SEIR Epidemiological Model: A Review

1 Basic SIR Model with demography

Model Assumptions:

1. The infection circulates in a population of size N, with a per capita background death rate, μ which is balanced by a birth rate μN. We also assume that
$$\frac{dN}{dt} = 0,$$
hence
$$N = S + I + R$$
remains constant.

2. The infection causes acute morbidity (not mortality); That is, in this version of the SIR model we assume we can ignore disease-induced mortality. This is reasonable for certain infections like chickenpox, but certainly not for others like rabies, SARS, or ebola.

3. Individuals are recruited directly into the susceptible class at birth (so we ignore perinatal maternal immunity).

4. Transmission of infection from infectious to susceptible individuals is controlled by a bilinear contact term βIS This stems from the assumption that the I infectious individuals are independently and randomly mixing with all other individuals, so the fraction S/N of the encounters is with susceptible individuals; β is the contact rate times the probability of transmission given a contact between a susceptible and an infectious individual.

5. Chances of recovery or death is assumed not to change during the course of infection.

6. Infectiousness is assumed not to change during the course of infection.

7. Infected individuals move directly into the the infectious class (as opposed to the SEIR model;and remains there for an average infectious period of $1/\gamma$ (assuming $\mu << \gamma$).

8. The model assumes that recovered individuals are immune from reinfection for life.

The model is characterised taking into account the manifold of Susceptible, Infectious and Recovered individuals, namely

$$\mathcal{M}_{SIR}(N) = \{(S, I, R) \in \mathbb{R}^3_+ : S + I + R = N\}$$

together the parameter manifold

$$\mathcal{P}_{SIR} = \{(\mu, \beta, \gamma) \in \mathbb{R}^3_+ : \mu << \gamma\}.$$

Then for a given an observation $(S_0, I_0, R_0) \in \mathcal{M}_N$ and $(\mu, \beta, \gamma) \in \mathcal{P}_{SIR}$ in time $t = 0$ the evolution of the system is characterised by the ODE:

$$\dot{S}(t) = \mu(N - S) - \beta S \frac{I}{N}, \tag{1}$$

$$\dot{I}(t) = \beta S \frac{I}{N} - (\mu + \gamma)I, \tag{2}$$

$$\dot{R}(t) = \gamma I - \mu R \tag{3}$$

Since $\frac{S}{N} + \frac{I}{N} + \frac{R}{N} = 1$ holds then without loss of generality we may assume that $S(t), I(t)$ and $R(t)$ is a system of time-dependent probabilities i.e. $S + I + R = 1$ satisfying the ODE:

$$\dot{S}(t) = \mu(1 - S) - \beta S\, I \tag{4}$$

$$\dot{I}(t) = \beta S\, I - (\mu + \gamma)I, \tag{5}$$

$$\dot{R}(t) = \gamma I - \mu R \tag{6}$$

For directly transmitted pathogens, R_0 is, per definition, the expected number of secondary cases that arise from a typical infectious index-case

in a completely susceptible host population. R_0 plays a critical role for a number of aspects of disease dynamics and is therefore the focus of much study in historical and contemporary infectious disease dynamics. (R_0) is a very important quantity in epidemiology. For this simple SIR model

$$R_0 = \frac{\beta}{\gamma + \mu}$$

We need to load the library to solve numerically an ODE:

```
library(deSolve)
```

We construct the SIR model function:

```
sirmod = function(t, y, parms) {
  # Pull state variables from y vector
  S = y[1]
  I = y[2]
  R = y[3]
  # Pull parameter values from parms vector beta = parms["beta"]
  mu = parms["mu"]
  gamma = parms["gamma"]
  N = parms["N"]
  beta = parms["beta"]
  # Define equations
  dS = mu * (1 - S) - beta * S * I
  dI = beta * S * I - (mu + gamma) * I
  dR = gamma * I - mu * R
  res = c(dS, dI, dR)
  # Return list of gradients
  list(res)
}
```

