Epidemics

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- SI model
- SIS model
- SIR model



Epidemic dynamics models

- Mathematical epidimiology
- W. O. Kermack and A. G. McKendrick, 1927
- Deterministic compartamental model (population classes) $\{S, I, T\}$
- *S*(*t*) succeptable, number of individuals not yet infected with the disease at time t
- *I*(*t*) infected, number of individuals who have been infected with the disease and are capable of spreading the disease.
- R(t) recoverd, number of individuals who have been infected and then recovered from the disease, can't be infected again or to transmit the infection to others.
- Fully-mixing model
- Closed population (no birth, death, migration)
- Models: SI, SIS, SIR, SIRS,...

•
$$S(t)$$
 -susceptible , $I(t)$ - infected

$$S \longrightarrow I$$

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

- β infection/contact rate, number of contacts per unit time
- Infection equation:

$$I(t + \delta t) = I(t) + \beta \frac{S(t)}{N} I(t) \delta t$$
$$\frac{dI(t)}{dt} = \beta \frac{S(t)}{N} I(t)$$

- Fractions: i(t) = I(t)/N, s(t) = S(t)/N
- Equations

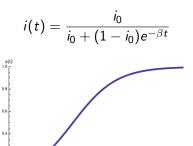
$$\begin{aligned} \frac{di(t)}{dt} &= \beta s(t)i(t) \\ \frac{ds(t)}{dt} &= -\beta s(t)i(t) \\ s(t) + i(t) &= 1 \end{aligned}$$

• Differential equation, $i(t = 0) = i_0$

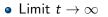
$$\frac{di(t)}{dt} = \beta(1-i(t))i(t)$$

Logistic growth function

• Solution:



10 1



0.2

$$egin{aligned} & i(t)
ightarrow 1 \ & s(t)
ightarrow 0 \end{aligned}$$

in image $i_0 = 0.05$, $\beta = 0.8$

SIS model

•
$$S(t)$$
 -susceptable , $I(t)$ - infected,
 $S \longrightarrow I \longrightarrow S$
 $S(t) + I(t) = N$

•
$$\beta$$
 - infection rate (on contact), γ - recovery rate
• Infection equations:

$$\frac{ds}{dt} = -\beta si + \gamma i$$
$$\frac{di}{dt} = \beta si - \gamma i$$
$$s + i = 1$$

• Differential equation, $i(t = 0) = i_0$

$$\frac{di}{dt} = (\beta - \gamma - i)i$$

Solution

$$i(t) = (1 - \frac{\gamma}{\beta}) \frac{C}{C + e^{-(\beta - \gamma)t}}$$

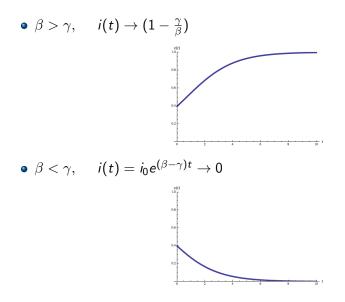
where

$$C = \frac{\beta i_0}{\beta - \gamma - \beta i_0}$$

• Limit $t \to \infty$

$$eta > \gamma \quad , \quad i(t) o (1 - rac{\gamma}{eta}) \ eta < \gamma \quad , \quad i(t) = i_0 e^{(eta - \gamma)t} o 0$$

Logistic function



• S(t) -susceptable , I(t) - infected, R(t) - recovered

$$S \longrightarrow I \longrightarrow R$$

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

•
$$eta$$
 - infection rate, γ - recovery rate

• Infection equation:

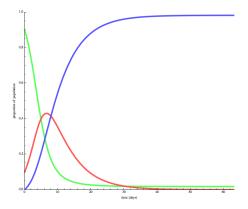
$$\begin{aligned} \frac{ds}{dt} &= -\beta si \\ \frac{di}{dt} &= \beta si - \gamma i \\ \frac{dr}{dt} &= \gamma i \\ s + i + r = 1 \end{aligned}$$

Equation

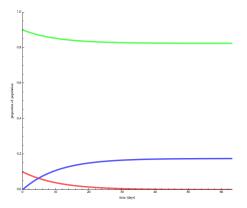
$$\frac{ds}{dt} = -\beta s \frac{dr}{dt} \frac{1}{\gamma}$$
$$s = s_0 e^{-\frac{\beta}{\gamma}r}$$
$$\frac{dr}{dt} = \gamma (1 - r - s_0 e^{-\frac{\beta}{\gamma}r})$$

