Week Five

Siva Sundar, EE23B151

July 2024

6th August

SEIR Model

- An extension to **"SIR model"**.
- The full-form is as follows:
  - ⋆ **'S'** stands for *"Susceptible"* to disease. Entities in this set are **vulnerable** to diseases.
  - ⋆ **'E'** stands for *"Exposed"*. Entities in this set **are infected**, but they are **not infectious** to other Entities in **S**.
  - ⋆ **'I'** stands for *"Infected"*. Entities in this set can **infect** others as well.
  - ⋆ **'R'** stands for *"Recovered"* from infection.
- **Assumptions:**
  - ⋆ For the entities in 'E' to infect others, it takes some time (ie, for moving from the set 'E' to 'I'). Let's assume this follows **"exponential distribution"** with parameter as "a" (hence, time average is a^{-1}).
  - ⋆ Birth rate Λ **equals** death rate $N\mu$, making N (population size, $S+E+I+R = N$) a constant. The term 'μ' is the *per capita death rate.*

7th August

- Set of **Differential Equations** for the model:

$$\frac{dS}{dt} = \mu N - \mu S - \frac{\beta IS}{N}$$

$$\frac{dE}{dt} = \frac{\beta IS}{N} - (\mu + a)E$$

$$\frac{dI}{dt} = aE - (\gamma + \mu)I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

  Notice that as $S + E + I + R = N$:

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

- **Reproduction Number:**
  The *basic reproduction number* is the **expected number** of cases **directly generated by one case** in a population where **all individuals are susceptible to infection.** (**Assuming**, individuals are **not** infected nor immunized (naturally or through vaccination)

For this model,

- ⋆ Exposed individuals become infectious with *probability* **'a'**.
- ⋆ *Total cases* for an exposed individual: $\mu + a$. (be infected or die)
- ⋆ Duration of infection: $(\gamma + \mu)^{-1}$.
- ⋆ Disease spreads from Infectious individuals with *probability* β.

$\therefore R_0 =$ (Prob. transmission per contact)$\times$(Duration of infection)
$\times$ (Probability of surviving 'Exposed' stage)

$$\Rightarrow R_0 = \beta \times \frac{1}{\mu + \gamma} \times \frac{a}{a + \gamma} \qquad \text{(See Ref.[2])}$$

- **States of Equilibrium**:
  - ⋆ *Disease-Free-Equilibrium (DFE)*: disease is **not** present in the population. Mathematically, $(S, E, I, R) = (N, 0, 0, 0)$.
  - ⋆ *Endemic Equilibrium (EE)*: disease **persists** in the population at a **constant level** over time. It represents a *steady-state* situation where the disease is constantly present in the population but at a *stable* level.

For a biologically meaningful initial condition as follows:

$$(S(0), E(0), I(0), R(0)) \in \{(S, E, I, R) \in [0, N]^4 : S, E, I, R \geqslant 0, S + E + I + R = N\}$$

it holds that:

$$R_o \leqslant 1 \Rightarrow \lim_{t\to\infty}(S(t), E(t), I(t), R(t)) = DFE = (N, 0, 0, 0)$$

$$R_o > 1, I(0) > 0 \Rightarrow \lim_{t\to\infty}(S(t), E(t), I(t), R(t)) = EE$$

8th August

CLICK HERE to see the **Julia** code which **solves** the **Differential Equations** seen above. Below are some output figures for different values of a, β, μ and γ.

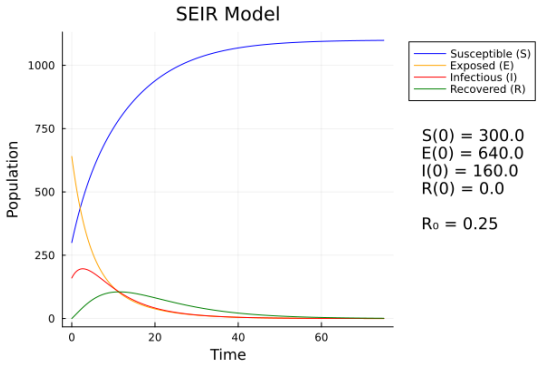

Figure 1: $a = \beta = \mu = \gamma = 0.1$ (DFE)

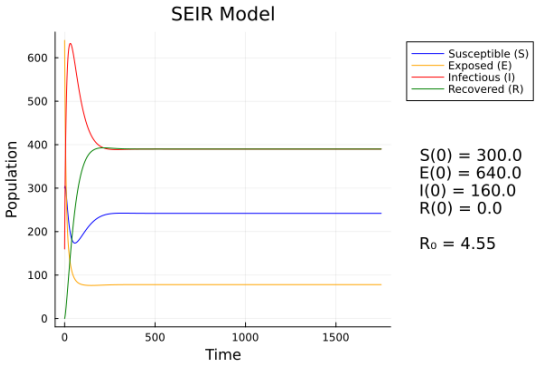

Figure 2: $a = \beta = 0.1$ & $\mu = \gamma = 0.01$ (EE)

10th August

How did we arrive at the Differential Equation set?

