Compartmental Models in Epidemiology
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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 as governed by conditions related to the infectious disease.

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

$$S(t) + I(t) + R(t) = N \tag{1}$$

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

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

where

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \tag{3}$$

and the parameters β and γ 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

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

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

$$s(t) + i(t) + r(t) = 1 \tag{5}$$

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

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). It is assumed that all newborns enter the susceptible class. The model is given by

$$dS/dt = \mu_b N - \beta IS/N - \mu_d S$$
$$dI/dt = \beta IS/N - \gamma I - \mu_d I \tag{7}$$
$$dR/dt = \gamma I - \mu_d R$$

where

$$\mu_b N \longrightarrow \text{birth rate of newborns into the susceptible class}$$
$$\mu_d S, \ \mu_d I, \ \mu_d R \longrightarrow \text{death rates in respective classes}$$

and in the special case when $\mu_b = \mu_d$,

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

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

$$ds/dt = \mu_b - \beta is - \mu_d s$$
$$di/dt = \beta is - (\gamma + \mu_d)i \tag{9}$$
$$dr/dt = \gamma i - \mu_d r$$

1.2 Threshold Quantities

Quantities such as R_o, σ and R are commonly used and reported to describe the overall potential for an epidemic to spread.

1.2.1 Basic Reproduction Number R_o

$$R_o \longrightarrow \text{the average number of secondary infections that occur when } one \text{ infective is introduced in}$$
$$\text{to an otherwise } completely \text{ susceptible population}$$

It is assumed that the infected individual is in the host population for their entire infectious period and interacts/mixes with the population exactly how the host population would do so natively. We may write R_o as

$$R_o = \frac{\beta}{\gamma} \tag{10}$$

which may be easier to interpret if formulated as $R_o = \beta D$. We may rewrite the differential equation for number of infectious individuals from eq. 2 to include R_o as

$$\frac{dI}{dt} = \left(R_o \frac{S_o}{N} - 1 \right) \gamma I \tag{11}$$

where $S(0) = S_o$. The number of infectives will increase, the disease will spread through the population, when

$$R_o > \frac{N}{S_o} \tag{12}$$

Or, in the case when the entire initial population is susceptible $N = S_o$, the infectious disease will spread if

$$R_o > 1 \tag{13}$$

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1.2.2 Contact Number σ

$\sigma \longrightarrow$ the average number of adequate contacts of a typical *infective* during the infectious period (note slight distinction from β)

1.2.3 Replacement/Reproduction Number R

$R \longrightarrow$ the average number of secondary infections produced by a typical infective during the infectious period

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

$$
\begin{aligned}
dS/dt &= -\beta IS/N \\
dE/dt &= \beta IS/N - \epsilon E \\
dI/dt &= \epsilon E - \gamma I \\
dR/dt &= \gamma I
\end{aligned}
\tag{14}
$$

where ϵ is a parameter (sometimes considered to be a random variable to introduce some stochasticity) such that the rate of transfer out of the exposed class and into the infected class is ϵE. The mean latent period of the infection is given by $1/\epsilon$.

Introducing vital dynamics, the model is given by

$$
\begin{aligned}
dS/dt &= \mu_b N - \beta IS/N - \mu_d S \\
dE/dt &= \beta IS/N - (\mu_d + \epsilon)E \\
dI/dt &= \epsilon E - (\gamma + \mu_d)I \\
dR/dt &= \gamma I - \mu_d R
\end{aligned}
\tag{15}
$$

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

$$
\begin{aligned}
dS/dt &= \mu_b N - \beta IS/N - \mu_d S \\
dE/dt &= \beta IS/N - (\mu_d + \epsilon)E \\
dI/dt &= \epsilon E - (\gamma + \mu_d)I \\
dR/dt &= \gamma I - \mu_d R \\
dD/dt &= \delta I
\end{aligned}
\tag{16}
$$

where δ is the mortality rate of the disease, given by

$$
\delta = \frac{\# \text{ of deaths}}{\text{total } \# \text{ of cases}}
\tag{17}
$$

Table 1: *Summary of Notation*

Symbol	Description
N	population size
$S(t), I(t), R(t)$	*number* of susceptible, infectious & recovered individuals
$s(t), i(t), r(t)$	*fraction* of population in respective classes above
β	average adequate contact rate
D	average infectious period
γ	$1/D$ (proportion of infected recovering per unit time)
μ_b and μ_d	birth/death (natural) proportion
ϵ	proportion of exposed becoming infective rate
δ	mortality rate of disease

4   Further Reading

Apart from those listed in *references*, there have been numerous sources (articles, videos, talks, etc.) that have been incredibly helpful for my understanding. I have compiled these here

  https://www.notion.so/karnav/COVID-19-Modelling-Reading-List-d420a00ce957423493545d1f23e54cd1

and will continue to update this list. I highly recommend looking at these!

References

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

[2] Compartmental models in epidemiology. (2020, 9 May). *Wikipedia*. Retrieved May 20, 2020, from https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology#The_SIR_model_is_dynamic_in_three_senses