Lecture Notes CS:4980 SIR Compartmental Models
Lecture 3 and 4: Jan 28th and 30th, 2020
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1 Compartmental Models

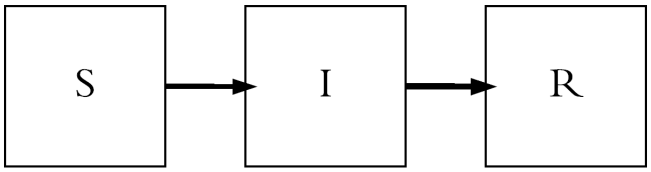
Before we analyze Compartmental Models, we must understand the definition and the concept of Compartmental Models.

Definition 1. *Compartmental Models are partitions of a set polulation into different distinct compartments. Each individual is one of the listed compartments in the model. Some examples of distinct compartments are as follows:*

1. $S \rightarrow Susceptible$
2. $E \rightarrow Exposed$
3. $M \rightarrow Immunity\ from\ mother$
4. $I \rightarrow Infected$
5. $R \rightarrow Resistant$

Compartmental Models can be created and used in many unique ways. A couple example models are SIR, SEIR, SIS, and MSIR. Below is a flow chart of a SIR model.

Consider this visualization of a SIR compartmental model.



Example 1.1: SIR
Compartmental Model

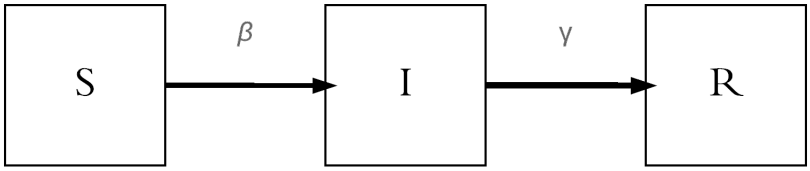
Transitions between compartments only go in the direction the arrow is pointing. Individuals are only allowed to follow the path within the model. i.e, an inidividual cannot go from susceptible to resistant in one time step.

2 SIR Model Specification

The SIR Compartmental Model is the model that is easily used and commonly used today. The SIR model contains a constant population, denoted as N. This population can only be one of the three states available. The three states that an individual can join are susceptible, infected, or resistant. Denoted as S, I, or R respectively. An individual **cannot** be part I and R, each individual can only be in one compartment at any given time. Time proceeds in discrete steps, also called Time Steps. (i.e. T = 1,2,...) Along with this, individuals can move to the next compartment in one time step, but cannot break the progression of the model. (i.e. Individual x cannot go from S to R in one time step.) Lastly, death is not possible in this model.

All Compartmental Models work in time steps. In every time step, many processes will happen within the model. For the SIR model, only three actions happen within the model. Each susceptible individual x will "contact" another individual y that is chosen uniformly from the population N. If y is infected, then x has a probability of β to become infected too. Each infected individual has a probability of γ to become resistant. All individuals who are resistant, stay resistant for the rest of all time steps.

Below is an updated visualization of a SIR model with β and γ probabilities.



Example 2.1: SIR Model with Probabilities β & γ

The probability of an infected individual to become resistant over any timestep is proven below. Let x denote the period of time for an infected person

$$\text{Prob}[x = 1] = \gamma$$

$$\text{Prob}[x = 2] = (1 - \gamma)\gamma$$

$$\text{Prob}[x = t] = (1 - \gamma)^{t-1}\gamma)$$

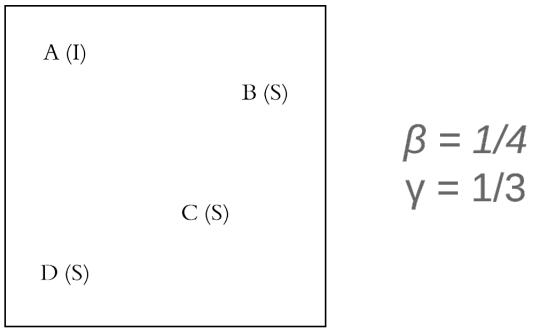
Therefore Geometric Disturbution

$$E[x] = 1/\gamma$$

2.1 Example SIR Problem

University of Iowa conducted a SIR computational study with four individuals named A, B, C, and D respectively. These fictional individuals are contained in a box with A being labeled with I and B, C, and D labeled as S.The probability β is 1/4 and the probability of γ is 1/3. Find the probabilty that B gets infected in time state 1 and that no one is infected after time state 1.

Below is the visual representation of the Example SIR Problmem.