We introduce the parameter values

```
times = seq(0, 26, by = 1/10)
parms = c(mu = 0.2, N = 1, beta = 2, gamma = 1/2)
start = c(S = 0.999, I = 0.001, R = 0.1)
```

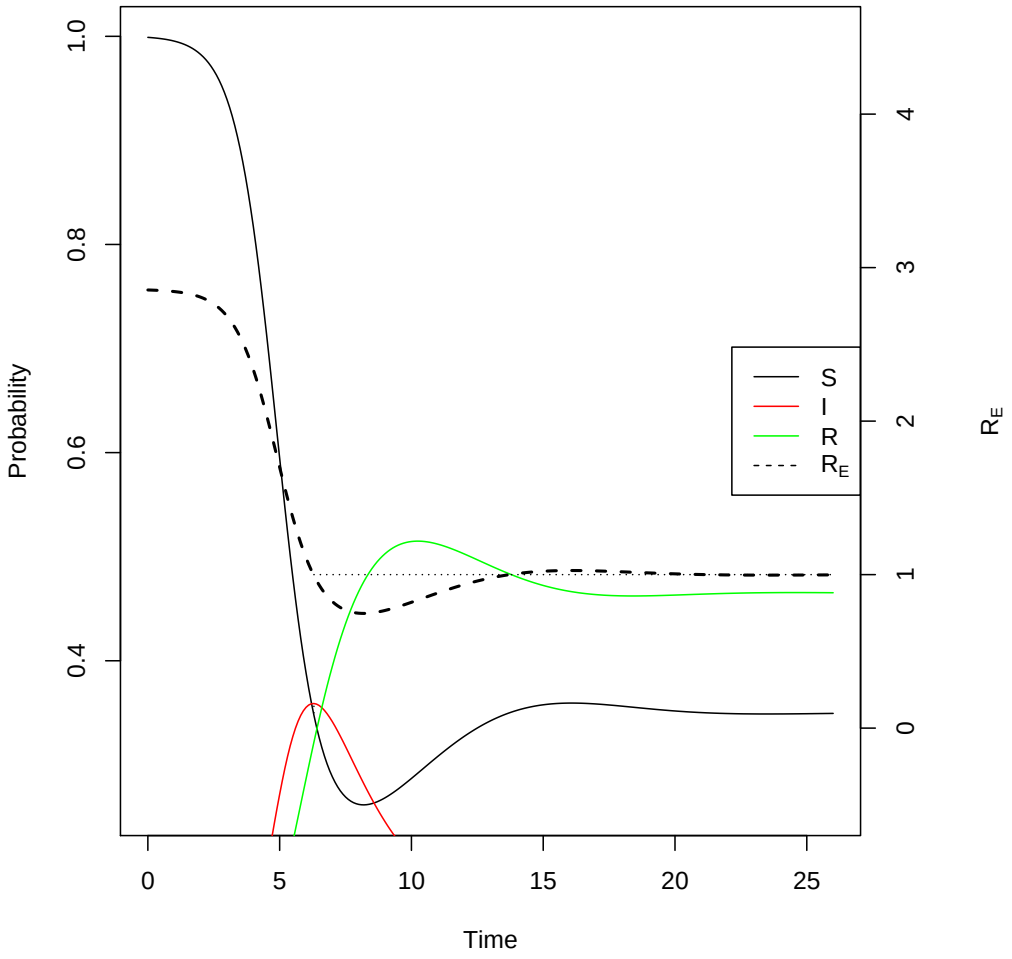
We integrate numerically (1)-(3)

```
out = ode(y=start, times=times, func=sirmod, parms= parms)
out = as.data.frame(out)
#head(round(out, 3))
```

