Epidemics

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Network Science
1. Epidemic models
   - SI model
   - SIS model
   - SIR model

2. Branching process
   - Galton-Watson process
Epidemic dynamics models

- Mathematical epidemiology
- W. O. Kermack and A. G. McKendrick, 1927
- Deterministic compartmental model (population classes) \{S, I, T\}
- \(S(t)\) - susceptible, 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.
- \(R(t)\) - recovered, 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,..
SI model

- $S(t)$ - susceptible, $I(t)$ - infected
  
  $$S \rightarrow I$$

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

- $\beta$ - infection/contact rate, number of contacts per unit time

- Infection equation:

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

  $$\frac{dI(t)}{dt} = \beta \frac{S(t)}{N} I(t)$$
SI model

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

\[
\frac{di(t)}{dt} = \beta s(t)i(t) \\
\frac{ds(t)}{dt} = -\beta s(t)i(t)
\]

$s(t) + i(t) = 1$

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

\[
\frac{di(t)}{dt} = \beta(1 - i(t))i(t)
\]
Logistic growth function

Solution:

\[ i(t) = \frac{i_0}{i_0 + (1 - i_0)e^{-\beta t}} \]

Limit \( t \to \infty \)

\[ i(t) \to 1 \]
\[ s(t) \to 0 \]

in image \( i_0 = 0.05, \ \beta = 0.8 \)
SIS model

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

\[ S \rightarrow I \rightarrow S \]

\[ S(t) + I(t) = N \]

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

\[ \frac{ds}{dt} = -\beta si + \gamma i \]
\[ \frac{di}{dt} = \beta si - \gamma i \]

\[ s + i = 1 \]

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

\[ \frac{di}{dt} = (\beta - \gamma - i)i \]
SIS model

Solution

\[ i(t) = \left(1 - \frac{\gamma}{\beta}\right) \frac{C}{C + e^{-(\beta-\gamma)t}} \]

where

\[ C = \frac{\beta i_0}{\beta - \gamma - \beta i_0} \]

Limit \( t \to \infty \)

\[ \beta > \gamma \ , \quad i(t) \to \left(1 - \frac{\gamma}{\beta}\right) \]

\[ \beta < \gamma \ , \quad i(t) = i_0 e^{(\beta-\gamma)t} \to 0 \]
Logistic function

- $\beta > \gamma$, \quad $i(t) \to (1 - \frac{\gamma}{\beta})$

- $\beta < \gamma$, \quad $i(t) = i_0 e^{(\beta - \gamma)t} \to 0$
SIR model

- $S(t)$ - susceptible, $I(t)$ - infected, $R(t)$ - recovered

\[ S \rightarrow I \rightarrow R \]

\[ S(t) + I(t) + R(t) = N \]

- $\beta$ - infection rate, $\gamma$ - recovery rate

Infection equation:

\[
\begin{align*}
\frac{ds}{dt} & = -\beta si \\
\frac{di}{dt} & = \beta si - \gamma i \\
\frac{dr}{dt} & = \gamma i \\

s + i + r & = 1
\end{align*}
\]
SIR model

- **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**

\[
t = \frac{1}{\gamma} \int_0^r \frac{dr}{1 - r - s_0 e^{-\frac{\beta}{\gamma} r}} \\
\]
\[ \frac{\beta}{\gamma} = 4 \]
\[ i_0 = 0.1 \]
$\frac{\beta}{\gamma} = 0.5$

$i_0 = 0.1$
SIR model

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

- Limits: \( t \to \infty, \) \( \frac{dr}{dt} = 0, \) \( r_\infty = \text{const} \),
  \[ 1 - r_\infty = s_0 e^{-\frac{\beta}{\gamma} r_\infty} \]

- Initial conditions: \( r(0) = 0, \) \( i(0) = c/N, \) \( s(0) = 1 - c/N \approx 1 \)
  \[ 1 - r_\infty = e^{-\frac{\beta}{\gamma} r_\infty} \]
SIR model

\[ r_\infty = 1 - e^{-R_0 r_\infty}, \quad R_0 = \frac{\beta}{\gamma} \]

\[ (r_\infty)'|_{r_\infty=0} = (1 - e^{-R_0 r_\infty})'|_{r_\infty=0}, \]

critical point: \( R_0 = 1 \)
SIR model

- \( r_\infty \) - the total size of the outbreak
- Epidemic threshold
  
  Epidemics: \( R_0 > 1, \quad \beta > \gamma \), \( r_\infty = \text{const} > 0 \)
  
  No epidemics: \( R_0 < 1, \quad \beta < \gamma \), \( r_\infty \to 0 \)

- \( \beta \) - infection rate, \( \gamma \) - recovery rate \( \to 1/\gamma \) - 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

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

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
Branching process

image from David Easley, Jon Kleinberg, 2010
Branching process

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

\[
(1 - pq_{n-1})^k \quad \text{- probability that will not spread through any of the subtries}
\]

\[
(1 - pq_{n-1})^k = 1 - q_n
\]
Branching process

- Recurrence ($q_n$ - probability that infection persists through $n$ steps)

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

- limiting probability \( q^* = \lim_{n \to \infty} q_n \)

\[
q^* = 1 - (1 - pq^*)^k
\]

- Slope:

\[
pk(1 - pq)^{k-1}\bigg|_{q=0} = 1
\]

- When \( R_0 = pk > 1 \), there is a non zero probability of infection persists
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.