10. Epidemics on networks

- Important topic of network science: spread of diseases (over networks)
  - e.g. human & animal diseases, computer viruses

- Simplified model: Susceptible-infected (SI) model, Susceptible-infected-recovered (SIR) model
  - SI-Susceptible (SIS) model ( reinfection), SIRS model

SI model

\[ S \rightarrow I \]

SIR model

\[ S \rightarrow I \rightarrow R \]

SIS model

\[ S \rightarrow I \]

SIRS model

\[ S \rightarrow I \rightarrow R \]

U) SI model

- Disease spreading

\( S(t) \): the number of susceptible individuals at time \( t \)

\( I(t) \): the number of infected individuals at time \( t \)

\( \beta \): the rate of disease spreading

\( n \): total population

- Average probability of susceptible person: \( \frac{S}{n} \)

- An infected person has contact with an average of \( \frac{\beta S}{n} \) susceptible person per unit time

- Overall average rate of new infections: \( \frac{\beta S \dot{X}}{n} \)

\[
\begin{align*}
\frac{dX}{dt} &= \beta \frac{S \dot{X}}{n} \quad \text{(increase)} \\
\frac{dS}{dt} &= -\beta \frac{S \dot{X}}{n} \quad \text{(decrease)}
\end{align*}
\]

Fully mixed susceptible-infected model (SI model)

By setting \( S = \frac{S}{n} \), \( X = \frac{X}{n} \)

\[
\begin{align*}
\frac{dX}{dt} &= \beta S \dot{X}, \quad \frac{dS}{dt} = -\beta S \dot{X}
\end{align*}
\]
\[ \frac{dS}{dt} = -\beta S I \]
\[ \frac{dI}{dt} = \beta S I - \gamma I \]
\[ \frac{dR}{dt} = \gamma I \]

\[ S + I + R = 1 \]

\[ S(0) = S_0, \quad I(0) = 0, \quad R(0) = 0 \]

\[ S(t) = \frac{S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ I(t) = \frac{\beta S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ R(t) = \frac{\gamma I(t)}{\beta} \]

\[ S(t) \rightarrow I(t) \rightarrow R(t) \]

\[ \frac{dS}{dt} = -\beta S I \]
\[ \frac{dI}{dt} = \beta S I - \gamma I \]
\[ \frac{dR}{dt} = \gamma I \]

\[ S(0) = S_0, \quad I(0) = 0, \quad R(0) = 0 \]

\[ S(t) = \frac{S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ I(t) = \frac{\beta S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ R(t) = \frac{\gamma I(t)}{\beta} \]

\[ S(t) \rightarrow I(t) \rightarrow R(t) \]

\[ \frac{dS}{dt} = -\beta S I \]
\[ \frac{dI}{dt} = \beta S I - \gamma I \]
\[ \frac{dR}{dt} = \gamma I \]

\[ S(0) = S_0, \quad I(0) = 0, \quad R(0) = 0 \]

\[ S(t) = \frac{S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ I(t) = \frac{\beta S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ R(t) = \frac{\gamma I(t)}{\beta} \]

\[ S(t) \rightarrow I(t) \rightarrow R(t) \]

\[ \frac{dS}{dt} = -\beta S I \]
\[ \frac{dI}{dt} = \beta S I - \gamma I \]
\[ \frac{dR}{dt} = \gamma I \]

\[ S(0) = S_0, \quad I(0) = 0, \quad R(0) = 0 \]

\[ S(t) = \frac{S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ I(t) = \frac{\beta S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ R(t) = \frac{\gamma I(t)}{\beta} \]

\[ S(t) \rightarrow I(t) \rightarrow R(t) \]

\[ \frac{dS}{dt} = -\beta S I \]
\[ \frac{dI}{dt} = \beta S I - \gamma I \]
\[ \frac{dR}{dt} = \gamma I \]

