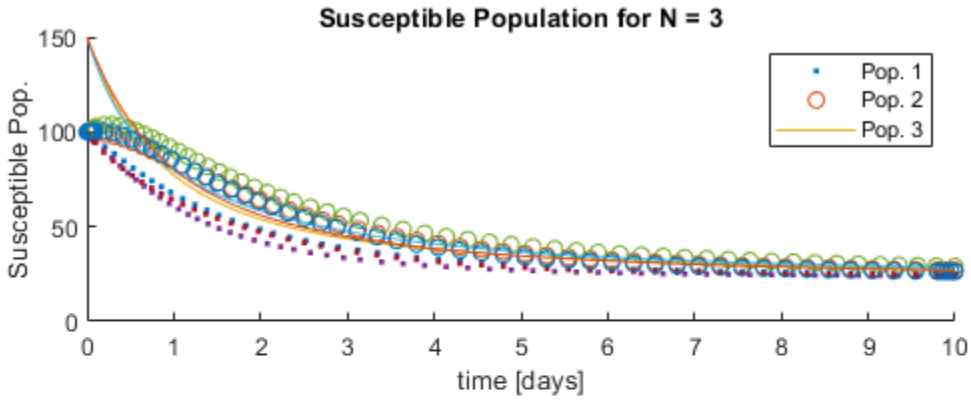
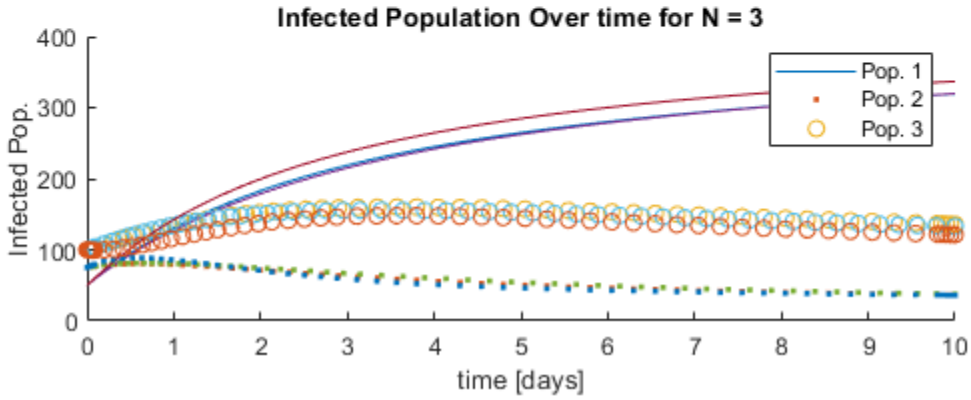
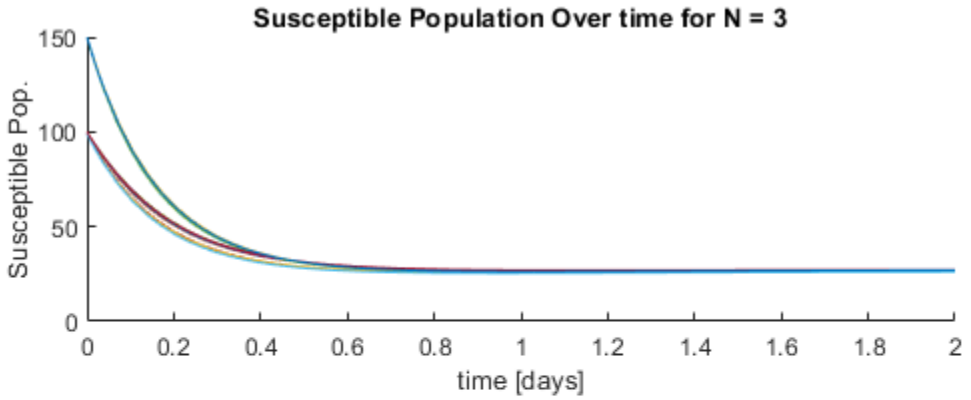
```
clear,clc;
%params
k1 = [5, 6, 7];
k2 = [100, 90, 70];
v1 = [0.8, 0.3, 0.7];
x0 = [99 50 100 75 150 100];

alpha = [0.05, 0.2, 0.15];
r = [0.1, 0.2, 0.15];

% Design choice, C_ij = 0 for all i=j, and C_ij = C_ji, so group A has same
% effect on group B same as B has on A.


figure
%want to see varied C and D matricies
for i=1:3

%random values in (0,1)
c12 = rand;
c13 = rand;
c23 = rand;

d12 = rand;
d13 = rand;
d23 = rand;

C = [0 c12 c13;
     c12 0 c23;
     c13 c23 0];
D = [0  d12 d13;
     d12 0 d23;
     d13 d23 0];

%sim
[t,x] = ode45(@(t,x) nonlin(t,x,k1,k2,v1,alpha,r,zeros(6),zeros(6,1),C,D),
[0 10], x0);

%plotting
subplot(2,1,1), hold on
plot(t,x(:,1),'.')
plot(t,x(:,3),'o')
plot(t,x(:,5))
hold off, xlabel("time [days]")
ylabel("Susceptible Pop.")
title("Susceptible Population for N = 3")
legend("Pop. 1", "Pop. 2", "Pop. 3")


subplot(2,1,2)
hold on
plot(t,x(:,2))
```

