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.

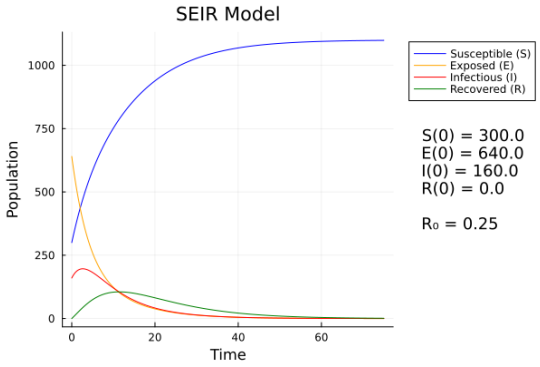

Figure 1: $a = \beta = \mu = \gamma = 0.1$ (DFE)

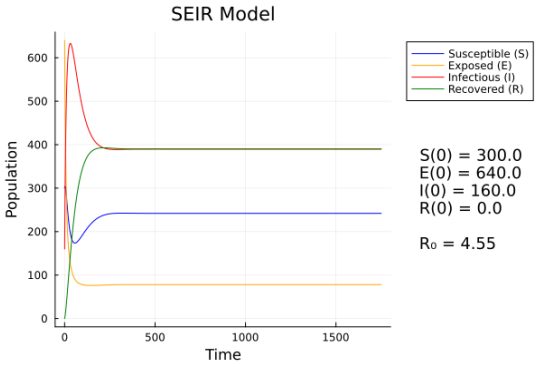

Figure 2: $a = \beta = 0.1$ & $\mu = \gamma = 0.01$ (EE)

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:

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

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.

Making a new model

Now, by taking inspiration from these models, let's make our own model for a particular disease, **Common Cold**! (I get it most frequently and I hate it.)

Let's first analyse this disease:

- Its an **Infectious** disease.
- Over **200 different viruses** can cause the common cold, with *rhinovirus* being the most common.
- After recovery, the individual gets a **passive immunity** for some time. After this duration, he/she is susceptible again.
- Prevention is through **hygiene**. Bad hygiene can reduce the *rate of recovery*.

Keeping these points in mind, lets make our model which is a *modification* to **SIR model**. Our model takes into account an important factor: **"Hygiene"**. We will have the following compartments:

- S_v: Susceptible individuals but are **vigilant** about health and hygiene.
- S_n: Susceptible individuals who are **negligent** about health and hygiene.
- I_v: Infected individuals who where in 'S_v'.
- I_n: Infected individuals who where in 'S_n'.
- R: Contains individuals who are recovered from the infection. These individuals are from both I_v and I_n.

Now lets talk about the different **interactions** and **properties** between the individuals in these compartments.

Interactions and Properties

In a real-life scenario such as a school or workspace with people from various households and habits, we can categorize individuals into groups with **good** and **bad hygiene**. Vigilant individuals, who practice **good hygiene**, are less likely to contract infections from their environment and only get infected through unavoidable interactions with others. The likelihood of these **vigilant** individuals getting infected is proportional to the number of infected individuals present. They themselves **will not infect others** due to their good hygiene.

On the other hand, negligent individuals, who practice **poor hygiene**, face a higher risk of infection both from their interactions and from their environment. For these individuals, the infection rate, denoted by α, is at its minimum when there are no infected individuals ($I_n = 0$), meaning their infection is solely due to environmental factors. As the number of infected individuals in their environment increases, their infection rate α increases accordingly, reaching its maximum when all susceptible individuals in the negligent group are infected.

Regarding recovery, individuals with **good hygiene** (I_v) experience a constant recovery rate, denoted by γ. Conversely, negligent individuals (I_n) have a recovery rate that starts at its maximum when there are no infected individuals in their group and gradually decreases as the number of infected individuals in their group increases. The recovery rate reaches its minimum when all individuals in the negligent group are infected.

Additionally, both **vigilant** and **negligent** individuals gain *temporary resistance* to infection for a period τ. During this period, they cannot contract the infection, providing them with temporary protection. After this, they **will become susceptible again**.