Solution

$$t = \frac{1}{\gamma} \int_0^r \frac{dr}{1 - r - s_0 e^{-\frac{\beta}{\gamma}r}}$$









Equation

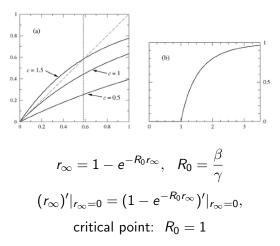
$$\frac{dr}{dt} = \gamma (1 - r - s_0 e^{-\frac{\beta}{\gamma}r})$$

• Limits:
$$t \to \infty$$
, $\frac{dr}{dt} = 0$, $r_{\infty} = const$,

$$1-r_{\infty}=s_0e^{-\frac{\beta}{\gamma}r_{\infty}}$$

• Initial conditions: r(0) = 0, i(0) = c/N, $s(0) = 1 - c/N \approx 1$

$$1-r_{\infty}=e^{-\frac{\beta}{\gamma}r_{\infty}}$$



- r_{∞} the total size of the outbreak
- Epidemic threshold

- β infection rate, γ recovery rate $\rightarrow 1/\gamma$ average time to recover
- Basic reproduction number

$$R_0 = \frac{\beta}{\gamma}$$

It is average number of people infected by a person before his recovery

$$R_0 = E[\beta\tau] = \beta \int_0^\infty \gamma \tau e^{-\gamma\tau} d\tau = \frac{\beta}{\gamma}$$

Simple model of contagion (decease transmission)

- 1st-wave: first infected person enters the population and transmits to each person he meets with probability *p*. Suppose he meets *k* people while contagious
- 2nd-wave: Each infected person from 1st wave meets k new people and independently transmits infection with probability p
- 3rd-wave:

This is Galton-Watson branching stochastic process (Proposed by Francis Galton 1889 as a model for extinction of family names) Population is organized as a tree

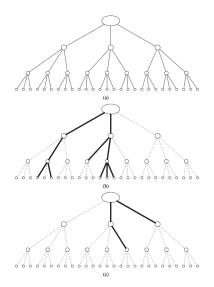
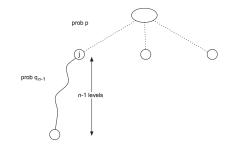


image from David Easley, Jon Kleinberg, 2010

Extinction probability

- let q_n probability that infection persists n steps (levels of the tree)
- pq_{n-1} probability that spreads through one first contact and then survives n-1 levels

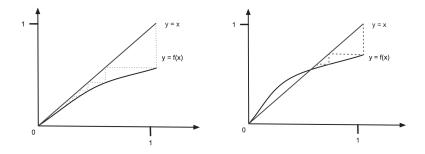


• $(1 - pq_{n-1})^k$ - probability that will not spread through any of the subtries

$$(1-pq_{n-1})^k=1-q_n$$

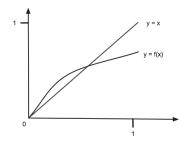
• Recurrence $(q_n - \text{probability that infection persists through n steps})$

$$q_n = 1 - (1 - pq_{n-1})^k, \ \ q_0 = 1$$



• limiting probability $q^* = \lim_{n \to \infty} q_n$

$$q^* = 1 - (1 - pq^*)^k$$



• Slope:

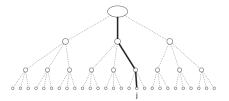
$$pk(1-pq)^{k-1}|_{q=0} = 1$$

• When $R_0 = pk > 1$, there is a non zero probability of infection persists

Leonid E. Zhukov (HSE)

Galton-Watson branching random process:

- if $R_0 = 1$, the mean of number of infected nodes does not change
- if $R_0 > 1$, the mean grows geometrically as R_0^n
- if $R_0 < 1$, the mean shrinks geometrically as R_0^n



 $R_0 = 1$ - point of phase transition

- A Contribution to the Mathematical Theory of Epidemics. , Kermack, W. O. and McKendrick, A. G. , Proc. Roy. Soc. Lond. A 115, 700-721, 1927.
- The Mathematics of Infectious Disease, Herbert W. Hethcote, SIAM Review, Vol. 42, No. 4, p. 599-653, 2000