Intro to deterministic models

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Effective Degree Equations

References

We will develop a system of differential equations which predicts disease spread by tracking the numbers of partnerships involving individuals of various statuses.

These have been developed by [1, 2, 3, 4] among many others.

Transition rates

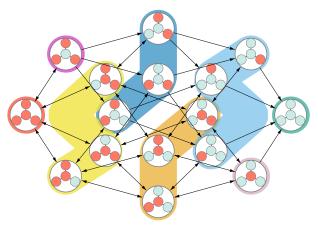
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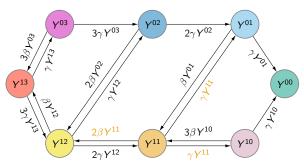
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$$\dot{S} = -\beta[SI] + \gamma I$$
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Can you see the problem?

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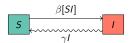
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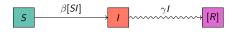
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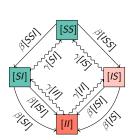
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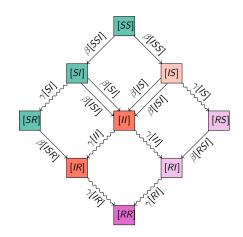
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- ► The fourth term represents the infected node in an SI pair recovering.









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The equations are equivalent to the Kermack-McKendrick equations 4 D > 4 P > 4 E > 4 E > E

Appropriateness of $[SI] = \langle K \rangle SI$

What assumptions are we making when we set $[SI] = \langle K \rangle SI$?

- We're assuming that nodes are <u>not</u> preferentially infected by degree.
- ▶ We're assuming that neighbors of infected nodes are no more likely to be infected than any other node.

When are these assumptions appropriate?

- Same degree, annealed network. Partnerships have zero duration.
- Large very similar degrees, transmission probability per edge very low, and low clustering.
- ▶ As a general rule if the disease will never transmit across the same partnership twice, we can use models that ignore partnership duration.

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▶ Set π_I to be the probability that a random stub in the population belongs to an infected node.

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$$\begin{split} \dot{S}_k &= -\beta k S_k \pi_I \\ \dot{I}_k &= \beta k S_k \pi_I - \gamma I_k \\ \dot{R}_k &= \gamma I_k \\ \pi_I &= \sum_{l=1}^M \ell[I_\ell] \left/ \sum_{l=1}^M \ell N_\ell \right. \end{split}$$

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 - So

$$\mathcal{R}_{0} = \sum_{k} \frac{kP(k)}{\langle K \rangle} k \frac{\beta}{\gamma} = \frac{\beta}{\gamma} \frac{\langle K^{2} \rangle}{\langle K \rangle}$$

Scale-free networks

 Many measurements of sexual partnership degree distribution suggests that it scales like

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- ▶ But if $\langle K^2 \rangle$ is finite, then there is an epidemic threshold.

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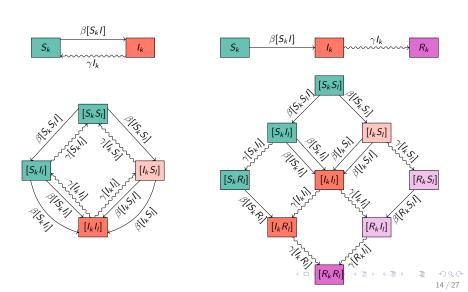
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- So susceptible high degree nodes tend to have more infected neighbors.
- ▶ We expect to see islands of infection surrounding high degree nodes. Eventually the disease spreads to other high degree nodes. So it can persist even if the naive estimate has $\mathcal{R}_0 < 1$.

An improved heterogeneous degree model

Use S_k , I_k , and R_k to denote the proportion of the population that is in each state and has degree k: $\sum_k S_k + I_k + R_k = 1$.



Improved closure

We close this with:

$$[AS_kB] = \frac{k-1}{k} \frac{[AS_k][S_kB]}{S_k}$$

This assumes that statuses of two neighbors of a susceptible node are independent.