Finally, we plot the numerical solution

```
#Calculate R0
R0=parms["beta"]/(parms["gamma"]+parms["mu"])
```

```
#Adjust margins to accommodate a second right axis
par(mar = c(5,5,2,5))
#Plot state variables
plot(x=out$time, y=out$S, ylab="Probability", xlab="Time",type="l")
lines(x=out$time, y=out$I, col="red")
lines(x=out$time, y=out$R, col="green")
#Add vertical line at turnover point
xx = out$time[which.max(out$I)]
lines(c(xx,xx), c(1/R0,max(out$I)), lty=3)
#prepare to superimpose 2nd plot
par(new=TRUE)
#plot effective reproductive ratio (w/o axes)
plot(x=out$time, y=R0*out$S, type="l", lty=2, lwd=2,
     col="black", axes=FALSE, xlab=NA, ylab=NA,
ylim=c(-.5, 4.5))
lines(c(xx, 26), c(1,1), lty=3)
#Add right-hand axis for RE
axis(side = 4)
mtext(side = 4, line = 4, expression(R[E])) #Add legend
legend("right", legend=c("S", "I", "R",expression(R[E])),
       lty=c(1,1,1,2), col=c("black", "red", "green", "black"))
```



2 The SEIR Model

We briefly introduce a refinement to the SIR model to take into account the latent period. The process of transmission often occurs due to an initial inoculation with a very small number of pathogen units (e.g., a few bacterial cells or virions). A period of time then ensues during which the pathogen reproduces rapidly within the host, relatively unchallenged by the immune system. During this stage, pathogen abundance is too low for active trans-

mission to other susceptible hosts, and yet the pathogen is present. Hence, the host cannot be categorized as susceptible, infectious, or recovered; we need to introduce a new category for these individuals who are infected but not yet infectious. These individuals are referred to as Exposed and are represented by the variable E in SEIR models.

We assume that:

- An average infective individual produces β new infections per unit of time when all contacts are with susceptible but that otherwise, this rate is reduced by the ratio S/N.
- Individuals in the exposed class E progress to the infective class at the per capita rate k.
- There is no disease-induced mortality or permanent immunity, and there is a mean infective period of $1/\sigma$.

Then the SEIR equations are:

$$\dot{S}(t) = \mu(N - S) - \beta S \frac{I}{N}, \tag{7}$$

$$\dot{E}(t) = \beta S \frac{I}{N} - (\mu + \sigma)E, \tag{8}$$

$$\dot{I}(t) = \sigma E - (\mu + \gamma)I, \tag{9}$$

$$\dot{R}(t) = \gamma I - \mu R \tag{10}$$

The model is characterised taking into account the manifold of Susceptible, Exposed, Infectious and Recovered individuals, namely

$$\mathcal{M}_{SEIR}(N) = \{(S, E, I, R) \in \mathbb{R}^4_+ : S + E + I + R = N\}$$

together the parameter manifold

$$\mathcal{P}_{SEIR} = \{(\mu, \beta, \gamma, \sigma) \in \mathbb{R}^4_+ : \mu << \gamma\}.$$

In a similar way as in the SIR model we can deduce the evolution of the corresponding time-dependent probabilities:

$$\dot{S}(t) = \mu(1 - S) - \beta S\, I, \tag{11}$$

$$\dot{E}(t) = \beta S\, I - (\mu + \sigma)E, \tag{12}$$

$$\dot{I}(t) = \sigma E - (\mu + \gamma)I, \tag{13}$$

$$\dot{R}(t) = \gamma I - \mu R \tag{14}$$

Moreover, in this model

$$R_0 = \frac{\beta + \sigma}{(\gamma + \mu)(\sigma + \mu)}.$$

We construct the SEIR model function:

```
seirmod = function(t, y, parms) {
  # Pull state variables from y vector
  S = y[1]
  E = y[2]
  I = y[3]
  R = y[4]
  # Pull parameter values from parms vector beta = parms["beta"]
  mu = parms["mu"]
  gamma = parms["gamma"]
  beta = parms["beta"]
  sigma = parms["sigma"]
  # Define equations
  dS = mu * (1 - S) - beta * S * I
  dE = beta * S * I - (mu + sigma) * E
  dI = sigma * E  - (mu + gamma) * I
  dR = gamma * I - mu * R
  res = c(dS, dE, dI, dR)
  # Return list of gradients
  list(res)
}
```

We introduce the parameter values

```
times = seq(0, 30, by = 1/10)
parms = c(mu = 0.01, N = 1, beta = 2, gamma = 1/2, sigma = 0.1)
start = c(S = 0.9, E=0.05, I = 0.02, R = 0.03)
```