Example 3.1 Initial State
of SIR Example

$$\text{Prob[B gets infected in time state 1]} = 1/4 * 1/4 = 1/16$$

$$\text{Prob[No one is infected after time state 1]} = (15/16)^3 * 1/3$$

2.2 Future Populations

Given that we know the populations of each compartment, we must find the future population of each compartment too. Using the SIR model, we can use γ, β, and the current populations to find the populations in the next time step. Given that $X(t)$, $Y(t)$, and $Z(t)$ are populations of susceptible, infected, and resistent at given time step t respectively. Therefore,

$$X(t) + Y(t) + Z(t) = N$$

Then we must find $X(t+1)$, $Y(t+1)$, and $Z(t+1)$.

X(t+1)
Let x ϵ S just before time step t.

$$\text{Prob}[x \text{ becomes infected in time step } t] = Y(t)/N * \beta = ((I's\ Pop./Pop)/N) * \beta$$

$$\text{E[No. of susceptible individuals who will become infected in time step } t] = X(t) * (Y(t)/N) * \beta$$

$$\text{E}[X(t+1)] = Y(t) + ((X(t) * Y(t) * \beta)/N)$$

Y(t+1)

$$\mathrm{E}[X(t+1)] = Y(t) + ((X(t) * Y(t) * \beta)/N) - \gamma * y(t)$$

Z(t+1)

$$\mathrm{E}[Z(t+1)] = Z(t) + \gamma * Y(t)$$

Implications for Computation

By assuming that the random variables X, Y, and Z behave exactly like their expectation. (also known as "mean field approximation") We can prove that this approximation is good when **populations are large** and **actions are independent**.

2.3 What Defines an "Epidemic?"

Over thousands of years, our human population has experienced several epidemics. But what defines an epidemic? Below, we will computationally find how an epidemic will occur. Please note: a disease is considered an epidemic even if it infects a very small fraction of the population. (e.g. 0.5%)

When $Y(t+1) > Y(t)$

$$\begin{gathered} \text{True when } ((X(t) * Y(t) * \beta)/N) - \gamma * Y(t) > 0, \\ \rightarrow (X(t) * \beta)/N - \gamma > 0 \\ \rightarrow \beta - \gamma > 0 \\ \beta/\gamma > 1 \end{gathered}$$

A Key property of a SIR model is that the disease becomes an epidemic if and only $\beta/\gamma > 1$

2.4 Epidemic Curve Graph

All epidemics follow a similar basic curve correlating the ammount of infected people over time. In the SIR model, the epidemic starts slow, but gradually increases over time till the epidemic hits it's peak, then gradually moves back down. This creates an inverted parbola. The peak of the curve denotes the peak of infection, where the most people are infected. The curve follows this equation given in class:

$$Y(t+1) = Y(t) + Y(t) * ((X(t) * \beta)/N - \gamma)^t$$

2.5 Basic Reproduction Number

Definition 2. *The Basic Reproduction Number, denoted as R_o, is the expected number of new infections caused by a single infection during the early stages of the infection.*

Within a SIR model, we can show that:

$$R_o = \beta/\gamma$$

Consider the situation just before time step 1. Suppose that $x \epsilon I$. Our goal is to find the expectation of individuals who will be infected by x. To spread the infection, we will create or

chose an arbitrary $y \epsilon S$.With these individuals, we can find the probability that y will be infected by x in any time step.

$$\text{Prob}[y \text{ will be infected by } x \text{ in time step 1}] = \beta/N$$

$$\text{Prob}[y \text{ will be infected by } x \text{ in time step 2}] = (1 - (\beta/N)) * (1 - \gamma) * (\beta/N)$$

$$\text{Prob}[y \text{ will be infected by } x \text{ in time step } t] = ((1 - (\beta/N)) * (1 - \gamma))^{t-1} * (\beta/N)$$

Let δ denote $(1 - (\beta/N)) * (1 - \gamma)$

$$\text{Prob}[y \text{ will be infected by } x] = \sum_{t=1}^{\infty} \delta^{t-1} * (\beta/N)$$

By the Definition of a Geomeric Series, we can get:

$$\sum_{t=1}^{\infty} \delta^{t-1} = (\beta/N) * (1/(1 - \delta))$$

Therefore the Expectation of number of people infected by x is $\beta * (1/(1 - \delta))$.
Assuming that while $N \to \infty$:

$$(1 - (\beta/N)) * (1 - \delta) \to 1 - \delta$$

Therefore, as $N \to \infty$ the Expectation of number of people infected by x is β/γ. Which correlates to the probability of infection over the probability of resistance. Along with this, we can note that to increase R_o, you can increase β or reduce γ. Vice Versa to decrease R_o.

3 Additional Compartmental Models

There are endless amount of different compartmental models that epidemiologists use. But a couple that will be covered in class at at a later date are: SEIR, SIS, MSIR, etc.

THIS IS A DRAFT AS OF THURS FEB 6TH