- People migrating from 'S' to 'E' can be thought of as a first order kinetic equation as its *similar* to **multiplication of bacteria** in a culture. Say, the rate constant be λ.

$$\frac{dS}{dt} = -\lambda S + \dots$$
$$\frac{dE}{dt} = +\lambda S + \dots$$

- As we know, the people in the set 'S' are **exposed** to infection due to the people in 'I'. Hence, the exposure rate λ depends on 'I':

$$\text{Rate of S to E } (\lambda) = (\text{Rate of Transmission } (\beta) \times \text{P(infection} \mid \text{contact occurred))}$$
$$\Rightarrow \lambda = \frac{\beta I}{N}$$

- By similar reasoning given in first point, we can also say transitions 'E to I' and 'I to R' follow first order kinetics as well, with rate constants σ (Incubation rate) and γ (Recovery rate) respectively:

$$\frac{dE}{dt} = +\lambda S - \sigma E + \dots$$
$$\frac{dI}{dt} = +\sigma E - \gamma I + \dots$$
$$\frac{dR}{dt} = \gamma I + \dots$$

  Up to this derivation, we used [3] as reference. In it, they then remove the dots $(\dots)$ stating that there are *no other influence* to the system. But in reality, there is **birth** (Λ) and **death rate** (μN) that affects the total system!

- Birth rate increases only susceptible individuals while death rate decreases all the groups. Hence:

$$\frac{dS}{dt} = \Lambda - \mu S - \frac{\beta IS}{N}$$
$$\frac{dE}{dt} = \frac{\beta IS}{N} - (\mu + a)E$$
$$\frac{dI}{dt} = aE - (\gamma + \mu)I$$
$$\frac{dR}{dt} = \gamma I - \mu R$$

  By, taking the sum of all the equations and taking $S + E + I + R = N$, the total population, we get:

$$\frac{dN}{dt} = \Lambda - \mu N$$

- So if we take a system with constant population N, then: $\Lambda = \mu N$. Replacing this in the **DE set** yields the required model!

11th August

There are other epidemic models as well, in fact, **we can create our own models** by considering the various **interactions** and **properties** these individuals have.

SIS model

Some infections (like common cold, influenza) may give temporary resistance upon recovery from infection, and individuals become susceptible again. This can be represented by the set of equations:

$$\frac{dS}{dt} = -\frac{\beta IS}{N} + \gamma I$$
$$\frac{dI}{dt} = +\frac{\beta IS}{N} - \gamma I$$

Here, we are not considering birth and death rates, and also its clear from the equations that we are assuming $N = S + I$ is **constant**. Substituting $S = N - I$ in second equation yields:

$$\frac{dI}{dt} = (\beta - \gamma)I - \frac{\beta I^2}{N}$$

The solution to this is the **logistic function**, hence, S and I are **positive**. Solving it, by making it *Linear DE*, we get:

$$\frac{1}{I(t)}e^{(\beta-\gamma)t} = \frac{\beta}{N(\beta-\gamma)}e^{(\beta-\gamma)t} + C$$

Here also, we can define something **like** the *reproduction number*

If $R_0 \leqslant 1$, we see that $I(t \to \infty) = 0$ and, if $R_0 \geqslant 1$, then we see $I(t \to \infty) = (1 - \frac{\gamma}{\beta})N$

$$R_0 = \frac{\text{Transmission Rate } (\beta)}{\text{Recovery Rate } (\gamma)}$$

SIRD model

Similar to SIR, but here, we consider an additional set '**D**' which contains all the *deceased* individuals who died due to infection **alone**. Considering a constant population, with no birth nor death rates:

$$\frac{dS}{dt} = -\frac{\beta IS}{N}$$
$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I - \mu I$$
$$\frac{dR}{dt} = \gamma I$$
$$\frac{dD}{dt} = \mu I$$

SIRV model

Instead of the set 'D', we use the set '**V**' which contains the *vaccinated* individuals. Only the individuals in 'S' gets vaccinated in this model, say by a rate 'v', then the difference from the above equation set are:

$$\frac{dS}{dt} = -\frac{\beta IS}{N} - vS, \quad \frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I \ \ \& \ \ \frac{dV}{dt} = vS$$

MSIR model

For infections like **measles**, babies born are **not** born into the *susceptible compartment* but are **immune** to the disease for the first few months of life due to protection from maternal antibodies *(Passive immunity)*. Hence, we make another compartment '**M**' for *maternally derived immunity*. The set of equations for this model are:

$$\begin{aligned}
\frac{dM}{dt} &= \Lambda - \delta M - \mu M \\
\frac{dS}{dt} &= \delta M - \frac{\beta I S}{N} - \mu I \\
\frac{dI}{dt} &= \frac{\beta I S}{N} - \gamma I - \mu I \\
\frac{dR}{dt} &= \gamma I - \mu R
\end{aligned}$$

Where,

- We consider birth rate Λ, death rate μ.
- As $M + S + I + R = N$, rate of change of population $= \Lambda - \mu N$
- δ is the rate at which individuals in 'M' lose their immunity and become susceptible to infection.

References:

[1] Wikipedia: Compartmental models in epidemiology

[2] Introduction to SEIR Models by Swiss TPH

[3] The SEIR model of infectious diseases