Topic B Assignment 2

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1. (i) Let $S(t)$, $I(t)$ and $R(t)$ be the number of susceptible, infected and recovered people respectively at time t. We are modelling the SIR model where recovered individuals will die with rate μ, and are reborn as susceptibles. This is simply a transition from $R \to S$ with rate μ. This is effectively an SIRS model. Writing out the transition table: Table (i) shows a naïve approach to the problem. Since rebirth occurs instantly after a recovered individual dies, N remains fixed.

   (ii) Without randomness, this is the system (using proportions)

$$\frac{di}{dt} = \beta is - \gamma i$$
$$\frac{ds}{dt} = -\beta is + \mu(1 - i - s)$$

   Where $I = Ni$ and $S = Ns$.

   (iii) Consider the equilibria for the model. I will consider the population proportions $()i, s)$ rather than numbers (I, S). First get the i nullclines:

$$\frac{di}{dt} = 0 = \beta is - \gamma i$$
$$\implies i = 0 \; or \; \beta s - \gamma = 0$$
$$s = \frac{\gamma}{\beta}$$

   And the s nullclines:

$$\frac{ds}{dt} = 0 = -\beta is + \mu(1 - i - s)$$
$$-\beta is - \mu S = -\mu(1 - i)$$
$$s(\beta i + \mu) = \mu(1 - i)$$
$$s = \frac{\mu(1 - i)}{\beta i + \mu}$$

Event	Transition	Rate
Infection	$(S, I, R) \to (S - 1, I + 1, R)$	$\frac{\beta IS}{S+I+R-1}$
Recovery	$(S, I, R) \to (S, I - 1, R + 1)$	γI
Rebirth	$(S, I, R) \to (S + 1, I, R - 1)$	μR

Event	Transition	Rate
Infection	$(S, I) \to (S - 1, I + 1)$	$\frac{\beta IS}{N-1}$
Recovery	$I \to I - 1$	γI
Rebirth	$S \to S + 1$	$\mu(N - I - S)$

Table 1: Top: full SIRS model description. Bottom: a simplified description to the model

So fixed points are: the trivial case: $i = 0, s = 1$, and the more interesting one:

$$\begin{aligned} s = \frac{\gamma}{\beta}, \quad \frac{di}{dt} &= -\beta i \frac{\gamma}{\beta} + \mu(1 - i - \frac{\gamma}{\beta}) \\ 0 &= -\gamma i + \mu - \mu i - \mu \frac{\gamma}{\beta} \\ \gamma i + \mu i &= \mu(1 - \frac{\gamma}{\beta}) \\ i &= \frac{\mu\left(1 - \frac{\gamma}{\beta}\right)}{\gamma + \mu} \end{aligned}$$

The fixed point for I exists in the relevant region only if

$$\begin{aligned} 1 - \frac{\gamma}{\beta} &\geq 0 \\ \gamma &\leq \beta \end{aligned}$$

So this fixed point exists only if $\gamma \leq \beta$
The stability of these steady states, using the Jacobian:

$$J(i, s) = \begin{pmatrix} \beta s - \gamma & \beta i \\ -\beta s - \mu & -\beta i - \mu \end{pmatrix}$$

And hence for the steady states

$$J(0, 1) = \begin{pmatrix} \beta - \gamma & 0 \\ -\beta - \mu & -\mu \end{pmatrix}$$

With eigenvalues $\beta - \gamma$ and $-\mu$. This is stable if $\gamma > \beta$ and $\mu > 0$. For the other steady state:

$$\begin{aligned} J\left(\frac{\mu\left(1 - \frac{\gamma}{\beta}\right)}{\gamma + \mu}, \frac{\gamma}{\beta}\right) &= \begin{pmatrix} \beta\frac{\gamma}{\beta} - \gamma & \beta\frac{\mu\left(1-\frac{\gamma}{\beta}\right)}{\gamma+\mu} \\ -\beta\frac{\gamma}{\beta} - \mu & -\beta\frac{\mu\left(1-\frac{\gamma}{\beta}\right)}{\gamma+\mu} - \mu \end{pmatrix} \\ &= \begin{pmatrix} 0 & \frac{\mu(\beta-\gamma)}{\gamma+\mu} \\ -\gamma - \mu & -\left(\frac{\mu(\beta-\gamma)}{\gamma+\mu} + \mu\right) \end{pmatrix} \\ &= \begin{pmatrix} 0 & \frac{\mu(\beta-\gamma)}{(\gamma+\mu)} \\ -(\gamma+\mu) & -\frac{\mu(\beta-\mu)}{(\gamma+\mu)} \end{pmatrix} \end{aligned}$$

