Epidemiology and SIR model final

↗ Class?	Simulation of Biological Systems

Epidemiology basics

Def - Epidemiology

> “*Branch of medicine which deals with the incidence, distribution, and possible control of diseases and other factors relating to health.” (Definition by: Oxford Languages)*

Epidemiological Triad

The epidemiological triad consists of three elements (Balasubramanian):

- Agent: *virus, bacteria, parasite or organism that is the cause of the disease*
- Host: *After being infected by an agent, hosts become carriers of the illness. Both carriers and hosts are susceptible to contracting the illness. Consider a situation when a coworker is ill with a cold. You could get sick or not, but when you return home, you could give the infection to your kids.*
- Environment: *The air, soil, water, climate change, and other elements that affect the transmission of disease are all considered to be parts of the environment.*

Disease transmission and spread

Germs get into the body through the mouth, skin, eyes, genitals.

Germs can spread:

- from **person to perso**n:
  - directly through close contact

    - indirectly from a susceptible individual to an object (food, benchtops, door handles, etc.) and subsequently to another individual who comes into contact with the contaminated item
    - Through: Aird as droplets o aerosols, faecal-oral spread, blood or other fluids, skin or mucous membranes, sexual contact
- from a **contaminated environmental source** (animal, soil, etc.) to a susceptible individual.
    - Through: contaminated food, water or environment

The SIR model

In epedemiology the SIR model is often used, which it is also a compartmental model. In this case, the individuals are divided over three different compartments:

- **S**usceptible: A susceptible individual is a healthy individual that has not yet contracted the diseas.
- **I**nfected: The infected individuals have contracted the disease and have the potential to spread it to others who are vulnerable.
- **R**emoved: A removed individual has already contracted the virus, and has been removed from the Infected compartment either due to recovery or death. In case of recovery, in these model, these individuals will become immune. This section may also be referred to as "resistant" or "recovered".

We express this compartments with the variables $S(t)$, $I(t)$ and $R(t)$, which tells us the amount of indiciduals at the compartments at any give time t. In this case, we counsider the total population number N to be constant. For this to happen, the birth rate, needs to be equal to the death rate.

The model is dynamic in that the numbers in each compartment may change over time, as suggested by the variable function in terms of time t. In an endemic disease with a brief infectious period, the significance of this dynamic aspect is most evident. Because of the fluctuations in the number of susceptible individuals ($S(t)$) over time, these diseases typically experience cycles of outbreaks. The number of susceptible people rapidly decreases during an epidemic as more become sick and go into the infectious and removed compartments. Until the number of susceptibles has increased once more, perhaps as a result of children being born into the susceptible compartment.

Each member of the population progresses from susceptible to infectious to recovered.

Parameters and variables

There are different versions of the SIR model. Some are more complicated and therefore take into consideration more parameters. However, there exist simplified versions of it, which are the ones we will look at today. These versions still help us to be able to understand how the model works. We could say that the number of assumptions is greater in these ‘simplified’ versions, with less assumptions, we could get closer to what would happen in the real-world.

Today, we will consider a model where we consider the population to be a fixed number, with only three compartments: susceptible $S(t)$, infections $I(t)$, and recovered $R(t)$*.

Therefore, using a fixed value for population we get:

$$N = S(t) + I(t) + R(t)$$

With initial conditions:

$$S(t=0), I(t=0), R(t=0)$$

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

$$\frac{dI}{dt} = \frac{\beta I S}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Therefore this represents the amount of people that are Sucenptible (S), Infected (I) or Recovered (R) at the start. If we want the SIR model to hold at all times, then these values are not independent.

Subsequently, the flow model updates the three variables for every time point with set values for β and γ . The simulation first updates the infected from the susceptible and then the removed category is updated from the infected category for the next time point ($t = 1$). This describes the flow of persons between the three categories. During an epidemic, the susceptible category is not shifted with this model, changes over the course of the epidemic and so does . These variables determine the length of the epidemic and would have to be updated with each cycle.

Assumptions:

- Every member of the population has the same chance of getting the disease as every other member of the population, with a rate of a and an equal proportion b of persons they come into contact with in a given amount of time.
- $\beta = a \cdot b$

  This is the product of the contact rate (b) and the transmission probability(a).
- An infected person contacts b people in a unit of time, but only a small percentage, S/N, of those people are susceptible.
- Every infective can infect $abS = \beta S$ susceptible persons, and therefore, the whole number of susceptibles infected by infected per unit time is βSI
- For the second and third equations, consider the population leaving the susceptible class as equal to the number entering the infected class. However, a number equal to the fraction γ (which represents the mean recovery/death rate, or $\frac{1}{\gamma}$ the mean infective period) of infectives are leaving this class per unit time to enter the removed class. These processes which occur simultaneously are referred to as the Law of Mass Action, a widely accepted idea that the rate of contact between two groups in a population is proportional to the size of each of the groups concerned.
- Finally, it is assumed that the rate of infection and recovery is much greater than the time scale of births and deaths and therefore, these factors are ignored in this model

