10.2 The Binomial SIR Epidemic Model

Definition. In this SIR model, the number of susceptible individuals that become infected in the interval $[t, t + dt]$ is a binomial random variable, say X, with parameters $S(t)$ and $\beta\, I(t)/N$. Also, the number of infected individuals that become removed is a binomial random variable, say Y, with parameters $I(t)$ and γ. The difference equations for this model take the form:

$$
\begin{cases}
S(j + 1) = S(j) - X, \\[2mm]
I(j + 1) = I(j) + X - Y, \quad , \quad j = 0, 1, 2, \ldots. \\[2mm]
R(j + 1) = R(j) + Y.
\end{cases}
$$

Note. In the deterministic SIR model, the random variables X and Y are replaced by their expected values.

Below we show how to simulate trajectories of S, I, and R, using SAS and R.

In SAS:

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

data SIR;
call streaminit(809197);
S=&N;
I=1;
time=0;
output;
do time=1 to &t;
X=rand("binomial", &beta*I/&N, S);
Y=rand("binomial", &gamma, I);
 S+(-X);
   I+X-Y;
      R+Y;
  output;
end;
run;
```

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


The Binomial SIR Epidemic Model
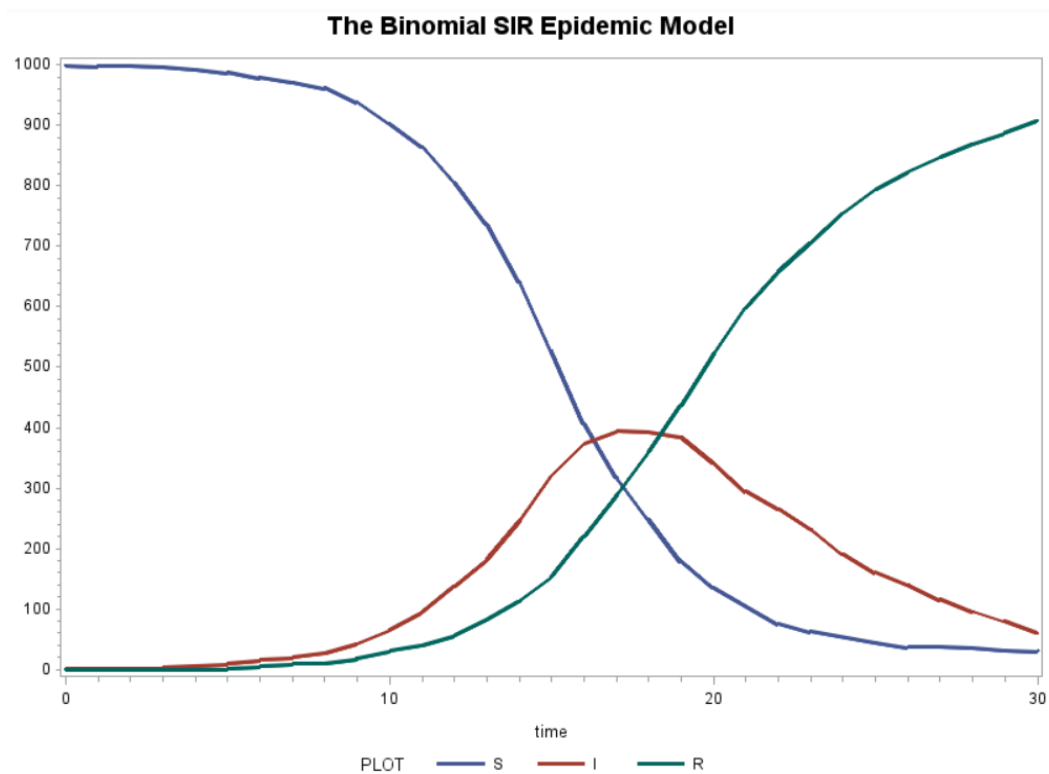
In R:
set.seed(191962)
N<- 1000
beta<- 0.7
gamma<- 0.2
S<- c()
I<- c()
R<- c()

S[1]<- N-1
I[1]<- 1
R[1]<- 0
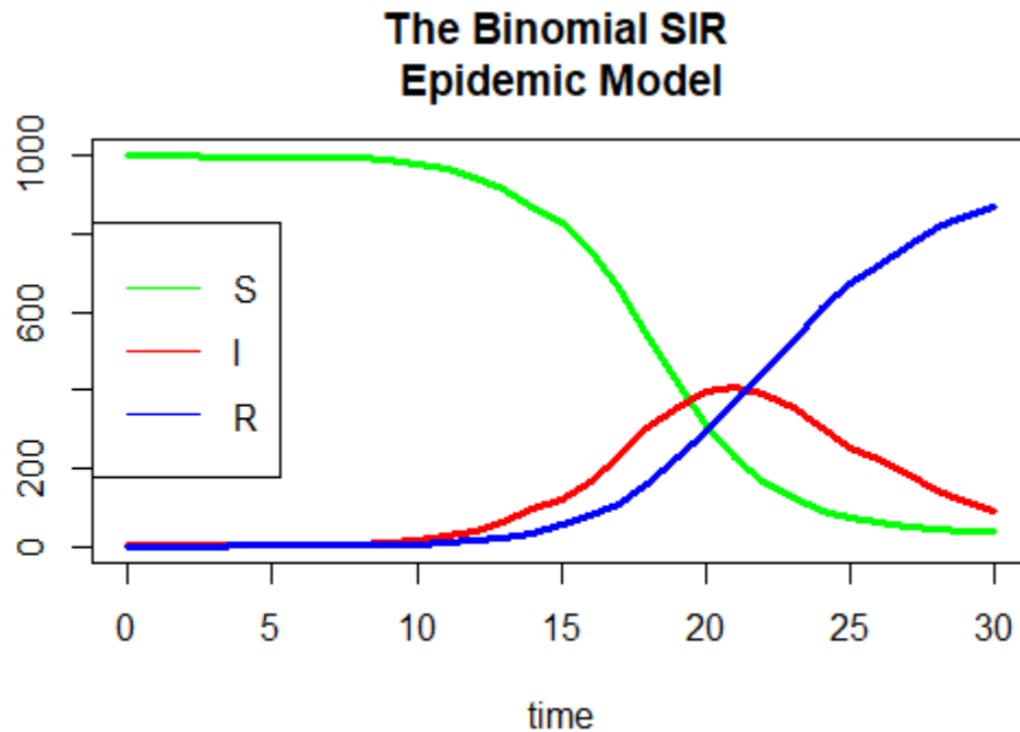
```
for (j in 1:30) {
X<- rbinom(1,S[j],beta*I[j]/N)
Y<- rbinom(1,I[j],gamma)
    S[j+1]<- S[j]-X
        I[j+1]<- I[j]+X-Y
            R[j+1]<- R[j]+Y
}

time<- 0:30
plot(time,S, type="l", lty=1, lwd=3, main="The Binomial SIR Epidemic
Model", ylim=c(0,N), col="green", ylab="")
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"))
```


The Binomial SIR Epidemic Model

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