

Introduction to Mathematical Models in Epidemiology

Glenn Ledder

Department of Mathematics
University of Nebraska-Lincoln
gledder@unl.edu

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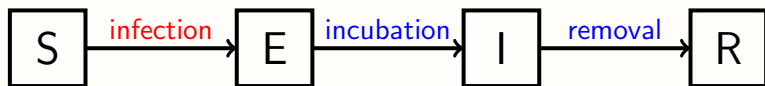
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1. Class structure

- ▶ Individuals in a population are divided into classes. These can vary from one model to another. Examples:
 - **S**: *Susceptible* – can be infected
 - **E**: *Exposed* – infected but not infectious
 - **I**: *Infectious* – can transmit the disease to susceptibles
 - **R**: *Removed* – no longer infectious
- ▶ Sometimes the names are misleading.
 - '*Exposed*' should be '*Latent*'
 - *Removed* includes people who are still sick and may include people who are deceased
- ▶ Models are designated by the class structure: SIR, SIS, SEIR, SEAIR, SEAIRHD etc

2. Processes

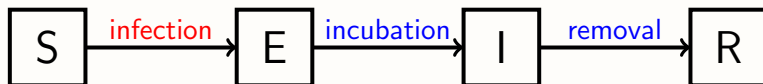
- ▶ Processes move individuals from one class to another.
 - Some models have processes that bring individuals into or out of the system.
- ▶ Example: Basic SEIR model



- Rate of change of S is $-\text{infection}$
- Rate of change of E is $\text{infection} - \text{incubation}$
- Rate of change of I is $\text{incubation} - \text{removal}$
- Rate of change of R is removal

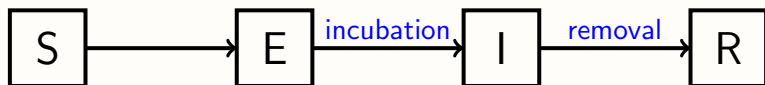
2. Processes – Two Types

- Processes are either **transmissions** or **transitions**.



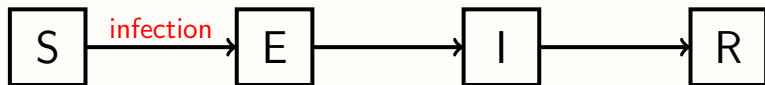
- **Transmissions** require interaction with another class.
 - Susceptibles are infected by Infectives.
- **Transitions** happen without any interaction.
 - Incubation of Latent individuals and removal of Infectious individuals happen spontaneously.

2.1 Processes – Transitions



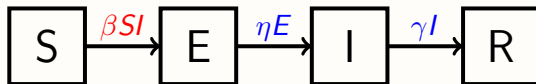
- ▶ Transition rates are (assumed to be) proportional to the **leaving** class
 - incubation rate = constant * $E = \eta E$
 - removal rate = constant * $I = \gamma I$
- ▶ **Rate constants are reciprocals of average time in class.**
 - Average removal time 10 days $\rightarrow \gamma = 0.1$

2.2 Processes – Transmissions



- ▶ Transmission rates are proportional to the **leaving** class size
 - infection rate = force of infection * $S = \lambda S$
- ▶ The force of infection is proportional to the sum of the **transmitting** classes (just I for SEIR)
 - force of infection = constant * $I = \beta I$
- ▶ The infection rate is $\beta I * S = \beta SI$

2.3 Summary – SEIR epidemic model



$$S' = -\beta SI$$

$$E' = \beta SI - \eta E$$

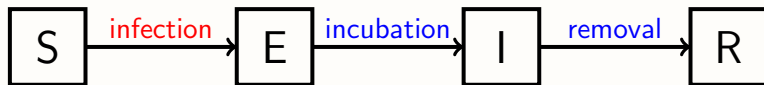
$$I' = \eta E - \gamma I$$

$$R' = \gamma I$$

- ▶ Let $N = S + E + I + R$. Then $N' = 0$, so N is constant.
 - The R equation is not needed because $R = N - S - E - I$.

3.1 Model Type – Epidemic

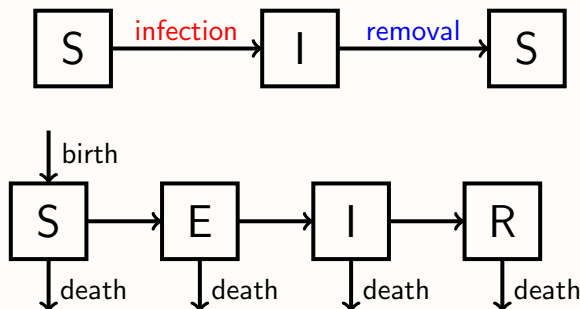
- ▶ **Epidemic** models have no means for replenishment of susceptibles.
 - These do not have births or natural deaths, so they are intended only for short time intervals (up to a few years).



- ▶ Including deceased individuals as 'Removed' makes the total population constant, which simplifies the model.

3.2 Model Type – Endemic

- ▶ **Endemic** models have some means for replenishment of susceptibles.
 - The focus of analysis is on determining long term behavior.