This will be stable if $\det J > 0$ and $trJ < 0$

$$\begin{aligned} \det J = \mu(\beta - \gamma) &> 0 \\ \beta - \gamma &> 0 \\ \beta &> \gamma \end{aligned}$$

And the trace has to be negative:

$$\begin{aligned} -\mu(\beta - \mu) &< 0 \\ \beta - \mu &> 0 \\ \beta &> \mu \end{aligned}$$

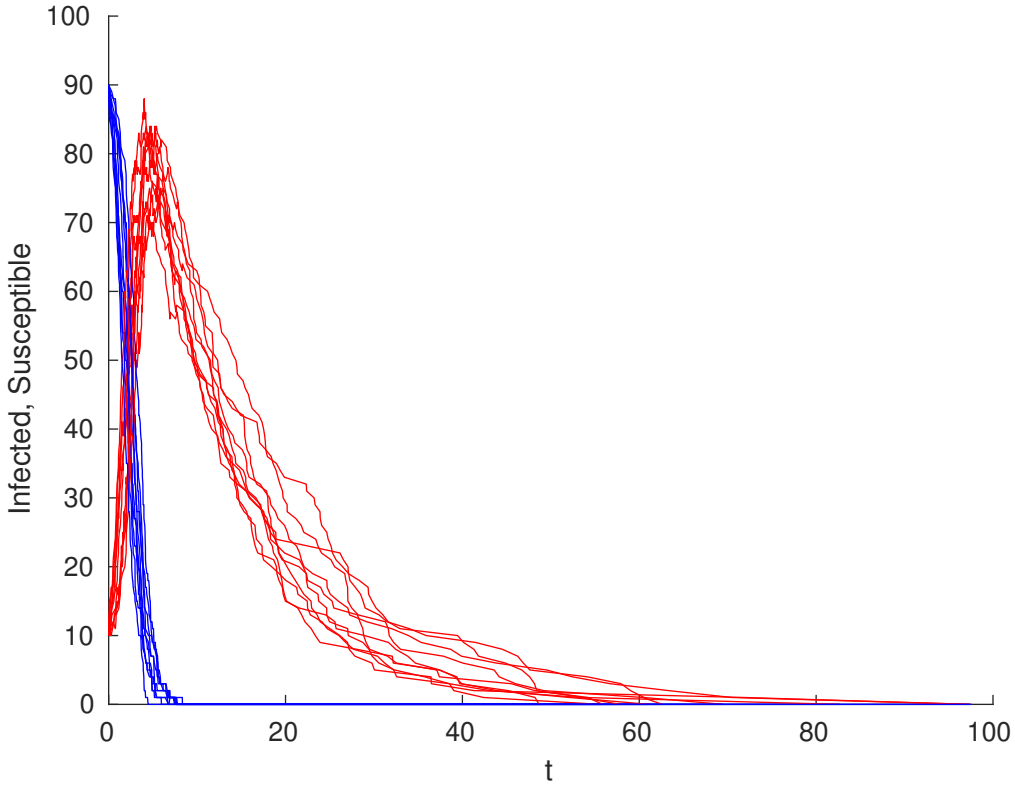

Figure 1: 10 Simulations of the model for $R_0 = 15$, $1/\gamma = 13$ and $1/\mu = \frac{60}{365}$. Blue: susceptible, red: infected

Hence this is a stable point so long as $\beta > \max\{\gamma, \mu\}$

If we have $\mu > \beta > \gamma > 0$ then there are no stable fixed points.

(iv) The code to simulate the model is shown in Code A. Figure 1 plots 10 simulations of the model. Clearly for this parameter set, the number of infected goes to 0. What is not shown in the plot is that as time goes to infinity $S \to N$.

(v) By simulating repeatedly, and rejecting points where $I(t) = 0$ for any t, we can estimate this $\mathbb{E}(I(t)|I(t) > 0)$

Figure 4 plots a comparison of the two models. Only $I(t)$ has been plotted for the deterministic and stochastic models, as this is the more interesting quantity. As shown in the figure, the two plots are very similar, overlapping for most of the region, but begin to separate slightly around $t = 60$ and above.

(vi) If **all** individuals die at a rate μ, and susceptibles are independently born at rate μ proportional to the total population, the model itself changes significantly. The total populaiton size N is no longer constant. The deterministic system of ODEs to model this is:

$$\begin{aligned}
\frac{dI}{dt} &= \frac{\beta IS}{S+I+R} - \gamma I - \mu I \\
\frac{dS}{dt} &= -\frac{\beta IS}{S+I+R} + \mu(I+R) \\
\frac{dR}{dt} &= \gamma I - \mu R
\end{aligned}$$

2. (i) The code for this is shown in A.3. It calls code A.2 to obtain the DA representation and then generates a Q_1 and Q_2 matrix for infection and recovery rates, respectively.