This is dubious when

- There is significant clustering.
- A node has transmitted to its neighbors and then recovered
 SIS.

$$\begin{split} [\dot{S_k}]_s &= \gamma[I_k]_s - \beta[S_k I]_s, \\ [\dot{I_k}]_s &= \beta[S_k I]_s - \gamma[I_k]_s, \\ [\dot{S_k}I_l]_s &= \gamma([I_k I_l]_s - [S_k I_l]_s) + \beta([S_k S_l I]_s - [IS_k I_l]_s - [S_k I_l]_s), \\ [\dot{S_k}\dot{S_l}]_s &= \gamma([S_k I_l]_s + [I_k S_l]_s) - \beta([S_k S_l I]_s + [IS_k S_l]_s) \\ [\dot{I_k}\dot{I_l}]_s &= \beta([S_k I_l]_s + [I_k S_l]_s) - 2\gamma[I_k I_l]_s + \beta([IS_k I_l]_s + [I_k S_l I]_s). \end{split}$$

SIS

$$\begin{split} [S_{k}]_{s} &= \gamma[I_{k}]_{s} - \beta[S_{k}I]_{s}, \\ [I_{k}]_{s} &= \beta[S_{k}I]_{s} - \gamma[I_{k}]_{s}, \\ [S_{k}I_{l}]_{s} &= \gamma([I_{k}I_{l}]_{s} - [S_{k}I_{l}]_{s}) + \beta([S_{k}S_{l}I]_{s} - [IS_{k}I_{l}]_{s} - [S_{k}I_{l}]_{s}), \\ [S_{k}S_{l}]_{s} &= \gamma([S_{k}I_{l}]_{s} + [I_{k}S_{l}]_{s}) - \beta([S_{k}S_{l}I]_{s} + [IS_{k}S_{l}]_{s}) \\ [I_{k}I_{l}]_{s} &= \beta([S_{k}I_{l}]_{s} + [I_{k}S_{l}]_{s}) - 2\gamma[I_{k}I_{l}]_{s} + \beta([IS_{k}I_{l}]_{s} + [I_{k}S_{l}I]_{s}). \end{split}$$

SIR

$$[S_{k}]_{s} = -\beta[S_{k}I]_{s},$$

$$[I_{k}]_{s} = \beta[S_{k}I]_{s} - \gamma[I_{k}]_{s},$$

$$[R_{k}]_{s} = \gamma[I_{k}]_{s},$$

$$[S_{k}I_{l}]_{s} = -\gamma[S_{k}I_{l}]_{s} + \beta([S_{k}S_{l}I]_{s} - [IS_{k}I_{l}]_{s} - [S_{k}I_{l}]_{s}),$$

$$[S_{k}S_{l}]_{s} = -\beta([S_{k}S_{l}I]_{s} + [IS_{k}S_{l}]_{s}).$$

Further simplifications are possible

We can further simplify the model if we assume that the probability a node's neighbor is susceptible is independent of the node's degree. (fails if there are degree correlations).

Pairwise Equations

Effective Degree Equations

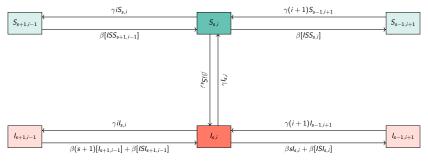
References

Effective Degree Equations <u>aka</u> Approximate Master Equations

Developed by [6, 7, 8, 9].

- ► The basic idea is that we can choose a different fundamental unit to study.
- ► Each node is the center of a "star", and its risk of infection depends on how many infected neighbors it has.
- ▶ We use $S_{s,i}$ to denote the proportion of the population that is susceptible and has s susceptible and i infected neighbors. Similarly $I_{s,i}$.
- ▶ We can ignore recovered neighbors (hence "effective degree")

SIS model



A term like $[ISS_{s+1,i-1}]$ represents (1/N) times) the number of paths that exist from an infected node to a susceptible node to a susceptible node having s+1 susceptible partners and i-1 infected partners.