\[ S(0) = S_0, \quad I(0) = 0, \quad R(0) = 0 \]

\[ S(t) = \frac{S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ I(t) = \frac{\beta S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ R(t) = \frac{\gamma I(t)}{\beta} \]

\[ S(t) \rightarrow I(t) \rightarrow R(t) \]

\[ \frac{dS}{dt} = -\beta S I \]
\[ \frac{dI}{dt} = \beta S I - \gamma I \]
\[ \frac{dR}{dt} = \gamma I \]

\[ S(0) = S_0, \quad I(0) = 0, \quad R(0) = 0 \]

\[ S(t) = \frac{S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ I(t) = \frac{\beta S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ R(t) = \frac{\gamma I(t)}{\beta} \]

\[ S(t) \rightarrow I(t) \rightarrow R(t) \]

\[ \frac{dS}{dt} = -\beta S I \]
\[ \frac{dI}{dt} = \beta S I - \gamma I \]
\[ \frac{dR}{dt} = \gamma I \]

\[ S(0) = S_0, \quad I(0) = 0, \quad R(0) = 0 \]

\[ S(t) = \frac{S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ I(t) = \frac{\beta S_0 e^{\beta t}}{1 + S_0 (1 - e^{\beta t})} \]

\[ R(t) = \frac{\gamma I(t)}{\beta} \]

\[ S(t) \rightarrow I(t) \rightarrow R(t) \]
\[ \frac{dr}{dt} = r \left( 1 - s - r \right) = r \left( 1 - s_0 e^{-\frac{tr}{r}} \right) \]

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

\[ \Rightarrow t = \frac{1}{r} \int_0^r \frac{du}{1-u-s_0 e^{-\frac{ru}{r}}} \quad \text{hard to get a closed-form evaluate numerically} \]

- susceptibles decrease monotonically \( (r = s = s_0 e^{-\frac{tr}{r}}) \)
- recovered individuals increase monotonically
- infected individuals go up at first, then down again as they recover

Asymptotic value of \( r \) \( (\frac{dr}{dt} = 0) \)

\[ r = 1 - s_0 e^{-\frac{tr}{r}} \]

With initial conditions \( s_0 = 1 - \frac{C}{n}, \quad \kappa_a = \frac{C}{n}, \quad T_0 = 0 \)

as \( n \to \infty \) \( s_0 \approx 1 \)

\[ r = 1 - e^{-\frac{tr}{r}} \]
4) SIS model

- allows "reinfection" (lifelong immunity on their victims after recovery)

\[
\begin{align*}
\frac{dS}{dt} &= \gamma I - \beta SI, \\
\frac{dI}{dt} &= \beta SI - \gamma I, \quad S + I = 1
\end{align*}
\]

\[
\frac{d\alpha}{dt} = \beta (1-\alpha) I - \gamma \alpha = (\beta - \gamma - \beta \alpha) \alpha
\]

\[\chi(t) = \left(1 - \frac{1}{\beta} \right) \frac{Ce^{(\beta-\gamma)t}}{1 + Ce^{(\beta-\gamma)t}}, \quad \text{where} \quad C = \frac{\beta \alpha_0}{\beta - \gamma - \beta \alpha_0}\]

\[\chi(0) = \alpha_0\]

\[
\lim_{t \to \infty} \chi(t) = 1 - \frac{\gamma}{\beta} = \frac{\beta - \gamma}{\beta} \quad \text{(cf. fixed point \(\beta - \gamma - \beta \alpha^* = 0, \quad \alpha^* = \frac{\beta - \gamma}{\beta}\))}
\]

(i) if \(\beta > \gamma\), logistic growth curve

as \(\beta \to \gamma\), \(\alpha^* \to 0\)

(ii) if \(\beta < \gamma\), the disease will die exponentially
(4) SIRS model

\[
\begin{align*}
\frac{dS}{dt} &= r - \beta S x
, \\
\frac{dI}{dt} &= \beta S x - \rho I
, \\
\frac{dR}{dt} &= \rho I - r - sR
, \\
S + I + R &= 1
\end{align*}
\]