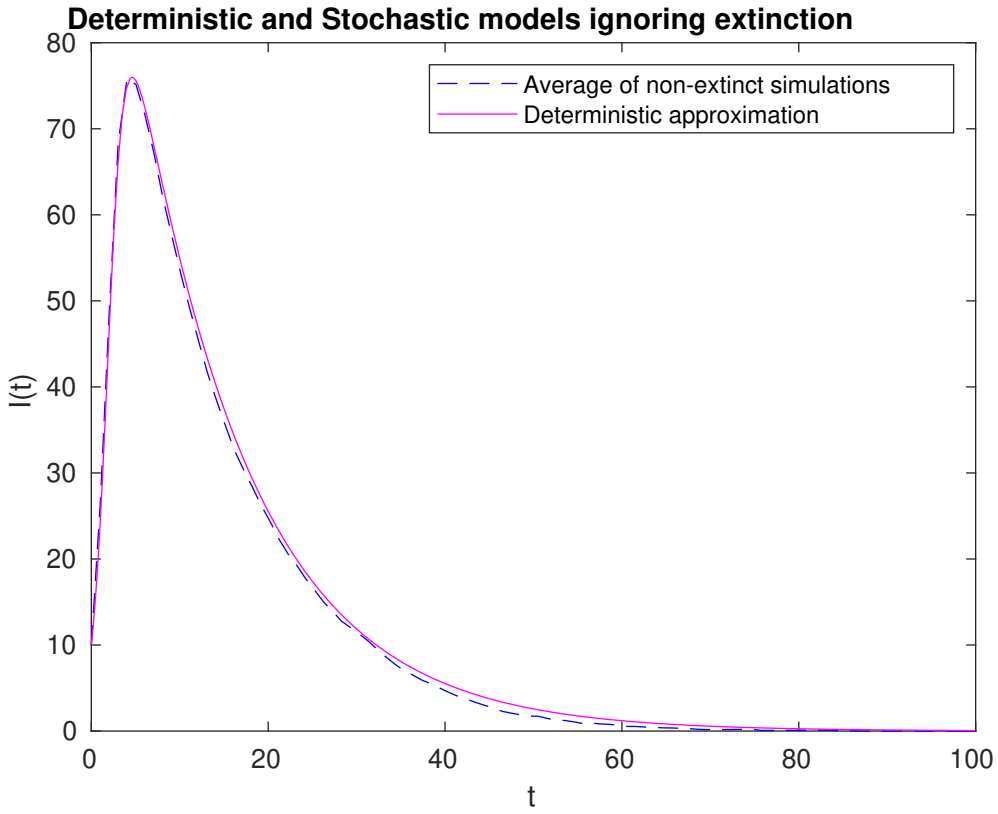

Figure 2: Comparison of the deterministic and stochastic models, where the stochastic solution is the average of 50 simulations.

(ii) Part 2 of code A utilises the SIRQ function and the code A.4.

(iii) The code A outputs the value, and it gives 0.0501 for the probability that a total of 12 people are infected over the epidemic.

(iv) The part labelled Question 4 Part 4 of code A solves this.

(v) To calculate the probability of a minor outbreak,

3. (i) So we now consider the SI(2)R model. Transitions are

$$S \overset{\frac{\beta IS}{N-1}}{\to} I_1 \overset{\gamma}{\to} I_2 \overset{\gamma}{\to} R$$

Since we are only considering a single individual in the system, the states correspond to those above. R is the absorbing state.

Since we consider an infinite population and we are only concerned with states that accumulate cost. So Q_B will be the Q matrix for I_1, I_2.

$$Q_B = \begin{pmatrix} -2\gamma & 2\gamma \\ 0 & -2\gamma \end{pmatrix}$$

With cost function (since you infect at rate β in either state):