We make the closures

$$[ISS_{s,i}] = \frac{[ISS]}{[SS]} sS_{s,i} \qquad [ISI_{s,i}] = \frac{[ISI]}{[SI]} sI_{s,i}$$

Which correspond to assuming that the susceptible neighbors of susceptible nodes are interchangeable and the susceptible neighbors of infected nodes are interchangeable.

SIS effective degree model

We get

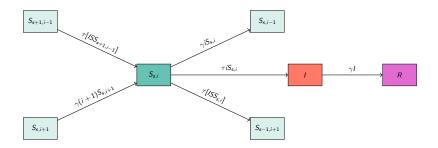
$$\begin{split} \dot{S}_{s,i} &= -\tau i S_{s,i} + \gamma I_{s,i} + \gamma \left((i+1) S_{s-1,i+1} - i S_{s,i} \right) \\ &+ \tau \frac{[ISS]}{[SS]} \left((s+1) S_{s+1,i-1} - s S_{s,i} \right), \\ \dot{I}_{s,i} &= \tau i S_{s,i} - \gamma I_{s,i} + \gamma \left((i+1) I_{s-1,i+1} - i I_{s,i} \right) \\ &+ \tau \left(\frac{[ISI]}{[SI]} + 1 \right) \left((s+1) I_{s+1,i-1} - s I_{s,i} \right), \end{split}$$

$$S = \sum_{s,i} S_{s,i}, \qquad I = \sum_{s,i} I_{s,i},$$

with

$$[SS] = \sum_{s,i} sS_{s,i}, \qquad [SI] = \sum_{s,i} iS_{s,i},$$
 $[ISS] = \sum_{s,i} isS_{s,i}, \qquad [ISI] = \sum_{s,i} i(i-1)S_{s,i}.$

SIR effective degree model



SIR effective degree equations

$$\begin{split} \dot{S}_{s,i} &= -\tau i S_{s,i} + \gamma ((i+1) S_{s,i+1} - i S_{s,i}) \\ &+ \tau \frac{[ISS]}{[SS]} [(s+1) S_{s+1,i-1} - s S_{s,i}] \\ \dot{R} &= \gamma I, \quad S = \sum_{s,i} S_{s,i}, \quad I = N - S - R, \end{split}$$

Pairwise Equations

Effective Degree Equations

References

References I

[1] M. J. Keeling.

The effects of local spatial structure on epidemiological invasions.

Proceedings of the Royal Society of London. Series B: Biological Sciences, 266(1421):859-867, 1999.

[2] M. J. Keeling and K. T. D. Eames.

Networks and epidemic models.

Journal of the Royal Society Interface, 2(4):295-307, 2005.

[3] R. Pastor-Satorras and A. Vespignani.

Epidemic dynamics and endemic states in complex networks.

Physical Review E, 63(6):066117, 2001.

[4] T. House and M.J. Keeling.

Insights from unifying modern approximations to infections on networks. Journal of the Royal Society Interface, 8(54):67–73, 2011.

[5] S. Chatterjee and R. Durrett.

Contact processes on random graphs with power law degree distributions have critical value 0. The Annals of Probability, 37(6):2332–2356, 2009.

[6] J. Lindquist, J. Ma, P. van den Driessche, and F.H. Willeboordse. Effective degree network disease models.

Journal of Mathematical Biology, 62(2):143-164, 2011.

7] F. Ball and P. Neal.

Network epidemic models with two levels of mixing.

Mathematical Biology, 212(1):69-87, 2008.

[8] J. P. Gleeson.

High-accuracy approximation of binary-state dynamics on networks.

Physical Review Letters, 107(6):068701, 2011.

References II

[9] James P Gleeson.

Binary-state dynamics on complex networks: pair approximation and beyond. Physical Review X, 3(2):021004, 2013.