, one gets,

$$\frac{\partial}{\partial t}\rho(I,t) = (\exp\frac{1}{N}\frac{\partial}{\partial I} - 1)Nb(I)\rho(I,t) + \exp -\frac{1}{N}\frac{\partial}{\partial I} - 1)Nd(I)\rho(I,t)$$
$$\approx \frac{\partial}{\partial I}[(b(I) - d(I))\rho(I,t)] + \mathcal{O}(\frac{1}{N})$$

, where $b(I) = \alpha(1-I)I$ and $d(I) = \beta I$ since $b_n = \alpha n\left(1 - \frac{n}{N}\right) = Nb(I)$ and $d_n = \beta n = Nd(I)$.

It then follows that,

$$\frac{dI}{dt} = b(I) - d(I) = \alpha(1-I)I - \beta I$$

,which is equal to the result of the deterministic model when the infection sustain ad infinitum in the model. This only hold for $T < T_{ext}$. After this limit, the stochastic dynamics will approximate an extinction of the epidemic due to fluctuations, while the deterministic limit predicts that the epidemic lasts ad infinitum. The fluctuations for the stochastic model are assumed to be of order $\frac{1}{N}$, i.e small, which is why long-lived quasi-steady state is expected in the limit of large values of N for the stochastic model. Thereby, in the limit of $T < T_{ext}$, the stochastic model has approximately the same dynamics as the deterministic.

(c) The probability distributions were found for each of the three sets of infection respectively recovery rates. The figures [6], [7] and [8] shows the result of the obtained logarithmized probability distributions for the first time t_b or t_d, where an infection or recovery event takes place.

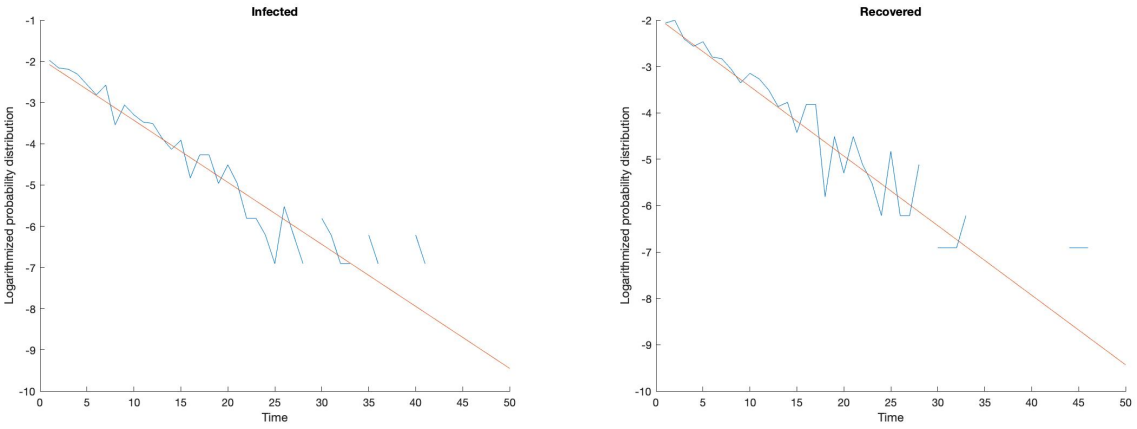

Figure 6: Plot with logarithmized probability distributions against time with parameters: $b_n = 0.1$ and $d_n = 0.2$. A superimposed straight line was also plotted, with slopes b_n/d_n.

As presented in the figures, it is possible to see that the logarithmized probability distributions follows the straight lines. This result verify that the distributions decay exponentially with exponent $-\lambda t$, where $\lambda = b_n/d_n$. The data in the plots origins from normalisation and from collecting the data from a histogram, which may be the reason for the gaps that can be seen in the plots.

