

## Compartmental Models in Epidemiology

Compartmental models in epidemiology are named as such because individuals of a population are assigned to distinct compartments pertaining to their state regarding an infectious disease. Individuals may transition/progress through these compartments.

### 1 SIR Model

The SIR model divides the population into 3 groups.

*Susceptible*  $\longrightarrow$  individuals who are able to contract the disease

*Infectious*  $\longrightarrow$  individuals who have contracted the disease are able to infect susceptibles

*Recovered*  $\longrightarrow$  individuals who have recovered from the disease and are unable to be re-infected

We may consider the model without *vital dynamics* as the dynamics of an epidemic are more prominent than those of birth and death, especially on short time scales. Therefore, the population size  $N$  remains constant. The number of susceptible, infectious and recovered individuals at time  $t$  are represented by  $S(t)$ ,  $I(t)$  and  $R(t)$ , respectively, such that

$$S(t) + I(t) + R(t) = N \quad (1)$$

The SIR model may be represented by a set of coupled differential equations

$$\begin{aligned} dS/dt &= -\beta IS/N \\ dI/dt &= \beta IS/N - \gamma I \\ dR/dt &= \gamma I \end{aligned} \quad (2)$$

where (could perhaps move this above model)

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \quad (3)$$

and the parameters  $\beta$  and  $\gamma$  are defined as

$\beta \longrightarrow$  average number of *adequate contacts* (sufficient for disease transmission) of an individual per unit time

$\gamma \longrightarrow$  if an individual is infectious for time period  $D$ , then  $\gamma = 1/D$

Dividing equations in (2) by  $N$  gives

$$\begin{aligned} ds/dt &= -\beta is \\ di/dt &= \beta is - \gamma i \\ dr/dt &= \gamma i \end{aligned} \quad (4)$$

where  $s(t)$ ,  $i(t)$  and  $r(t)$  are the susceptible, infectious and recovered fractions of the population, respectively, such that

$$s(t) + i(t) + r(t) = 1 \quad (5)$$

$$\dot{s}(t) + \dot{i}(t) + \dot{r}(t) = 0 \quad (6)$$

for all  $t \geq 0$ .

## 1.1 Vital Dynamics

We may consider the infectious disease's behaviour over a longer period by extending the SIR model to include births and natural deaths (by causes other than the disease). The model is given by

$$\begin{aligned} dS/dt &= \mu N - \beta IS/N - \mu S \\ dI/dt &= \beta IS/N - \gamma I - \mu I \\ dR/dt &= \gamma I - \mu R \end{aligned} \tag{7}$$

where

$$\begin{aligned} \mu N &\longrightarrow \text{birth rate of newborns into the susceptible class} \\ \mu S, \mu I, \mu R &\longrightarrow \text{death rates in respective classes} \end{aligned}$$

and

$$S(t) + I(t) + R(t) = N = \text{constant} \tag{8}$$

for all  $t \geq 0$  if the births balance the deaths, however,  $N$  is variable in the general case. Dividing equations (7) by  $N$  gives

$$\begin{aligned} ds/dt &= \mu - \beta is - \mu s \\ di/dt &= \beta is - (\gamma + \mu)i \\ dr/dt &= \gamma i - \mu r \end{aligned} \tag{9}$$

## 2 SEIR Model

Many infectious diseases have a latent period during which the host has been infected but cannot yet infect others. Note that this is distinct from incubation time, which is the period before the onset of symptoms. We may extend the SIR model by introducing a new class of *exposed* individuals.

The SEIR model without vital dynamics is given by

$$\begin{aligned} dS/dt &= -\beta IS/N \\ dE/dt &= \beta IS/N - \epsilon E \\ dI/dt &= \epsilon E - \gamma I \\ dR/dt &= \gamma I \end{aligned} \tag{10}$$

where  $\epsilon$  is a parameter (random variable?) such that the rate of transfer out of the exposed class is  $\epsilon E$ . The mean latent period of the infection is given by  $1/\epsilon$ .

Introducing vital dynamics, the model is given by

$$\begin{aligned} dS/dt &= \mu N - \beta IS/N - \mu S \\ dE/dt &= \beta IS/N - (\mu + \epsilon)E \\ dI/dt &= \epsilon E - (\gamma + \mu)I \\ dR/dt &= \gamma I - \mu R \end{aligned} \tag{11}$$

## 3 SEIRD Model

The SEIR model may be further extended by considering deaths caused by the disease and introducing a *deceased* class. The SEIRD model (with vital dynamics as before) is thus represented by

$$\begin{aligned}
dS/dt &= \mu N - \beta IS/N - \mu S \\
dE/dt &= \beta IS/N - (\mu + \epsilon)E \\
dI/dt &= \epsilon E - (\gamma + \mu)I \\
dR/dt &= \gamma I - \mu R \\
dD/dt &= \delta I
\end{aligned} \tag{12}$$

where  $\delta$  is the mortality rate of the disease, given by

$$\delta = \frac{\# \text{ of deaths}}{\text{total } \# \text{ of cases}} \tag{13}$$

Table 1: *Summary of Notation*

Symbol	Description
$N$	population size
$S(t), I(t), R(t)$	<i>number</i> of susceptible, infectious & recovered individuals
$s(t), i(t), r(t)$	<i>fraction</i> of population in respective classes above
$\beta$	average adequate contact rate
$D$	average infectious period
$\gamma$	$1/D$ (proportion of infected recovering per unit time)
$\mu$	birth/death (natural) proportion
$\epsilon$	aksjh
$\delta$	mortality rate of disease

## References

- [1] Hethcote, H. W. (2000). The Mathematics of Infectious Diseases. *SIAM Review*, 42(4), 599–653. doi: <https://doi.org/10.1137/S0036144500371907>