Introduction to Mathematical Epidemiology: Basic Models

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Thanks to NSERC, collaborators

Deterministic compartmental models suitable for the spread of infectious diseases among humans

Simple models that leave out a lot of the biology but give some observed qualitative behavior "A scientific theory should be as simple as possible but no simpler" Albert Einstein

Concentrate on models formulated as ordinary differential equations starting with a simplified version of the model introduced by Kermack, McKendrick 1929, and use the modeling framework



Susceptible-Infectious-Recovered plus demographics

 Biological Problem: Will measles become endemic in the population? Currently measles is a leading cause of death among young children in India

2. Assumptions: Measles is a viral disease, so SIR model appropriate Include demographics, but ignore death due to measles

3. Formulation of Model:

S, I, R denote the number of susceptible, infectious, recovered people

with N = S + I + R as the total population

A denotes the rate of input into S

d denotes the natural death rate

 γ denotes the rate of recovery

 λ denotes the number of contacts in unit time by an infectious person

called the transmission parameter

Assume standard incidence, and all parameters are positive



$$\frac{dS}{dt} = A - dS - \frac{\lambda SI}{N}$$
$$\frac{dI}{dt} = \frac{\lambda SI}{N} - (d + \gamma)I$$
$$\frac{dR}{dt} = \gamma I - dR$$

Initial conditions are $S(0) > 0 \simeq N$, I(0) > 0 small, R(0) = 0

$$\frac{dS}{dt} = A - dS - \frac{\lambda SI}{N}, \quad \frac{dI}{dt} = \frac{\lambda SI}{N} - (d + \gamma)I$$

4. Analysis of Model:

The model is well posed, solutions remain nonnegative and are bounded

There is a disease free equilibrium (DFE): $S = \frac{A}{d}, I = 0, R = 0$

Linearizing about the DFE gives

$$rac{dI}{dt}=(\lambda-(d+\gamma))I=(d+\gamma)(\mathcal{R}_0-1)I$$
 where $\mathcal{R}_0=rac{\lambda}{d+\gamma}$

There is also an endemic equilibrium $I^* > 0$ with

$$I^* = rac{A}{d+\gamma}(1-rac{1}{\mathcal{R}_0})$$

provided the bracket is positive, i.e. $\mathcal{R}_0 > 1$

5. Interpret Solution:

 $\mathcal{R}_0 = \frac{\lambda}{d+\gamma}$ is the basic reproduction number and is the product of the contact rate λ and the average death adjusted infectious time $1/(d+\gamma)$

If $\mathcal{R}_0 < 1$ then the DFE is (locally) stable, measles dies out

If $\mathcal{R}_0 > 1$ then there is an endemic equilibrium $I^*, R^* = \gamma I^*/d$ and $I \to I^*$ as $t \to \infty$ so measles is endemic in the population

 \mathcal{R}_0 determines a sharp threshold with a forward bifurcation at $\mathcal{R}_0=1$

6. Validate Model:

Sometimes measles and other viral diseases die out quickly but other times they give rise to an endemic situation

Data for \mathcal{R}_0 in countries where measles is endemic confirms that $\mathcal{R}_0>1$ but data is confounded by vaccination

7. Use Model Results:

If a fraction p of the population is vaccinated so that $(1-p)\mathcal{R}_0 < 1$ then measles will be eradicated

$$p > (1-rac{1}{\mathcal{R}_0})$$

is the fraction needed to give herd immunity

For example:

if $\mathcal{R}_0=5$ then need to vaccinate 80%

if $\mathcal{R}_0 = 10$ then need to vaccinate 90%

In some regions of India measles has \mathcal{R}_0 of about 15 so need to vaccinate over 93% WHO estimate for 2013: 87% – 90% of Indian children received at least 1 measles vaccination Since 2010 a second dose is recommended in high-risk states Susceptible-Infectious-Recovered without demographics

Influenza is usually a short epidemic so demographics can be ignored

If demographics are ignored, A = d = 0, then the previous analysis fails!

Putting this assumption into the previous model gives

$$\frac{dS}{dt} = -\frac{\lambda SI}{N}, \quad \frac{dI}{dt} = \frac{\lambda SI}{N} - \gamma I, \quad \frac{dR}{dt} = \gamma I$$

Thus I = 0 is the only equilibrium and $I(t) \rightarrow 0$ as $t \rightarrow \infty$ To see how the dynamics evolve consider

$$\frac{dI}{dS} = -1 + \frac{\gamma N}{\lambda S}$$

integrating gives

$$I + S - rac{\gamma N}{\lambda} \log S = C$$

where C is a constant

$$I + S - \frac{\gamma N}{\lambda} \log S = C$$

Initial conditions are $S(0) > 0 \cong N$, I(0) > 0 small, R(0) = 0so C is finite, giving $S(\infty) \neq 0$

The parameter $\mathcal{R}_0=rac{\lambda}{\gamma}$ still acts as a threshold

If $\mathcal{R}_0 < 1$, then $I \rightarrow 0$ monotonically, influenza dies out If $\mathcal{R}_0 > 1$, then I first increases to a peak, then $I \rightarrow 0$

Approximating: I(0) = 0, $I(\infty) = 0$ the final size equation can be written

$$\log \frac{S(0)}{S(\infty)} = \mathcal{R}_0(1 - \frac{S(\infty)}{N})$$

The total number of people infected is $I(0) + S(0) - S(\infty)$ Not everyone becomes infectious, $S(\infty)$ escape infection

The attack ratio, i.e. fraction of people infected is approx. $1 - \frac{S(\infty)}{N}$



Simulation of the influenza SIR model showing the number of infectious people against time, with $\lambda = 0.5, \gamma = 0.25, N = 1,000, I(0) = 5$

For small time $I(t) \approx I(0) \exp{\{\gamma(\mathcal{R}_0 - 1)t\}}$ can be used to estimate \mathcal{R}_0 from data

The maximum number of infectious people can be found from $\frac{dl}{dt} = 0$ and l(t) can be fitted to data on influenza epidemics

For seasonal influenza \mathcal{R}_0 is usually 1.4 to 2.4 Herd immunity applies: $p > 1 - \frac{1}{\mathcal{R}_0}$ giving around 50% vaccination needed to eliminate influenza

BUT there are many strains of influenza, the virus mutates, some people are asymptomatic, some are latently infected, age structure is important...

In November 2014, influenza subtype B was predominant in India