10.1 The Deterministic Susceptible-Infected-Removed (SIR) Epidemic Model

Definition. In the **deterministic SIR (Susceptible-Infected-Removed)** model of epidemics, individuals in the population are assigned to three subgroups or **compartments**, each representing a specific stage of the epidemic. The stages are: **susceptibles** (those who have not yet been exposed to the disease), **infected** (those who have been infected themselves and can infect others), and **removed** (recovered and immune, or dead) (those who no longer have the disease and cannot get it again). The population of size N is assumed a **closed population**, meaning that no immigration or emigration takes place. Denote by $S(t), t \geq 0$ the number of susceptible at time t, by $I(t), t \geq 0$, the number of infected at time t, and by $R(t), t \geq 0$, the number of removed at time t. Note that in a closed population, $N = S(t) + I(t) + R(t) = constant$. Further, in this model, the number of individuals in each compartment changes over time in a deterministic manner. At time 0, there is one infected $(I(0) = 1)$, the number of susceptible is the entire population size minus the one infected $(S(0) = N - 1)$, and there are zero removed $(R(0) = 0)$. Modeling in a continuous time frame, the functions $S(t), I(t)$, and $R(t)$, $t \geq 0$ satisfy the system of ordinal differential equations:

$$
\begin{cases}
\dfrac{dS(t)}{dt} = -\beta \, \dfrac{S(t) \, I(t)}{N}, \\[2em]
\dfrac{dI(t)}{dt} = \beta \, \dfrac{S(t) \, I(t)}{N} - \gamma I(t), \\[2em]
\dfrac{dR(t)}{dt} = \gamma I(t)
\end{cases}
$$

with the initial conditions $S(0) = N - 1$, $I(0) = 1$, and $R(0) = 0$. Here β is the **rate of infection** and γ is the **rate of removal**. The argument goes as follows. It is assumed that in an infinitesimally small interval $[t, t + dt]$, any susceptible individual meets exactly one individual from the population, so the probability that this individual is an infected one is $I(t)/N$. It is also assumed that an infected individual will pass the infection with probability β. Thus, the chance for a susceptible individual to become infected is $\beta \, I(t)/N$ and, on average, $\beta \, S(t)I(t)/N$ susceptible individuals become infected. This justifies the first equation. Also, it is assumed that each infected individual will recover or die with probability γ, and so, on average, $\gamma I(t)$ infected individuals will leave the infected compartment (and $\beta \, S(t)I(t)/N$ susceptible individuals will join the infected), hence, the second equation holds. Finally, all removed individuals stay removed, so a change over time can happen only

if infected individuals become removed (or, on average, $\gamma I(t)$ will join the removed), which supports the last equation.

Further, it is not very practical (if not impossible) to solve the given equations explicitly. Instead, these differential equations are turned into discrete **difference equations**, numerical solutions for which can be found recursively and plotted on a graph.

Consider discrete time points, a unit interval apart $(1, 2, 3,$ etc.). The above equations become:

$$
\begin{cases}
S(j+1) = S(j) - \beta \dfrac{S(j)\,I(j)}{N}, \\[2em]
I(j+1) = I(j) + \beta \dfrac{S(j)\,I(j)}{N} - \gamma I(j), \quad , \quad j = 0, 1, 2, \dots \\[2em]
R(j+1) = R(j) + \gamma I(j).
\end{cases}
$$