- Cannot be solved analytically, rely on numerical methods

- Epidemic models on networks
  - Previous models assume that every individual has an equal chance to contact with other people
    (people mingle and meet completely at random; fully mixed)
  - In the real world, most people have a set of regular acquaintances, neighbors, and coworkers
    Most other members of the world population can be ignored
    \( \Rightarrow \) network structure has a strong effect on disease spread
  - Disease spreads between any two individuals connected by an edge
    (fully mixed model: fully connected network)
  - Infection (transmission) rate depends on diseases, social behaviors, etc.

- Late-time properties of epidemics on networks
  - SI model: \( n \) individuals
    At \( t=0 \), most vertices are in the susceptible state.
a small fraction \( x_0 \) are in the infected state as \( t \to \infty \), the disease spreads to all the vertices in the same component.

\[ G_{T_0} \]

\[ G_{T_0} \]

\( \text{infected} \)
\( \text{not infected} \)

\( A \)
\( B \)

no path between \( A \) and \( B \) (different from fully mixed model)

- Fully mixed model depends on: \( \beta \) and \( x_0 \), \( \lim_{t \to \infty} x(t) = 1 \)
- Network model depends on:
  - \( \beta \) and \( x_0 \)
  - Network structure
  - The position of the first infected individual, \( \lim_{t \to \infty} x(t) = \frac{|S_0|}{n} \)

**Time-dependent properties of SI model**

\( s_i(t) \): probability that vertex \( i \) is susceptible at \( t \)

\( x_i(t) \): probability that vertex \( i \) is infected at \( t \)

\[
\begin{align*}
\frac{ds_i}{dt} &= -\beta s_i \sum_j A_{ij} x_j = -\beta s_i \sum_j A_{ij} (1 - S_j) \\
\frac{dx_i}{dt} &= \beta s_i \sum_j A_{ij} x_j = \beta (1 - x_i) \sum_j A_{ij} x_j \\
S_i + x_i &= 1
\end{align*}
\]

- Fully mixed model

\[
\begin{align*}
\frac{ds_i}{dt} &= -\beta s_i (1 - s) \\
\frac{dx_i}{dt} &= \beta (1 - x_i) x \\
S_i + x_i &= 1
\end{align*}
\]
Note that SI model over networks is an example of general first-order equation

\[ \frac{dx_i}{dt} = \beta \sum_{j} A_{ij} x_j (1-x_j) \]

(see lecture 9 for fixed point analysis and stability analysis)

SI model over networks is not solvable in closed form for general \( A_{ij} \)

(fixed-point analysis)

Focusing on early times: \( x_i \) is very small, \( 1-x_i \approx 1 \).

\[ \frac{dx_i}{dt} = \beta \sum_{j} A_{ij} x_j \]

\[ \frac{dx}{dt} = \beta A x \quad \text{(matrix form)} \]

\[ x(t) = \sum_{r} a_r(t) v_r \quad (v_r: \text{eigenvectors, } \lambda_r: \text{eigenvalues of } A) \]

\[ \frac{dx}{dt} = \sum_{r} \frac{da_r}{dt} v_r = \beta A \sum_{r} a_r v_r = \beta \sum_{r} \lambda_r a_r(t) v_r \]

\[ \frac{da_r}{dt} = \beta \lambda_r a_r(t) \quad a_r(t) = a_r(0) e^{\lambda_r t} \]

\[ x(t) = \sum_{r} a_r(0) e^{\lambda_r t} v_r \]

the fastest growing term corresponds to the largest eigenvalue \( \lambda_1 \)

\[ x(t) \sim e^{\lambda_1 t} v_1 \]

\( \beta \): infection rate (disease property)

\( \lambda_1, v_1 \): network structure