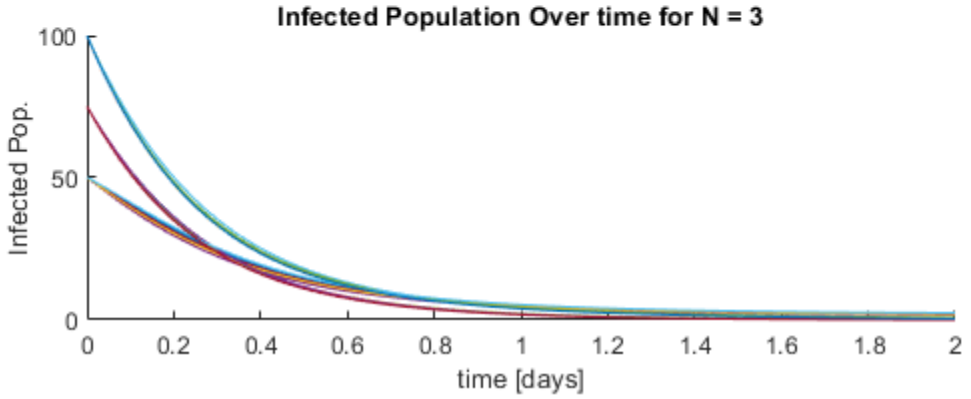
```
plot(t,x(:,4), '.')
plot(t,x(:,6), 'o')
hold off, xlabel("time [days]")
ylabel("Infected Pop.")
title("Infected Population Over time for N = 3")
legend("Pop. 1", "Pop. 2", "Pop. 3")
end


figure
%Controlled Network model, more iterations this time
for i=1:5
c12 = rand;
c13 = rand;
c23 = rand;

d12 = rand;
d13 = rand;
d23 = rand;

C = [0 c12 c13;
     c12 0 c23;
     c13 c23 0];
D = [0  d12 d13;
     d12 0 d23;
     d13 d23 0];
%control method from smaller dimensional no networking
KforN1 = [5.5 0; 0 4];
uforN1 = [150; 0];

%K is still diagonal
z = zeros(2);
K = [KforN1 z z; z KforN1 z; z z KforN1];

%u only nonzero for u_1i, or susceptible people
u = [uforN1;uforN1;uforN1];

%sim
[t,x] = ode45(@(t,x) nonlin(t,x,k1,k2,v1,alpha,r,K,u,C,D), [0 2], x0);

%plotting
subplot(2,1,1), hold on
plot(t,x(:,1))
plot(t,x(:,3))
plot(t,x(:,5))
hold off, xlabel("time [days]")
ylabel("Susceptible Pop.")
title("Susceptible Population Over time for N = 3")



subplot(2,1,2)
hold on
plot(t,x(:,2))
```

```
plot(t,x(:,4))
plot(t,x(:,6))
hold off, xlabel("time [days]")
ylabel("Infected Pop.")
title("Infected Population Over time for N = 3")


end



%nonlinear system generalized for N neighborhoods, also assumes params for
%all neighborhoods are the same
function dxdt = nonlin(t,x,k1,k2,v1,alpha,r,K,input,C,D)
    u = -K*x + input;

    dxdt = [];
    for i = 0:(length(x)/2-1)

        viral = v1(i+1)*x(1 + 2*i)*x(2+2*i)/(k1(i+1)+x(2+2*i));
        lossImm = alpha(i+1)*x(2+2*i);

        x1Rela = 0;
        x2Rela = 0;
        for j = 0:(length(x)/2-1)
            x1Rela = x1Rela + C(i+1,j+1)*(x(1+2*i)-x(1+2*j));
            x2Rela = x2Rela + D(i+1,j+1)*(x(1+2*i)-x(1+2*j));
        end
        dxdt = cat(1, dxdt,[-1*viral + lossImm - x1Rela;
                viral - lossImm - r(i+1)*x(2+2*i)/(x(2+2*i)+k2(i+1)) -
x2Rela]);
    end

    dxdt = dxdt + u;

end
```


Susceptible Population for N = 3
Susceptible Pop.
time [days]
Pop. 1
Pop. 2
Pop. 3


Infected Population Over time for N = 3
Infected Pop.
time [days]
Pop. 1
Pop. 2
Pop. 3


Susceptible Population Over time for N = 3
Susceptible Pop.
time [days]


Infected Population Over time for N = 3
Infected Pop.
time [days]

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