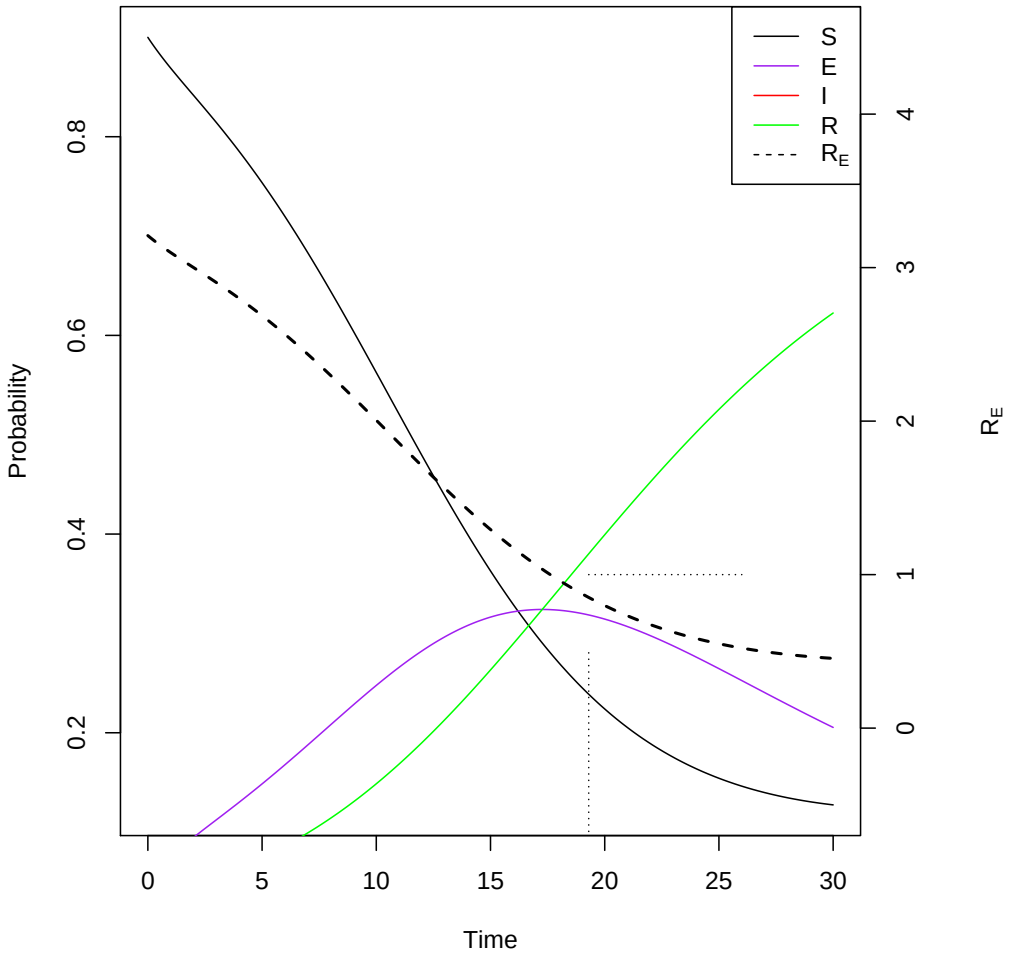
We integrate numerically (7)-(10)

```
out = ode(y=start, times=times, func=seirmod, parms= parms)
out = as.data.frame(out)
#head(round(out, 3))
```