The average time until an infection or recovery occurs were calculated and presented in table 1, for all sets of rates. The time to reach an infection respectively a recovery depends on the rate of the infection and recovery. For the two first sets, the recovery rate is twice as large as the infection rate and thereby the average time to reach a recovery is twice as fast. The same but opposite argument holds for the third set, i.e the larger

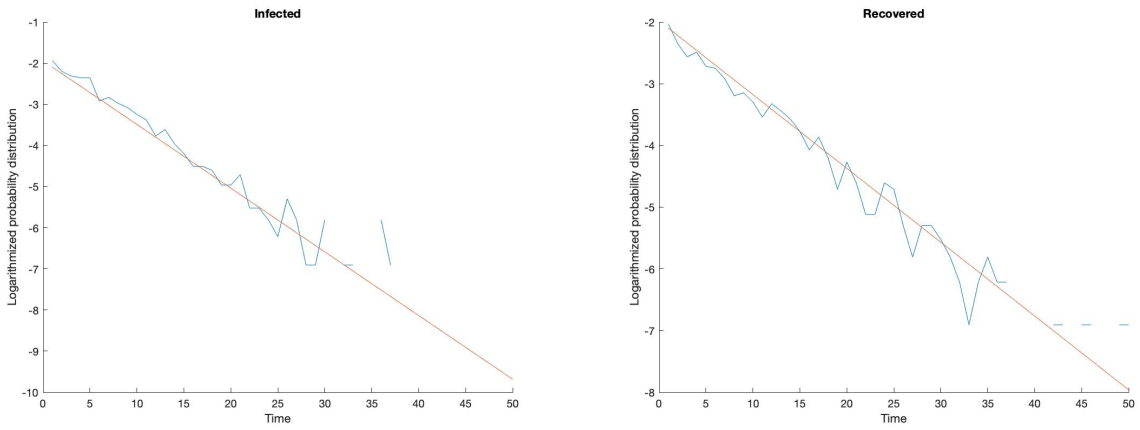

Figure 7: Plot with logarithmized probability distributions against time with parameters: $b_n = 1$ and $d_n = 2$. A superimposed straight line was also plotted, with slopes b_n/d_n.

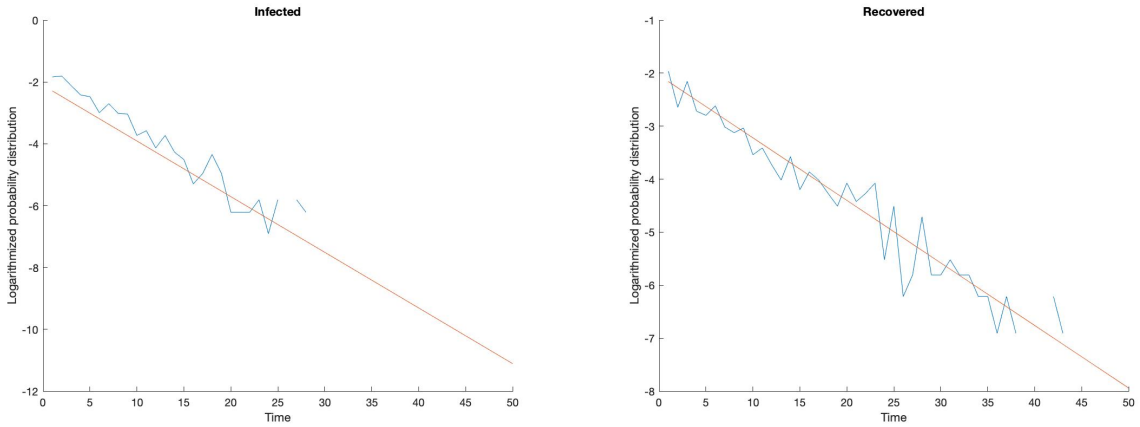

Figure 8: Plot with logarithmized probability distributions against time with parameters $b_n = 5$ and $d_n = 10$. A superimposed straight line was also plotted, with slopes b_n/d_n.

infection rate generates a faster time (twice as fast) to reach infection than recovery. One can also see that each average time is the inverse of its corresponding rate.