$$\boldsymbol{f} = \begin{bmatrix} \beta \\ \beta \end{bmatrix}$$

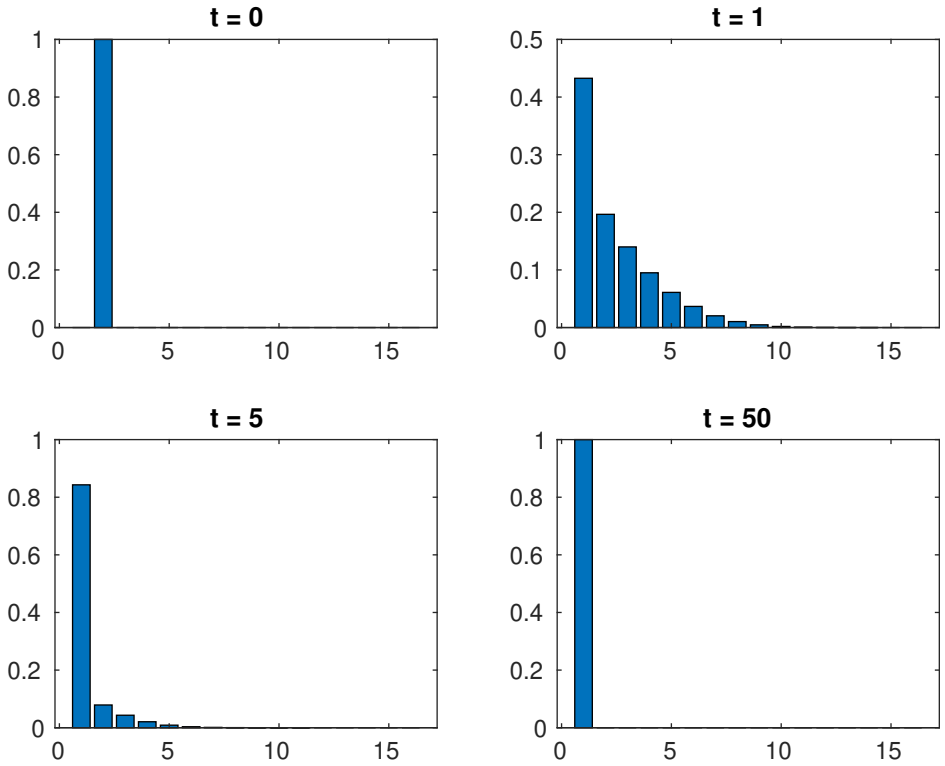

Figure 3: Probability mass function of $I(t)$ calculated using the implicit Euler method for various times

Hence

$$\begin{aligned} Q_B \boldsymbol{d} &= -\boldsymbol{f} \\ \begin{pmatrix} -2\gamma & 2\gamma \\ 0 & -2\gamma \end{pmatrix} \begin{bmatrix} d_1 \\ d_2 \end{bmatrix} &= \begin{bmatrix} -\beta \\ -\beta \end{bmatrix} \\ \implies d_2 &= \frac{\beta}{2\gamma} \\ -2\gamma d_1 + \beta &= -\beta \\ d_1 &= \frac{\beta}{\gamma} \end{aligned}$$

Since d_i are the expected cost for state i. So the expected total cost for one individual will be

$$d_1 + d_2 = \frac{3\beta}{2\gamma} = R_0$$

(ii) SIR model. We want to calculate

$$D = \mathbb{E}\left(\int_0^\infty f(X(t))dt \right)$$

With $N = 20, \beta = 0.6$ and $1/\gamma = 3$, and the cost per day to take care of i infected individuals will be:

$$f(i) = ai + b\lceil \frac{i}{4} \rceil = 2i + 5\lceil \frac{i}{4} \rceil, \quad f(0) = 0$$