Below we present SAS and R codes that plot the solutions on the time interval $[0,\ 30]$ for $N = 1000$, $\beta = 0.7$, and $\gamma = 0.2$.
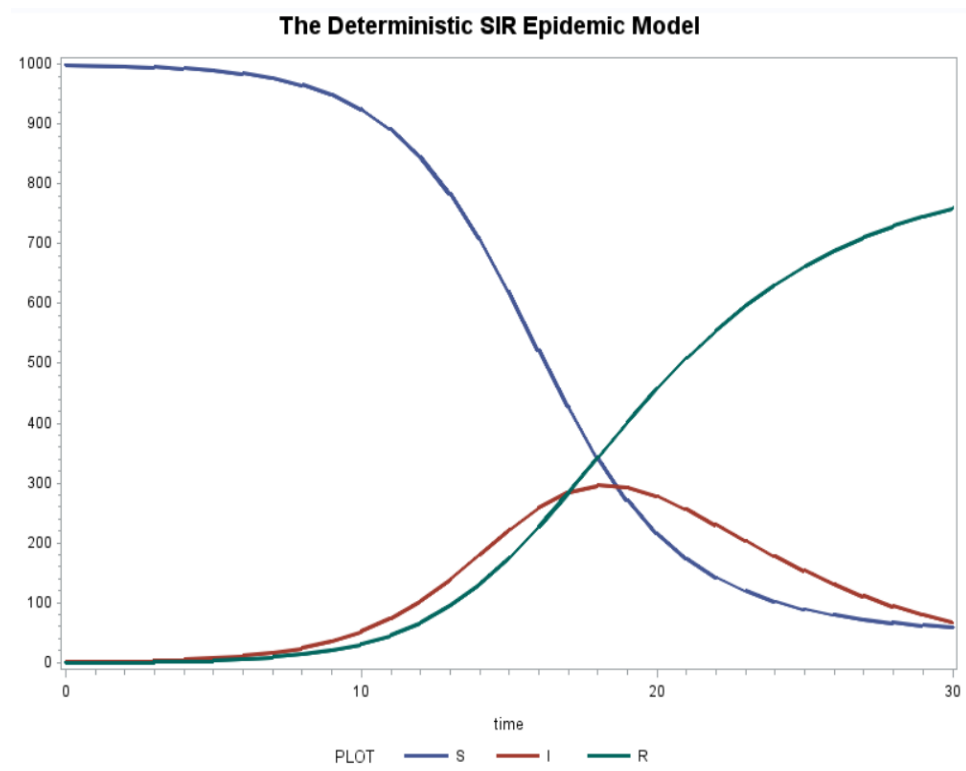
In SAS:

```
%let N=1000;
%let beta=0.7;
%let gamma=0.2;
%let t=30;

data SIR;
S=&N-1;
I=1;
R=0;
time=0;
output;
do time=1 to &t;
 S+(-&beta*S*I/&N);
   I+&beta*S*I/&N-&gamma*I;
     R+&gamma*I;
  output;
end;
run;
```

```
symbol interpol=join value=none width=2;
axis label=none;
title "The Deterministic SIR Epidemic Model";
proc gplot data=SIR;
plot (S I R)*time/overlay legend vaxis=axis;
run;
```


The Deterministic SIR Epidemic Model

In R:
N<- 1000
ta<- 0.7
gamma<- 0.2
S<- c()
I<- c()
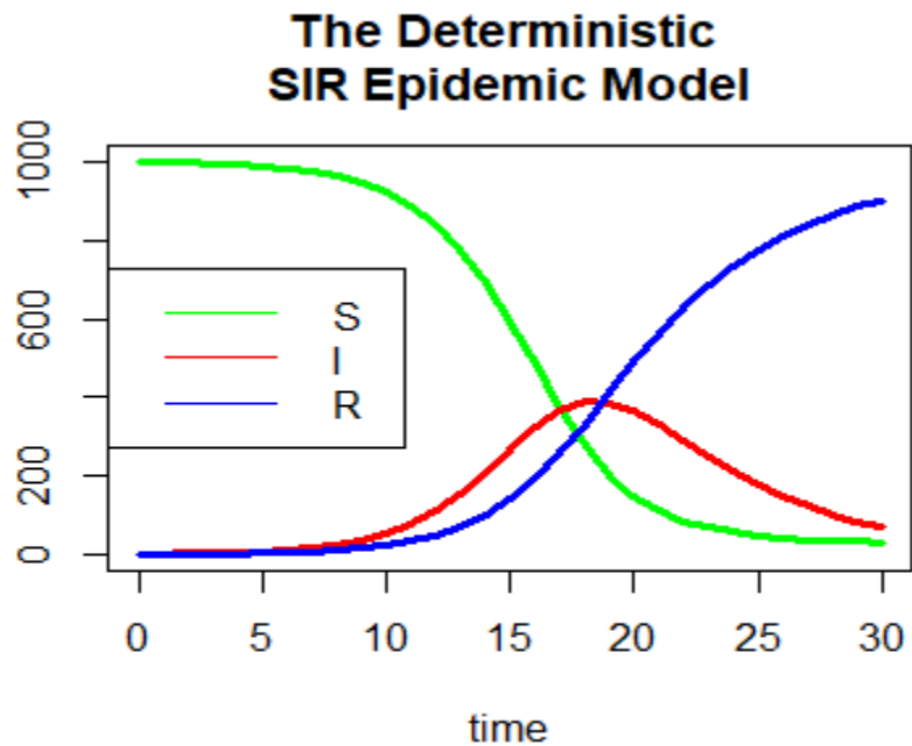R<- c()

S[1]<- N-1
I[1]<- 1
R[1]<- 0

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```
for (j in 1:30) {
    S[j+1]<- S[j-1]-beta*S[j]*I[j]/N
      I[j+1]<- I[j]+beta*S[j]*I[j]/N-gamma*I[j]
        R[j+1]<- R[j]+gamma*I[j]
}

time<- 0:30
plot(time,S, type="l", lty=1, lwd=3, main="The Deterministic SIR Epi-
demic
Model", ylim=c(0,N), col="green")
lines(time,I,lwd=3, col="red")
lines(time,R,lwd=3, col="blue")
legend("left", c("S","I","R"), lty=1, col=c("green","red","blue"))
```


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