Table 1: Average times until an infection or recovery occurred for all sets of rates

Set/Rate	b_n	d_n
1	9.6211	5.2083
2	1.0109	0.5070
3	0.1137	0.2166

Matlab code

Exercise 1

```
% Problem 1, 1c i)
clc
clear

L=100;
t=10000;
dt=0.01;
h=1;
a=0.1;
b=1;
d=0.5;
K=30;
D=1;

S=zeros(t,L+2);
I=zeros(t,L+2);

%First patch
S(1,2)=b/a;
S(1,102)=b/a;
I(1,2)=(-b+a*b*K-a*d*K)/a;
I(1,102)=(-b+a*b*K-a*d*K)/a;

for i=1:t-1
    for j=2:L+1
        I(i+1,j)=I(i,j)+dt*(-d*I(i,j)-I(i,j)*(S(i,j)+I(i,j))/K+...
            a*S(i,j)*I(i,j)+D*(I(i,j+1)+I(i,j-1)-2*I(i,j))/h^2);

        S(i+1,j)= S(i,j)+dt*(b*(I(i,j)+S(i,j))-d*S(i,j)...
            -S(i,j)*(I(i,j)+S(i,j))/K-a*S(i,j)*I(i,j)+...
            D*(S(i,j+1)+S(i,j-1)-2*S(i,j))/h^2);
    end
    S(i+1,1)=S(i+1,101);
    S(i+1,102)=S(i+1,2);
    I(i+1,1)=I(i+1,101);
    I(i+1,102)=I(i+1,2);
end

N=I+S;
figure(1)
contourf(N)
col=colorbar;
set(get(col,'title'),'string','Population density (ascending order)')
title('Population')

figure(2)
contourf(S)
col=colorbar;
set(get(col,'title'),'string','Susceptibles (ascending order)')
title('Susceptibles')

figure(3)
contourf(I)
col=colorbar;
set(get(col,'title'),'string','Infected (ascending order)')
title('Infected')

%% 1c ii)

% I=I(1000,:); %changing value of t before the population reaches homogenous state to get ↩
    different x for n0=0.1
% S=S(1000,:);
% x=linspace(0,120,102);
% n=I+S;
% figure(1)
% plot(x,n)
% xlabel('x')
% ylabel('n')
% legend('Population')
```

```
timeVector=[100 500 1000 1400 1800 2200 3000];
xVector=[5.9406 13.0690 21.3861 27.3267 33.2673 40.3960 48.7129];

figure
plot(timeVector,xVector)
xlabel('t')
ylabel('x')
legend('time against x, slope = 0.0150*10^2')
b = polyfit(timeVector,xVector,1);
slope=b(1);



%% 1d

I=I(3000,:);
S=S(3000,:);
x=linspace(0,120,102);
figure(1)
plot(x,S,x,I)
xlabel('x')
ylabel('S and I')
legend('Susceptibles','Infected')

figure(2)
plot(S,I)
xlabel('Susceptibles')
ylabel('Infected')
```

Exercise 2

```
%% Problem 2c
clear
clc


infeRecRateMatrix= [0.1, 0.2; 1, 2; 10, 5];
dt=0.01;

for i=1:size(infeRecRateMatrix,1)
    bn=infeRecRateMatrix(i,1);
    dn=infeRecRateMatrix(i,2);

    count=0;

I=[];
R=[];

    while length(I)<1000
        r=rand;

        if r <= bn*dt

            I=[I count*dt];
            count=1;

        end

        count=count+1;

    end

    count=0;

     while length(R)<1000

            r=rand;

        if r <= dn*dt

            R=[R count*dt];
```

```
            count=1;

        end

        count=count+1;

    end

figure(i)
hold on
numberOfBins=50;
[NI,XI]=hist(I,numberOfBins);
probI=NI/sum(NI);
plot(log(probI))
plot(-infeRecRateMatrix(i,1)*XI-2)

meanValueI(i)=mean(I);

xlabel('Time')
ylabel('Probability distribution (log)')
title('Infected')


figure(i+3)
hold on
numberOfBins=50;
[NR,X]=hist(R,numberOfBins);
probR=NR/sum(NR);
plot(log(probR))
plot(-infeRecRateMatrix(i,2)*X-2)

meanValueR(i)=mean(R);

xlabel('Time')
ylabel('Logarithmized probability distribution')
title('Recovered')

end
```