Where $i = 0$ is an absorbing state Have to solve the system

$$\boldsymbol{d} = -\boldsymbol{f} \backslash Q_b$$

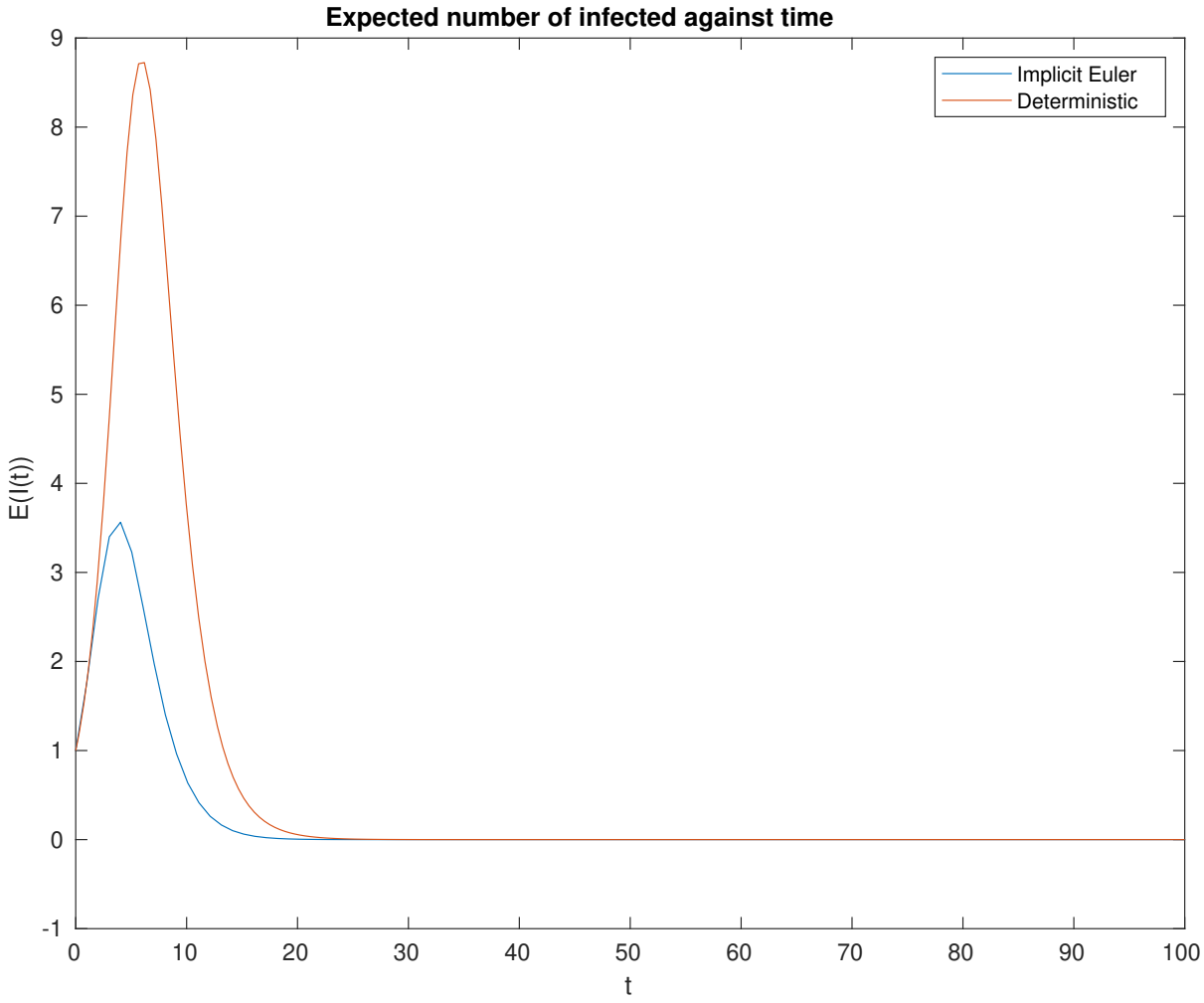

Figure 4: Comparison of the deterministic value and Implicit Euler approximation of $E[I(t)]$.

Where d_i is the expected cost for caring for individuals given the process starts in state i. Since this is the SIR model, we will use the DA state space. To extract the number of infected from this, $I = Z_2 - Z_1$