Finally, we plot the numerical solution

```
#Calculate R0
R0=(parms["beta"]*parms["sigma"])/
((parms["gamma"]+parms["mu"])*(parms["sigma"]+parms["mu"]))
#Adjust margins to accommodate a second right axis
par(mar = c(5,5,2,5))
#Plot state variables
```

```
plot(x=out$time, y=out$S, ylab="Probability", xlab="Time",type="l")
lines(x=out$time, y=out$E, col="purple")
lines(x=out$time, y=out$I, col="red")
lines(x=out$time, y=out$R, col="green")
#Add vertical line at turnover point
xx = out$time[which.max(out$I)]
lines(c(xx,xx), c(1/R0,max(out$I)), lty=3)
#prepare to superimpose 2nd plot
par(new=TRUE)
#plot effective reproductive ratio (w/o axes)
plot(x=out$time, y=R0*out$S, type="l", lty=2, lwd=2,
     col="black", axes=FALSE, xlab=NA, ylab=NA,
ylim=c(-.5, 4.5))
lines(c(xx, 26), c(1,1), lty=3)
#Add right-hand axis for RE
axis(side = 4)
mtext(side = 4, line = 4, expression(R[E])) #Add legend
legend("topright", legend=c("S","E" ,"I", "R",expression(R[E])),
  lty=c(1,1,1,1,2), col=c("black","purple" , "red", "green", "black"))
```



The relationship with the model given in the web site

http://gabgoh.github.io/COVID/index.html

is the following: Take in (11)-(14) the value $\mu = 0$ and also introduce the notation

$$T_{inf} = \frac{1}{\sigma}$$

for the Infectious Period,

$$T_{inc} = \frac{1}{\gamma}$$

for the Incubation Period, and

$$\beta = \frac{R_t}{T_{inf}} = \sigma\, R_t$$

where R_t the probability of transmission given a contact between a susceptible and an infectious individual. Observe that

$$R_0 = \frac{\beta + \sigma}{\gamma\sigma} = \frac{\beta}{\gamma\sigma} + \frac{1}{\gamma} = T_{inc}(R_t + 1),$$

thus

$$R_t = \frac{R_0}{T_{inc}} - 1.$$

In conclusion, for a given parameter values (R_0, T_{inf}, T_{inc}) and an initial condition $(S(0), E(0), I(0), R(0))$ such that $S(0) + E(0) + I(0) + R(0) = 1$ holds, we need to solve:

$$\dot{S}(t) = -T_{inf}^{-1}(T_{inc}^{-1}R_0 - 1)\, S\, I, \tag{15}$$

$$\dot{E}(t) = T_{inf}^{-1}(T_{inc}^{-1}R_0 - 1)\, S\, I - T_{inf}^{-1}\, E, \tag{16}$$

$$\dot{I}(t) = T_{inf}^{-1}\, E - T_{inc}^{-1}\, I, \tag{17}$$

$$\dot{R}(t) = T_{inc}^{-1}\, I \tag{18}$$

The R-code for this particular SEIR model is

```
pseirmod = function(t, y, parms) {
  # Pull state variables from y vector
  S = y[1]
  E = y[2]
  I = y[3]
  R = y[4]
  # Pull parameter values from parms vector beta = parms["beta"]
  R0 = parms["R0"]
  Tinc = parms["Tinc"]
  Tinf = parms["Tinf"]
  sigma = 1/Tinf
  gamma = 1/Tinc
  beta = sigma*(R0/Tinc-1)
  # Define equations
  dS = - beta * S * I
  dE = beta * S * I - sigma * E
  dI = sigma * E  - gamma * I
```