Model Variations and Extensions

Importance

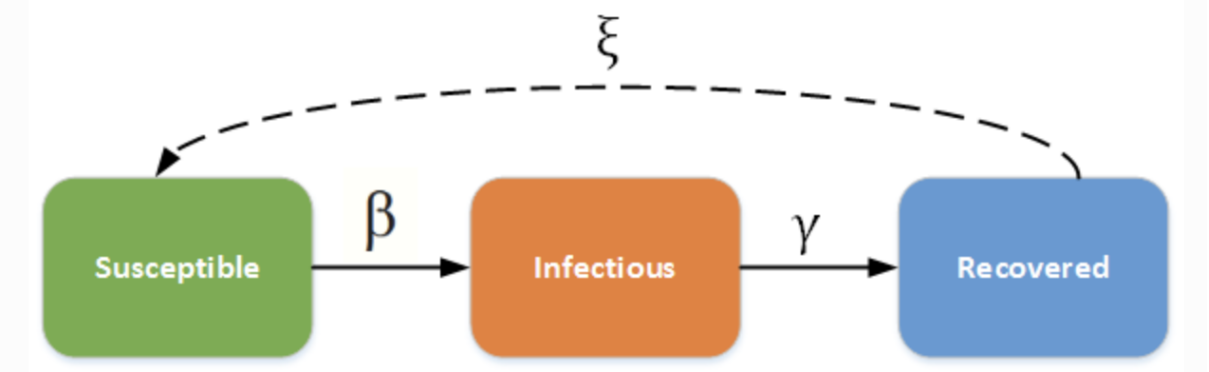
Variations on the basic SIR model are important because they allow for a more realistic representation of disease dynamics and enable researchers to account for specific characteristics and complexities of different infectious diseases. Here are several reasons why variations on the SIR model are valuable:

1. **Incorporating Demographic Factors**: The basic SIR model assumes a closed population with no births or deaths. Variations, such as the SIRS model, consider demographic factors like births, deaths, and aging, which are crucial in studying diseases with long-lasting or temporary immunity, like the common cold or seasonal flu.

2. **Accounting for Asymptomatic and Pre-Symptomatic Cases**: Many diseases, including COVID-19, have asymptomatic or pre-symptomatic carriers who can transmit the disease. Models like the SEIR model add compartments for exposed (pre-symptomatic) individuals, improving the accuracy of predictions and intervention strategies.
3. **Vaccination and Immunization**: Variations of the SIR model are essential for evaluating the impact of vaccination campaigns, different vaccine coverage rates, and the dynamics of immunity waning over time. The SIRV (SIR with vaccination) and SIRS models are common examples.
4. **Seasonality and Environmental Factors**: Some diseases exhibit seasonality and are influenced by environmental factors. Models like the SEIRS model can incorporate these elements to better understand how diseases like the flu or vector-borne diseases (e.g., dengue) fluctuate with changing seasons.
5. **Interventions and Control Measures**: Variations allow for the evaluation of various interventions, such as social distancing, isolation, quarantine, mask-wearing, and travel restrictions. These models are essential for policymakers to make informed decisions during disease outbreaks, such as the COVID-19 pandemic.
6. **Multi-Strain Pathogens**: Some diseases involve multiple strains or subtypes. Extensions of the SIR model, such as the SIRX model, consider multiple strains and competition between them, as seen in the case of influenza with different strains co-circulating.

SIRS

The difference between SIR and SIRS model is that in SIRS the recovered individuals do not gain total immunity and this wanes over times. Therefore they can get infected again. The flow diagram would look the following way then:



Where ξ is the rate at which recovered individuals return to the susceptible state.

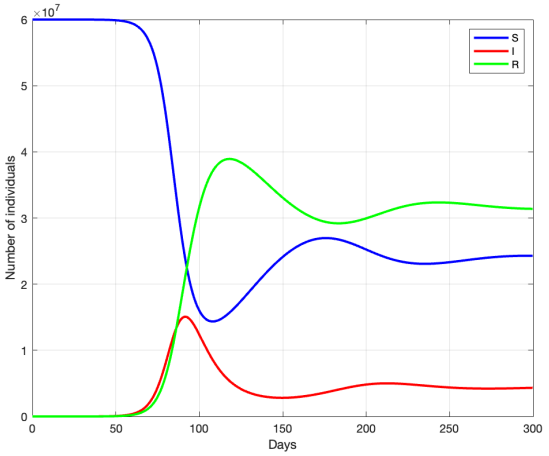
The system of differential equations looks the following:

$$\frac{dS}{dt} = \frac{\beta SI}{N} + \xi R$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I$$