A Code

A.1 Main Script

```

clear all
close all
%%Question 1
%part 4
%simulate the SIRS model
tbounds = [0,100];
beta = 15/13;
gamma = 1/13;
mu = 1/(60*365) ;
N = 100;
i0 = 10;

figure
hold on
for i=1:10
[t,IS] = SIRS_Sim(tbounds,beta,gamma,mu,N,i0);
plot(t,IS(:,1), '-r')
plot(t,IS(:,2), '-b')
end
axis ([0,100,0,100])
xlabel("t")
ylabel("Infected, Susceptible")
%%Try, Catch so it doesn't get cranky since
%my file hierarchy is dodgy
%if the Assignments folder doesn't exist
try
    saveas(gcf,"Assignments/TopicBA2Q14.eps",'epsc')
catch
    saveas(gcf,"TopicBA2Q14.eps",'epsc')
end

%%
%%Question 1
%part 5
close all
clear all
tbounds = [0,100];
beta = 15/13;
gamma = 1/13;
mu = 1/(60*365) ;
N = 100;
i0 = 10;

total = 0;
%number of cases we want without rejection
numberWanted = 50;
maxFailCount = 10000;
```

```
failcount = 0;
AverageIS = zeros(tbounds(2),2);

equispacedTime = linspace(0,tbounds(2));
%We want to at least succeed numberWanted times
%and not fail too many times
totals = zeros(length(equispacedTime),1);
for i=1:numberWanted
[t,IS] = SIRS_Sim(tbounds,beta,gamma,mu,N,i0);
%bin the times into equispace
    for i=1:length(equispacedTime)
        timeSnapshot = find(t >= equispacedTime(i),1,'first');
        %if we get a value
        if timeSnapshot
            AverageIS(i,:) = AverageIS(i,:) + IS(timeSnapshot,:);
            totals(i) = totals(i)+1;
        end
    end
end


AverageIS = AverageIS./totals;
plot(equispacedTime,AverageIS(:,1),'--b')
hold on
params =[N,beta,gamma,mu];
%solve the deterministic model numerically
[t,deterministicIS] = ode45(@SIRS_DE_deterministic,[0,100],[i0,N-i0],[],params);

plot(t,deterministicIS (:,1), '-m')
hold off
title("Deterministic and Stochastic models ignoring extinction")
xlabel("t")
ylabel("I(t)")
legend("Average of non-extinct simulations","Deterministic approximation",'location','northeast')


%my file hierarchy is dodgy
try
    saveas(gcf,"Assignments/TopicBA2Q15.eps",'epsc')
catch
    saveas(gcf,"TopicBA2Q15.eps",'epsc')
end

%%
%%Question 2
%part 2
close all
N = 15;
beta = 1.6;
gamma = 1;
InfectedAndSusceptible = [N-1,1];
```

```
[Q1,Q2] = SIRQ(N);
Q=beta*Q1+gamma*Q2;
%Cleaner, more memory efficient way to allocate the initial state since it
%only has one element
initState = sparse(1,2,1,1,length(Q),1);
probt = IEMethodReturnAll(Q,initState,[0,1,5,50]);
%probt0 = IEMethodReturnAll(Q,initState, 0);
%probt1 = IEMethodReturnAll(Q,initState, 1);
%probt5 = IEMethodReturnAll(Q,initState, 5);
%probt50 = IEMethodReturnAll(Q,initState, 50);

probt0NumInfected = InvertDaMap(probt(1,:),N);
probt1NumInfected = InvertDaMap(probt(2,:),N);
probt5NumInfected = InvertDaMap(probt(3,:),N);
probt50NumInfected = InvertDaMap(probt(4,:),N);
figure
title("Probability distributions of number infected at various times")
subplot(2,2,1)
bar(probt0NumInfected)
title("t = 0")
subplot(2,2,2)
bar(probt1NumInfected)
title("t = 1")
subplot(2,2,3)
bar(probt5NumInfected)
title("t = 5")
subplot(2,2,4)
bar(probt50NumInfected)
title("t = 50")
hold off
%my file hierarchy is dodgy
try
    saveas(gcf,"Assignments/TopicBA2Q22.eps",'epsc')
catch
    saveas(gcf,"TopicBA2Q22.eps",'epsc')
end


%%Question 2
%Part 3
Z = SIR_DA_mapping(N);
probt50TotalInfected = zeros(size(probt50));
for i=1:N
    %i infection events is Z(:,1)==i
probt50TotalInfected(i)= sum(probt50(Z(:,1) ==i));
end
probt50TotalInfected(12)

%%
%%Question 2
%Part 4
```

```
N=100;
beta = 1.6;
gamma = 1;
[Q1,Q2] = SIRQ(N);
Q=beta*Q1+gamma*Q2;
%Cleaner, more memory efficient way to allocate the initial state since it
%only has one element
initState = sparse(1,2,1,1,length(Q),1);
indexArray = 0:N;
expectationAtT = zeros(1,100);
t = linspace(0,100);

probt = IEMethodReturnAll(Q,initState, t);
invertedprobt = zeros(length(t),N+1);
for i=1:length(t)
    invertedprobt(i,:) = InvertDaMap(probt(i,:),N,true);
end
expectationAtT = sum(invertedprobt.*indexArray,2);
params = [N,beta,gamma,0];
%We can just use the SIRS DE model and set mu =0
[deterministicT,deterministicIS] = ode45(@SIRS_DE_deterministic,[0,100],[1,N-1],[],params);
plot(t,expectationAtT)
hold on
plot(deterministicT,deterministicIS(:,1))
hold off
title("Expected number of infected against time")
xlabel("t")
ylabel("E(I(t))")
legend("Implicit Euler","Deterministic")
%my file hierarchy is -wait-for-it- dodgy
try
    saveas(gcf,"Assignments/TopicBA2Q24.eps",'epsc')
catch
    saveas(gcf,"TopicBA2Q24.eps",'epsc')
end
%%
%%Question 3
%Part 2
%solve q = -f\Qb
%params
N = 20;
beta = 0.6;
gamma = 1/3;
a = 2;
b = 5;
%get the DA mapping
Z = SIR_DA_mapping(N);
[Q1,Q2] = SIRQ(N);
%full Q matrix
Q = beta*Q1 + gamma*Q2;
%get the number of infected
```

```
indexer = Z(:,1) - Z(:,2);
%non-absorbing states are those for Z1 - Z2 ~= 0
%nonZeroI = indexer(indexer~=0);
f = a*indexer + b*ceil(indexer/5);
%all states where 0 infected accumulate 0 cost
f(indexer==0) = 0;
%f = f(nonZeroI)
%f = a*nonZeroI + b*ceil(nonZeroI/5);
%Qb = Q(nonZeroI,nonZeroI);
Q(indexer==0,indexer==0)=0;
q = -f\Qb;
q = InvertDaMap(q,N,false);
plot(q)
```