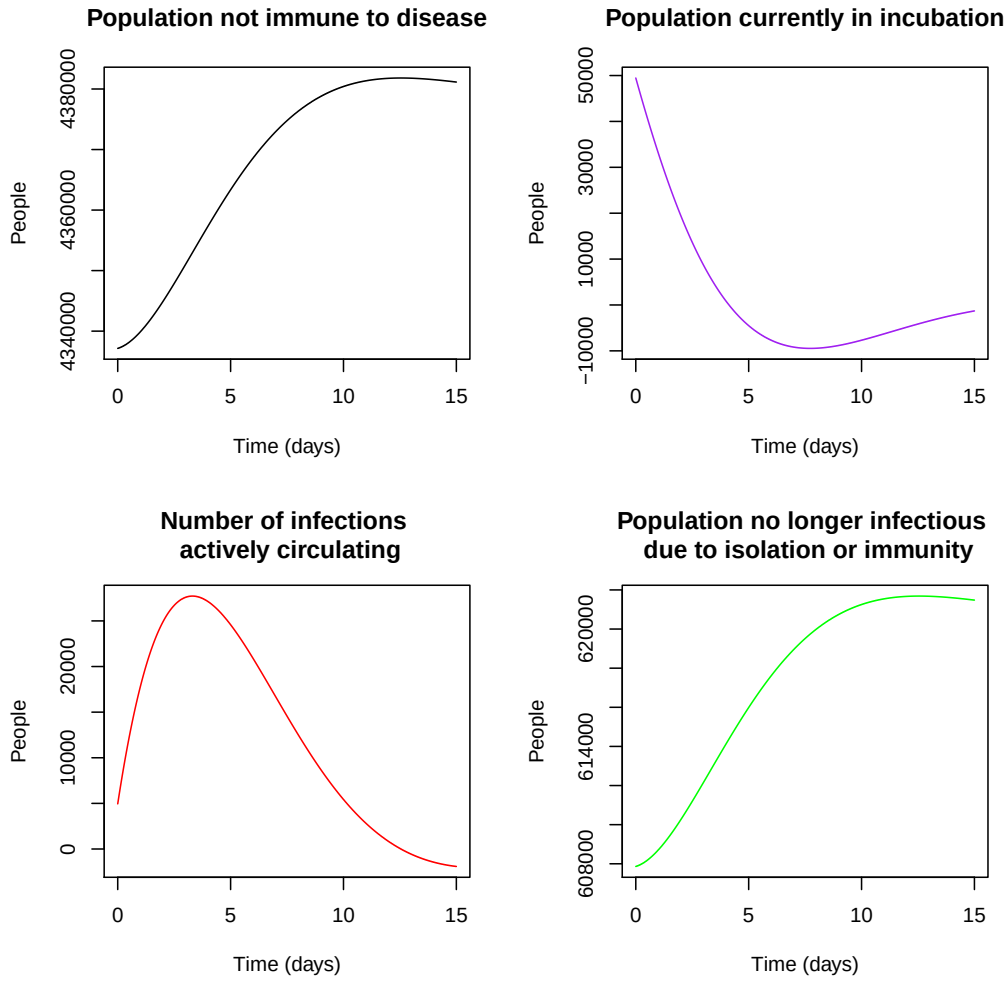
```
  dR = gamma * I
  res = c(dS, dE, dI, dR)
  # Return list of gradients
  list(res)
}
```

```
#####################################
# Model parameters
# R0   Reproduction Number
# Tinc Incubation Period (in days)
# Tinf Infectious Period (in days)
parms = c(R0 =3,Tinc = 14, Tinf=3)
#######################################
# Model variables
# S  Rate of population not immune to disease
# E  Rate of population currently in incubation
# I  Rate of population infected actively circulating
# R  Rate of population no longer infected due
#    to isolation or immunity
#####################################
# Initial Values
#####################################
start = c(S = 0.8769, E=0.01, I = 0.001, R = 0.1229)
### Time scale (in days)
times = seq(0,15, by = 1/1000)
### Population (CV)
N = 4946000
```

We integrate numerically (15)-(18)

```
out = ode(y=start, times=times, func=pseirmod, parms= parms)
out = as.data.frame(out)
```

```
par(mfrow=c(2,2))
plot(x=out$time, y=N*out$S, ylab="People", xlab="Time (days)"
        ,col="black",type="l"
  ,main="Population not immune to disease")
plot(x=out$time, y=N*out$E, ylab="People", xlab="Time (days)"
        ,col="purple",type="l"
  ,main="Population currently in incubation")
plot(x=out$time, y=N*out$I, col="red",type="l",ylab="People"
        , xlab="Time (days)"
  ,main = "Number of infections \n actively circulating")
plot(x=out$time, y=N*out$R, col="green",type="l"
        ,ylab="People"
  , xlab="Time (days)"
  ,main="Population no longer infectious \n due to isolation or immunity")
```