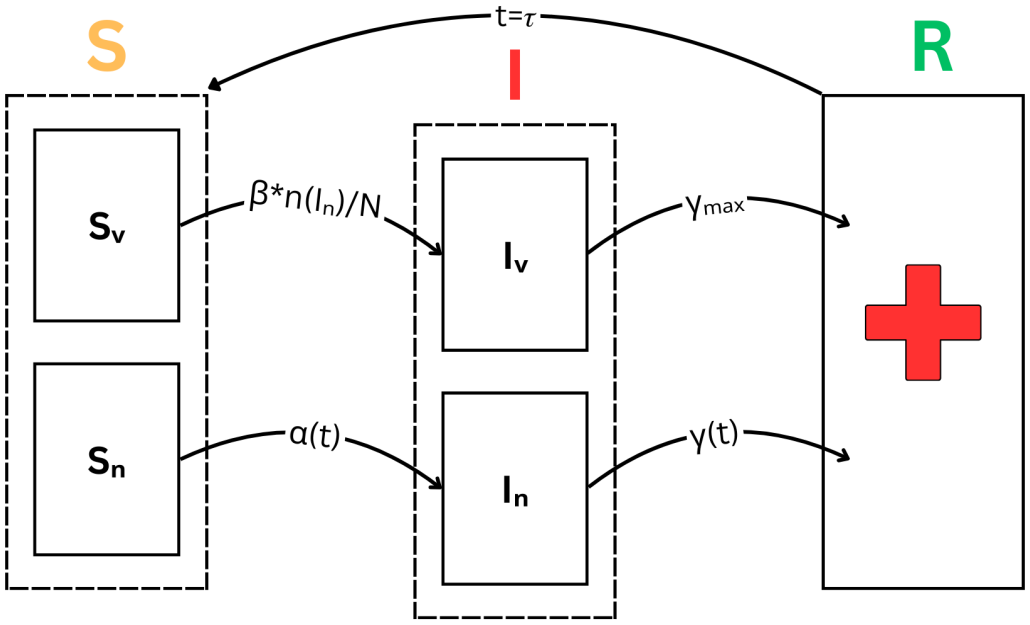

Figure 3: Pictorial representation of the model

I am going to be focusing more on the **elements in the sets**, compared to other models. So I won't be solving differential equations. I would like to *simulate* the model using elements of the type: **{State, Hygiene, Time recovered}**. The last data is needed to check the condition for transition from 'R to S'.

Simulation

Made a **C code** (as it is fast), which simulates the model. **CLICK HERE** to see it. The code outputs points in a file which is to be read using a plotting software (I chose octave). Below are some output plots for different values of parameters.

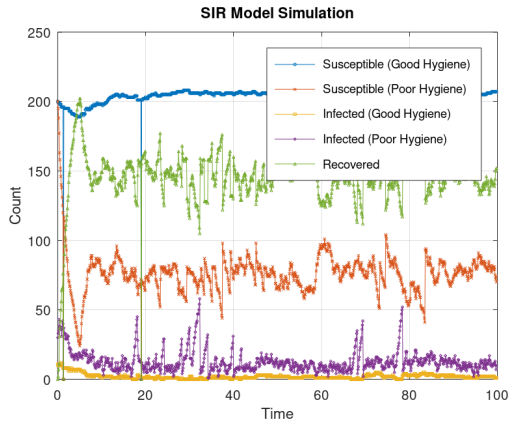

Figure 4(a): $\alpha_0 = 0.3, \alpha_{\max} = 0.7, \gamma_0 = 0.1, \gamma_{\max} = 0.5, \beta = 0.1, \tau = 5.0$

