Network Epidemic

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Rensselaer
Recall of epidemic models without network—basic states

- **S**: Susceptible (healthy)
- **I**: Infected (sick)
- **R**: Removed (immune / dead)

**Processes**:
- Infection
- Recovery
- Removal
Recall of epidemic models without network – definitions

- Each individual has <k> contacts (degrees)

- Likelihood that the disease will be transmitted from an infected to a healthy individual in a unit time: $\beta$

- Number of infected individuals: $I$. Infected ratio $i = I/N$

- Number of susceptible individuals: $S$. Susceptible ratio $s = S/N$
Recall of epidemic models without network – comparisons

- **Exponential regime:** $i = \frac{i_0 e^{\beta(k)t}}{1-i_0+i_0 e^{\beta(k)t}}$
- **Final regime:** $i(\infty) = 1$
- **Epidemic threshold:** No threshold

- **Exponential regime:** $i = \left(1 - \frac{\mu}{\beta(k)}\right) e^{\beta(k)t - \mu t}$
- **Final regime:** $i(\infty) = 1 - \frac{\mu}{\beta(k)}$
- **Epidemic threshold:** $R_0 = 1$

- **Exponential regime:** No closed solution
- **Final regime:** $i(\infty) = 0$
- **Epidemic threshold:** $R_0 = 1$
Real networks are not homogeneous

- Real contagions are regional
  - Individuals can transmit a pathogen only to those they come into contact with
  - Epidemics spread along links in a network

- Real networks are often scale-free
  - Nodes have different degrees
  - $\langle k \rangle$ is not sufficient to characterize the topology

Homogeneous mixing model is not realistic!

The black death pandemic
Comparison between homogeneous mixing and real network
Degree block approximation

- Degrees is the only variable that matters in network epidemic model
  - Place all nodes that have the same degree into the same block
  - No elimination of the compartments based on the state of an individual
  - Independent of its degree an individual can be susceptible to the disease (empty circles) or infected (full circles).
Network epidemic – SI model

Split nodes by their degrees

\[ i_k = \frac{I_k}{N_k}, \quad i = \sum_k P(k)i_k \]

**SI model:**

\[ \frac{di_k(t)}{dt} = \beta (1 - i_k(t))k\Theta_k(t) \]

I am susceptible with \( k \) neighbors, and \( \Theta_k(t) \)

of my neighbors are infected.

Density of infected neighbors of nodes with degree \( k \)

\[ i_k = i_0(1 + \frac{k(k-1)}{\langle k^2 \rangle - \langle k \rangle} (e^{\frac{t}{\tau^{SI}}} - 1)) \]

Average degree of the block \( k \)

\[ \tau^{SI} = \frac{\langle k \rangle}{\beta (\langle k^2 \rangle - \langle k \rangle)} \]

characteristic time for the spread of the pathogen

\[ i = \sum i_k p_k = i_0(1 + \frac{\langle k \rangle^2 - \langle k \rangle}{\langle k^2 \rangle - \langle k \rangle} (e^{\frac{t}{\tau^{SI}}} - 1)) \]
Network epidemic – SI model

- An ER random network with $<k> = 2$
- At any time, the fraction of high degree nodes that are infected is higher than the fraction of low degree nodes.
- All hubs are infected at any time
Network epidemic – SIS model

Split nodes by their degrees

\[ i_k = \frac{I_k}{N_k}, \quad i = \sum_k P(k)i_k \]

SI model:

\[ \frac{di_k(t)}{dt} = \beta(1 - i_k(t))k\Theta_k(t) - \mu i_k(t) \]

Recovery term

Average degree of the block \( k \)

Density of infected neighbors of nodes with degree \( k \)

I am susceptible with \( k \) neighbors, and \( \Theta_k(t) \) of my neighbors are infected.

\[ T^{SIS} = \frac{\langle k \rangle}{\beta\langle k^2 \rangle - \mu\langle k \rangle} \]

characteristic time for the spread of the pathogen

spreading rate:

High \( \lambda \) indicates high spreading likelihood

Threshold \( \lambda_c \)
Epidemic threshold

- $\lambda_c = \frac{1}{(k)+1}$
- Exceeds threshold: spread until it reaches an endemic state
- Less than threshold: dies out
Network epidemic – SIS model on scale-free network

- **Epidemic threshold**
  - $\lambda_c = \frac{\langle k \rangle}{\langle k^2 \rangle}$
  - In large networks: $\lambda_c \to 0$, $\tau \to 0$
  - This is bad: even viruses that are hard to pass from individual to individual can spread successfully!
  - Why? Hubs can broadcast a pathogen to a large number of other nodes!

\[\begin{align*}
\gamma = 3 & \quad \lambda_c = 0 \\
\Theta(\lambda) & \approx \frac{e^{-1/k_{min} \lambda}}{\lambda k_{min}} \left(1 - e^{-1/k_{min} \lambda}\right)^{-1} \\
i(\lambda) & \approx 2e^{-1/k_{min} \lambda}
\end{align*}\]

\[\begin{align*}
\gamma > 3 & \quad \lambda_c > 0 \\
\Theta(\lambda) & \approx \left(\frac{\lambda - \frac{\gamma - 3}{k_{min} (\gamma - 2)}}{\lambda_{min} (\gamma - 2)}\right)^{1/(\gamma - 3)} \\
i(\lambda) & \approx \lambda - \frac{\gamma - 3}{k_{min} (\gamma - 2)}
\end{align*}\]
## Comparison of the network epidemic models

<table>
<thead>
<tr>
<th>Model</th>
<th>Continuum Equation</th>
<th>$\tau$</th>
<th>$\lambda c$</th>
</tr>
</thead>
<tbody>
<tr>
<td>SI</td>
<td>$\frac{di_k}{dt} = \beta [1 - i_k] k \theta_k$</td>
<td>$\frac{\langle k \rangle}{\beta (\langle k^2 \rangle - \langle k \rangle)}$</td>
<td>0</td>
</tr>
<tr>
<td>SIS</td>
<td>$\frac{di_k}{dt} = \beta [1 - i_k] k \theta_k - \mu i_k$</td>
<td>$\frac{\langle k \rangle}{\beta \langle k^2 \rangle - \mu \langle k \rangle}$</td>
<td>$\frac{\langle k \rangle}{\langle k^2 \rangle}$</td>
</tr>
<tr>
<td>SIR</td>
<td>$\frac{di_k}{dt} = \beta [1 - i_k] k \theta_k - \mu i_k$</td>
<td>$\frac{\langle k \rangle}{\beta \langle k^2 \rangle - (\mu + \beta) \langle k \rangle}$</td>
<td>$\frac{1}{\langle k^2 \rangle - \langle k \rangle - 1}$</td>
</tr>
</tbody>
</table>

$s_k = 1 - i_l - r_k$
Summary

- Network epidemics behave very differently than simple epidemic models.
- Nodes with higher degree (hubs) are more vulnerable than those with lower degree.
- In SIS and SIR models, even pathogen with low spreading rate persists in scale-free networks because of the broadcasting ability of the hubs.