Population not immune to disease
People
4340000
4360000
4380000
0
5
10
15
Time (days)
Population currently in incubation
People
−10000
10000
30000
50000
0
5
10
15
Time (days)
Number of infections
actively circulating
People
0
10000
20000
0
5
10
15
Time (days)
Population no longer infectious
due to isolation or immunity
People
608000
614000
620000
0
5
10
15
Time (days)

3 A stochastic SEIR Model

Let us start by considering the following SEIR Model

$$\dot{S} = -\widehat{\beta} S\, I, \tag{19}$$
$$\dot{E} = \widehat{\beta} S\, I - \sigma E, \tag{20}$$
$$\dot{I} = \sigma E - \gamma I, \tag{21}$$
$$\dot{R} = \gamma I \tag{22}$$

where $S + E + I + R = N$, $\dot{S} + \dot{I} + \dot{I} + \dot{R} = 0$, and $\widehat{\beta} = \beta/N$. Then the Euler discretization with temporal step Δt gives us

$$S_{t+\Delta t} - S_t = -\widehat{\beta} S_t\, I_t\, \Delta t, \tag{23}$$
$$E_{t+\Delta t} - E_t = (\widehat{\beta} S_t\, I_t - \sigma E_t)\, \Delta t, \tag{24}$$
$$I_{t+\Delta t} - I_t = (\sigma E_t - \gamma I_t)\, \Delta t, \tag{25}$$
$$R_{t+\Delta t} - R_t = \gamma I_t\, \Delta t \tag{26}$$

We will assume that $\Delta t = 1$ day and then we finally obtain the following discrete dynamical system,

$$S_{t+\Delta t} - S_t = -\widehat{\beta} S_t\, I_t, \tag{27}$$
$$E_{t+\Delta t} - E_t = \widehat{\beta} S_t\, I_t - \sigma E_t, \tag{28}$$
$$I_{t+\Delta t} - I_t = \sigma E_t - \gamma I_t, \tag{29}$$
$$R_{t+\Delta t} - R_t = \gamma I_t. \tag{30}$$

To introduce the randomness in this model we will consider that

$$\{(S_t, E_t, I_t, R_t) : t \in \{0, 1, \ldots, T\}\}$$

is an $\mathcal{F}$-adapted stochastic process on a probability space $(\Omega, \mathcal{F}, \mathbb{P})$ where the filtration $\mathcal{F} = (\mathcal{F}_t)_{t=0}^{T}$ and hence (S_t, E_t, I_t, R_t) is a $\mathcal{F}_t$-measurable random variable. Thus,

$$\mathbb{E}[S_{t+\Delta t}|\mathcal{F}_t] = S_t - \widehat{\beta} S_t\, I_t, \tag{31}$$
$$\mathbb{E}[E_{t+\Delta t}|\mathcal{F}_t] = E_t + \widehat{\beta} S_t\, I_t - \sigma E_t, \tag{32}$$
$$\mathbb{E}[I_{t+\Delta t}|\mathcal{F}_t] = I_t + \sigma E_t - \gamma I_t, \tag{33}$$
$$\mathbb{E}[R_{t+\Delta t}|\mathcal{F}_t] = R_t + \gamma I_t. \tag{34}$$

Under the assumption $E_t \in \mathbb{N}$ we can consider a sequence $X_1, \ldots, X_{E_t}$ of independent random variables from $X \sim \mathcal{B}(\sigma)$, then we can write

$$\sigma\, E_t = \mathbb{E}\left[\sum_{k=1}^{E_t} X_k \middle| \mathcal{F}_t\right] = \mathbb{E}\left[\sum_{k=1}^{E_t} X_k\right],$$

and also if $I_t \in \mathbb{N}$ we can consider a sequence $Y_1, \ldots, Y_{I_t}$ of independent random variables from $Y \sim \mathcal{B}(\gamma)$, then we can write

$$\gamma\, I_t = \mathbb{E}\left[\sum_{k=1}^{I_t} Y_k \middle| \mathcal{F}_t\right] = \mathbb{E}\left[\sum_{k=1}^{Y_t} Y_k\right].$$