4. Basic reproductive number

- ▶ **Basic reproductive number \mathcal{R}_0 :**
the average number of secondary infections caused by one primary infective in a fully susceptible population.
 - $\mathcal{R}_0 > 1$ is needed to start an epidemic.
- ▶ The total number is the average rate times the average time.
- ▶ Calculation of average transmission rate:
 - Recall that the **transmission rate** is βSI
 - Transmission rate **per infective**: βS
 - Rate per infective in a **fully-susceptible population**: βN

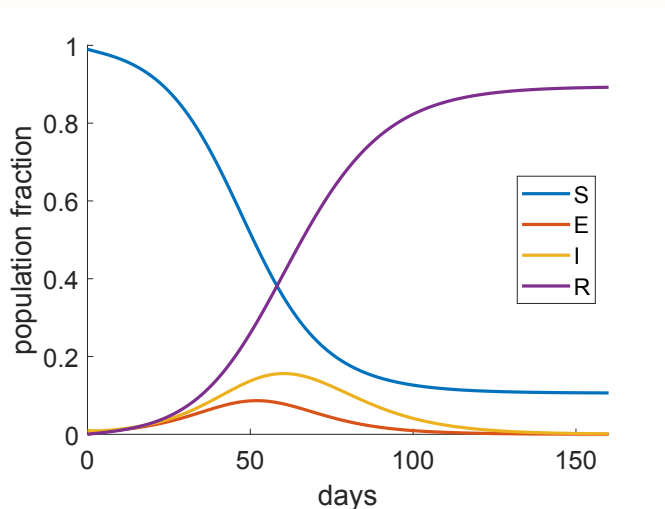
4. Basic reproductive number

- ▶ **Basic reproductive number \mathcal{R}_0 :**
transmission rate per infective in a fully susceptible population multiplied by average time in the Infectious class.
- ▶ Average transmission rate: βN
- ▶ Calculation of average time:
 - Recall that the **removal rate** is γI .
 - The average time is $1/\gamma$.

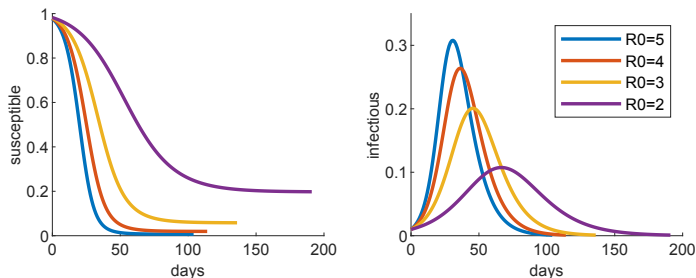
$$\mathcal{R}_0 = \beta N \cdot \frac{1}{\gamma} = \frac{\beta N}{\gamma}.$$

- ▶ Other diseases (like COVID-19) can be more complicated.

5 Behavior of Epidemic Models – Typical history



5. Behavior of Epidemic Models – Importance of \mathcal{R}_0



► Conjectures based on simulations:

1. Not everyone gets the disease.
 - Larger \mathcal{R}_0 means fewer escape.
2. The epidemic ends (in theory) with $I = 0$.
 - This is because we ignored births.

5.1 Epidemic Models – Not everyone gets the disease

$$\frac{dR}{dS} = \frac{R'}{S'} = \frac{\gamma I}{-\beta SI} = -\frac{\gamma}{\beta} \frac{1}{S}.$$

1. Integrate this equation using the fact that at time 0 we have $S = S(0)$ and $R = R(0)$.
2. Let $s = S/N$, $r = R/N$, $s_0 = S(0)/N$, $r_0 = R(0)/N$.
Rearrange the solution from Question 1 to get

$$\ln \frac{s_0}{s} = \mathcal{R}_0(r - r_0). \quad (1)$$

3. Solve for s and use the result to show that $s \geq s_0 e^{-\mathcal{R}_0} > 0$.
- The fraction of susceptibles is always decreasing, but never 0.

5.2 Epidemic Models – The epidemic ends with $I = 0$

4. Rewrite the S' equation as $I dt = -\beta^{-1} dS/S$ and integrate from time 0 to time ∞ .
 - Just leave the integral on the left side because you don't have a formula for I
 - Do the integral on the right side. You may assume $\lim_{t \rightarrow \infty} S = S_\infty > 0$. (Why?)
5. You have just shown that $\int_0^\infty I dt$ is a finite number. What can you conclude about $\lim_{t \rightarrow \infty} I$?

5.3 Epidemic Models – Final size relation

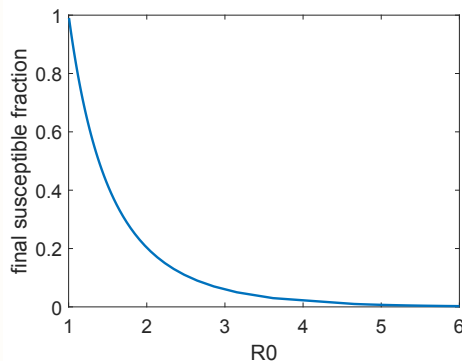
6. You now know that $I \rightarrow 0$. Explain why that means $E \rightarrow 0$ also. Conclude that $s_\infty + r_\infty = 1$.
7. Use the result of Question 6 with Equation (1) to get the final size relation

$$\ln \frac{s_0}{s_\infty} = \mathcal{R}_0(1 - r_0 - s_\infty). \quad (2)$$

- This result can be used to estimate \mathcal{R}_0 for an epidemic that is finished (assuming no interventions).
8. Explain why $1 - r_0 - s_\infty$ is the fraction of people who have the disease at some point in the epidemic.

5.3 Epidemic Models – Final size relation

- ▶ Assume no initial immunity.



- ▶ \mathcal{R}_0 for COVID-19 is about 5.7.