A.2 SIRS_Sim.m

```
function [t,IS] = SIRS_Sim(tbounds,beta,gamma,mu,n,i0)
%%%SIRS_Sim simulates the SIRS model until tbounds(2) or until extinction
%%%IN
%%%tbounds is the vector of the simulation's [initial time, end time]
%%%beta - infection rate
%%%gamma - recovery rate
%%%mu - replenishment rate (death of recovery & birth of susceptible)
%%%n - population size
%%%i0 - initial number of infected individuals
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%OUT
%%%t - vector of the times corresponding to event occurrences
%%%IS - vector of the state space for each time



%initial time
t(1) =tbounds(1);
%termination time
 tfinish = tbounds(2);
IS = [i0,n-i0];
%transition rates as an vector anonymous function
%qis = @(in) [beta*in(1)*in(2)/(n-1) - gamma*in(1),...
%     -beta*in(1)*in(2)/(n-1), mu(n-in(1)-in(2))];
events = @(in) [beta*in(1)*in(2)/(n-1),...
    gamma*in(1), mu*(n-in(1)-in(2))];

while t(end) <tfinish && IS(end,1) > 0
    currentInfected = IS(end,:);
    currentEvents = events(currentInfected);
    sumq = sum(currentEvents);
    t = [t ; t(end)+ exprnd(1/sumq)];
    %if infection event
    if rand*sumq < currentEvents(1)
        IS = [IS;IS(end,1)+1,IS(end,2)-1];
    %if recovery event
```

```
37        elseif  rand*sumq < currentEvents(1)+currentEvents(2)
38            IS = [IS;IS(end,1)-1,IS(end,2)];
39        %otherwise someone is reborn
40        else
41            IS = [IS;IS(end,1),IS(end,2)+1];
42
43        end
44
45
46  end
47
48
49
50  end
```

A.3 SIR_DA_mapping.m

```
1   function Z = SIR_DA_mapping(N)
2   %SIR_DA_mapping(N) returns a matrix corresponding to
3   %[number of infection events, number of recovery events]
4   %For a population of size N
5   %N - population size for the model (must be a positive integer)
6   %for any given row:
7   %I = z1-z2
8   %S = N-z1-2z2
9
10  %bad input handling
11  if(N<= 0)
12      error("N must be a positive integer")
13  end
14  %number of rows for Z
15  K = (N+1) * (N+2)/2;
16  Z = zeros(K,2);
17  %row indexer for z
18  i = 1;
19  for z2 = 0:N
20      for z1 = z2:N
21          Z(i,:) = [z1,z2];
22          i=i+1;
23      end
24  end
25
26  end
```

A.4 SIRQ.m

```
1   function [Q1,Q2] = SIRQ(N)
2   %Generate the Q matrix using the DA representation
3
4   %dim of final matrix
5   K = (N+1)*(N+2)/2;
6   Z = SIR_DA_mapping(N);
7
```

```
%Q1
%Q1 effectively contains the infection rates if beta = 1
%become infected with: IS/(N-1)
%I = z1-z2
%S = N-z1
qIe = (N-Z(:,1)).*(Z(:,1)-Z(:,2))/(N-1);
%positive values correspond to possible infection events
rowsI = find(qIe > 0);
%Using the DA representation, it
%moves to one state higher for infection event
columnsI = rowsI + 1;
%grab all the non-zero elements of qIe
qI = qIe(rowsI);

Q1 = sparse(rowsI,columnsI,qI,K,K) + sparse(rowsI,rowsI,-qI,K,K);

%Q2
%Q2 is the recovery rates
%recover with I = (z1-z2)
qRe = (Z(:,1)-Z(:,2));
%positive values correspond to possible recovery events
rowsR = find(qRe >0);
%recovery event - we move down by N-Z2
columnsR = rowsR+N-Z(rowsR,2);
qR = qRe(rowsR);
Q2 = sparse(rowsR,columnsR,qR,K,K) + sparse(rowsR,rowsR,-qR,K,K);
end
```