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

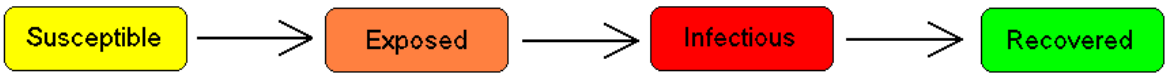
Again, we have a constant value for the total population $N = S + I + R$



SIR model with immunity loss (SIRS) with the following parameters:
Rate of infection: β=6·10^(−9)
Rate of recovery: γ=0.12
Rate of immunity loss: ξ=1/60
Total population: N=6·10^7
Initial number of infected: I_0=10

SEIR

Before we used the example of Covid-19 with MATLAB to see the plotting of an SIR with different parameters. However, in the case of Covid for example, we should also consider the latency period during which individuals have been infected but are not yet infectious themselves. We will call this new compartment Exposed (E). Therefore we have the following flow diagram



We will assume that the latency period is a random variable that has exponential distribution with parameter a. Again, we are assuming that N is constant, ($N = S + E + I + R$).

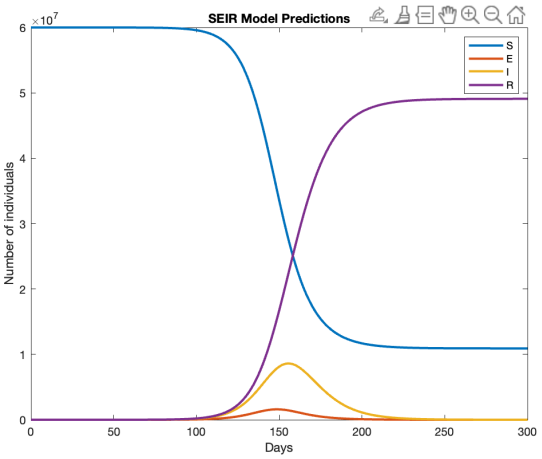
Thus, we have the following system of differential equations:

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

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

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

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



Example of SEIR model made with MATLAB with the following values:
Rate of infection = β=6·10^(−9)
Rate of recovery: γ=0.12
Rate of susceptability: μ =0.721
Total population: N=6·10^7
Initial number of infected: I_0=10

Assumptions and limitations

While the SIR model is a powerful tool, it's essential to acknowledge its assumptions and limitations. For instance, it assumes a well-mixed population, constant parameters, and homogeneous disease transmission. It also assumes that once individuals recover, they gain lifelong immunity, which might not hold true for all diseases.

Real-world scenarios often feature complex dynamics, heterogeneity in populations, and the introduction of interventions like vaccinations and treatments, which can be addressed with variations of the SIR model. For instance, the SIRS model considers waning immunity, while the SEIR model accounts for an exposed (latent) period before becoming infectious.

Bibliography

Works Cited

Balasubramanian, Chandana. “Epidemiological Triad.” *GIDEON*, 26 Sept. 2026,

www.gideononline.com/blogs/epidemiological-triad/#:~:text=The%20epidemiological%20triad%20consists%20of.

British Medical Journal. “What Is Epidemiology?” *Bmj.com*, 2019, www.bmj.com/about-bmj/resources-readers/publications/epidemiology-uninitiated/1-what-epidemiology.

Ezekiel, D, et al. *Stability Analysis of an SIR Infectious Disease Model*.

“How Infectious Diseases Spread.” *Ministry of Health NZ*, 2016, www.health.govt.nz/your-health/healthy-living/environmental-health/infectious-disease-prevention-and-control/how-infectious-diseases-spread.

K. Alexander, Lorraine, et al. *Common Measures and Statistics in Epidemiological Literature*.

“SIR and SIRS Models — Generic Model Documentation.” *Docs.idmod.org*, docs.idmod.org/projects/emod-generic/en/2.20_a/model-sir.html.

“SIR Model, Part 5.” *Services.math.duke.edu*, services.math.duke.edu/education/postcalc/sir/sir5.html.

Smith, David, and Lang Moore. “The SIR Model for Spread of Disease - the Differential Equation Model | Mathematical Association of America.” *Maa.org*, Dec. 2004, maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-the-differential-equation-model.

Wikipedia Contributors. “Compartmental Models in Epidemiology.” *Wikipedia*, Wikimedia Foundation, 30 Jan. 2019, en.wikipedia.org/wiki/Compartmental_models_in_epidemiology.