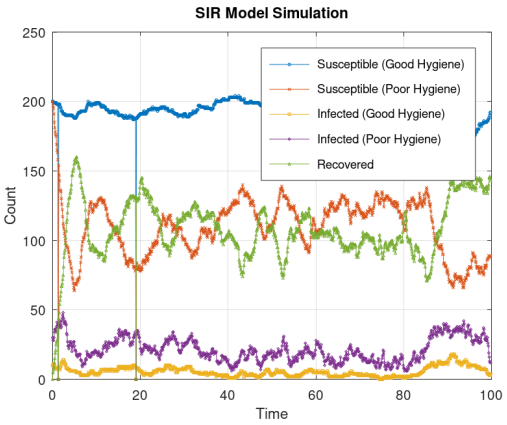

Figure 4(b): $\alpha_0 = 0.1, \alpha_{\max} = 0.5, \gamma_0 = 0.1, \gamma_{\max} = 0.3, \beta = 0.2, \tau = 5.0$

Figure 4: Using $S_v = 200$, $Sn = 200$, $Iv = 10$, $In = 30$

In both graphs, it is evident that individuals adhering to good hygiene largely remain healthy throughout the simulation period. In contrast, those with poor hygiene and recovered individuals exhibit significant fluctuations, indicating a recurrent pattern where individuals recover from illness only to become infected again. This cycle highlights the persistent vulnerability of the negligent population and the challenges they face in maintaining long-term health despite recovering from infections.

There is a small issue, which I couldn't resolve in the code. Some times the data turns to (0,0,0,0,0) at just a random point without altering other points near it.

References:

[1] Wikipedia: Compartmental models in epidemiology

[2] Introduction to SEIR Models by Swiss TPH

[3] The SEIR model of infectious diseases

13th August

Research Paper report

- Category Theory concepts required:
  - ⋆ Operads and Operadic Algebra.
  - ⋆ Copresheaves.
  - ⋆ Spans, Cospans, Structured cospans, Multicospans.
  - ⋆ Pullbacks.
- A **span** is similar to a "**multirelation**". It is similar to graphs. eg: $S \leftarrow I \rightarrow T$.

- *Whole-grain* Petri-nets: is a combinatorial description of a dynamic process. It consists of a sets for **input arcs**, **output arcs**, **species** and **transitions**. They are closed systems. eg: SIR model can be treated as a petri-net.
- **Undirected Wiring Diagrams** (UWDs): helps to visualize composition of multiple petri-nets. eg: combination of two petri-nets, SIR+SIvR.

  It also consists of:

  - ⋆ **Boxes**: represents a petri-net.
  - ⋆ **Ports**: subparts of petri-nets which can be connected to other such subparts in another petri-net.
  - ⋆ **Junctions**: multiple ports connected together forms a junction.

  Mathematically speaking, they create something called an **Operad**.
- Julia packages for implementing these are: **AlgebraicPetri** and **AlgebraicDynamics**.
- For simulation purposes, we can use discrete sampling algorithms, or we can convert the petri-net into **ODEs** or **DDEs** using **Law of Mass Action**, and solve them.
- **Advantage** of using petri-nets to make models is that transformation of a Petri net into an ODE via the law of mass action automatically and accurately translates local changes to the Petri net model into global changes to the corresponding ODE.

  eg: Ross-Macdonald class of equational models

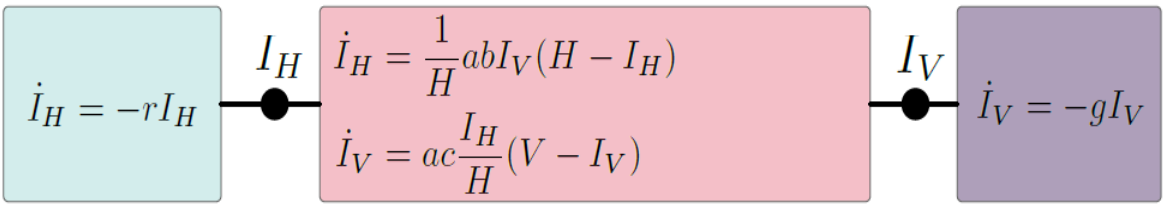

Figure 5: UWD model for the spread of a vector-borne pathogen

From the diagram, directly using Law of Mass Action, we can write:

$$\dot{I}_H = ab\frac{I_V}{H}(H - I_H) - rI_H, \quad \dot{I}_V = ac\frac{I_H}{H}(V - I_V) - gI_V.$$