A.5 IEMethodReturnAll.m

```
function probMatrix = IEMethodReturnAll(Q,initState,t)
%An improved version of the Implicit Euler method
%returns a Matrix with columns corresponding to the times contained in
%time vector t
%if t is a scalar then it will simply return the probability vector at
%time t
%prob is the probability mass function for the number of infected people at
%time t
prob = initState;
N = length(Q);
probMatrix = sparse ([],[],[], length(t),N,length(t)*N);

if t(1) ==0
    probMatrix(1,:)=prob;
end
tstep=0.02;
invertedPart =speye(N)-tstep*Q ;
%allocate the sparse matrix
for i=tstep:tstep:t(end)
    prob = prob/invertedPart ;
    %if there is a point within tstep of i
    tIndex= find(abs(t-i) < tstep);
```

```
23      if (tIndex)
24          probMatrix(tIndex,:) = prob;
25      end
26  end
27  end
```

A.6 SIRS_DE_deterministic.m

```
1  function dIS = SIRS_DE_deterministic(t,IS,params)
2  I = IS(1);
3  S = IS(2);
4  N = params(1);
5  beta = params(2);
6  gamma = params(3);
7  mu = params(4);
8  dIS = [beta*I.*S/(N) - gamma*I;-beta*I.*S/(N) + mu*(N-I-S)];
9  end
```

Assignment II

Worth 10% of course assessment; due by 1pm on Friday 10th May, 2019.

Relevant lectures: Lectures 1 – 18.

Individual marks are noted in [] at start of each question; total marks for assignment is 50.

Please provide an explanation/discussion with all answers, and code where appropriate.

Q1: Specifying models, and deterministic approximations
[16 marks]

In the lectures we looked at the basic SIR model. Now consider what would happen if we also add in demography (births and deaths). Assume that recovered individuals die at a rate μ and are immediately reborn as a susceptible.

(i) Specify the CTMC version of this model.

(ii) Derive a deterministic approximation to the stochastic dynamics.

(iii) What is the long term behaviour of the deterministic approximation?

(iv) Simulate the stochastic model and compare the long term dynamics with the deterministic version. Consider the parameters: $R_0 = 15$, $1/\gamma = 13$ days, $1/\mu = 60$ years, and frequency-dependent mixing.

(v) Calculate $E(I(t))$ conditional on the disease not going extinct and compare with the deterministic model.

(vi) How would the model change if all individuals can die at a rate μ and susceptible individuals are born independently at rate μ proportional to the total population?

Q2: Degree of advancement, and branching processes
[18 marks]

(i) Write code that generates the complete Q matrix for an SIR model (population size N) using the degree-of-advancement representation.

(ii) For $N = 15$, $\beta = 1.6$ and $\gamma = 1$, and starting with initial condition of $(S(0), I(0)) = (N-1, 1)$, produce some figures showing the probability mass function of I(t) at times 0, 1, 5 and 50. Use an implicit-Euler method to numerically solve the forward equation.

(iii) What is the probability that exactly 12 people are infected over the course of the epidemic? (Use the parameters from part (ii).)

(vi) For $N = 100$, $\beta = 1.6$ and $\gamma = 1$, plot the expected value of $I(t)$ as a function of time by solving the forward equation numerically, and compare to the deterministic approximation we derived in lectures.

(v) For $N = 50, 100$ and 500, $\beta = 1.6$ and $\gamma = 1$, calculate the probability of a minor outbreak using the same methods as in part (iii). How do these compare to the results derived using the branching process approximation?

Q3: Path integrals

[16 marks]

(i) In class, you evaluated R_0 and the probability mass function of secondary infections arising from a single individual with an exponentially-distributed infectious period, in an infinite population. Investigate how these two quantities (R_0 and the pmf of secondary infections) changes, if in place of an exponentially-distributed infectious period the individual has an Erlang-2-distributed infectious period with the same mean (i.e., $1/\gamma$).

(ii) Consider the SIR CTMC model of disease dynamics, in a population with $N = 20$ individuals. Assume that infectious individuals require care during their infectious period. Wards in the care facility are such that four individuals can be in each ward. Each individual has a per unit cost of $\$a$ per unit time whilst infectious, and each ward has a cost of $\$b$ per unit time whilst open. Assuming the CEO of the care facility is operating to minimise cost, that $a = 2$, $b = 5$, the effective transmission rate parameter $\beta = 0.6$, and that the average infectious period is 3 days, what is the expected cost of caring for individuals during an outbreak?