

L4, Modeling using networks and other heterogeneities

Tom Britton

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Different heterogeneities

In reality individuals behave differently both

- in terms of susceptibility and infectivity given that a "contact" takes place, and
- in terms of whom they have contact with

Previous results assumed individuals have equal susceptibility and infectivity AND that they "mix" uniformly

Question: Does this simplification make results useless?

Qualitative answer: The more infectious a disease is the less "problematic" is this simplification

⇒ ok for measles (except immunity) but not "valid" for STDs

Individual heterogeneities

In several situations individuals can be grouped into different *types* of individual

Different types may differ in terms of susceptibility + infectivity

Examples: infants – school children – adults, male – females, partially immune (vaccinated) – fully susceptible

Natural extension: **Multitype epidemic model**

- Let $\pi_j =$ community fraction of type j , $j = 1, \dots, k$
- Suppose an i -individual infects a given type- j individual at rate β_{ij}/n and recovers at rate $1/\nu$

Exercise 21 How many j -individuals does an i -individual on average infect when everyone is susceptible?

Multitype epidemics

Answer: $n_j \frac{\beta_{ij}}{n} \nu$ (=numbers at risk * infection rate * average length of infectious period) = $\beta_{ij} \nu \pi_j$

The matrix with these elements defines the expected number of new infections of various types caused by individuals of various types:

$$M = (m_{ij}) = (\beta_{ij} \nu \pi_j)$$

Often referred to as *next generation matrix*

R_0 = largest eigenvalue to this matrix (same interpretations as before)

In general no explicit expression, but if $\beta_{ij} = \alpha_i \gamma_j$ ("separable mixing") then $R_0 = \sum_i \alpha_i \gamma_i \nu \pi_i$

Exercise 22 Interpret α_i and γ_j

Exercise 23 Compute R_0 for the case: $\pi_1 = \pi_2 = 0.5$, $\nu = 1$ and $\beta_{11} = 1$, $\beta_{12} = \beta_{21} = 2$ and $\beta_{22} = 4$ which obeys separable mixing assumption. Is the answer surprising?

Previous heterogeneity mainly for "individual heterogeneities"

Equally (or more!) important: which individuals people have contact with

For many diseases (influenza, childhood disease, common cold) transmission within *households* is high

⇒ Important with models allowing for higher transmission within households

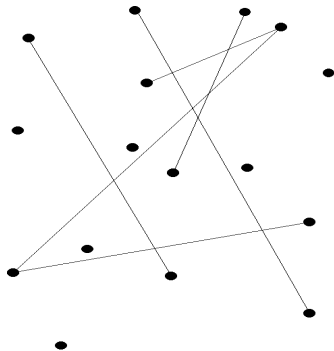
Households are small ⇒ randomness important

More about household epidemic models later in module

Networks

For other diseases (e.g. STDs) individuals are not connected in small sub-units

Common representation of social structure: network/graph **nodes** (individuals) and **edges** (“friendship”)



Social structure only partly known: modelled using random graph/network **with structure**

Some (potentially observed) local structures

- $D = \#$ friends of randomly selected individual (*degree distribution*)
- $c = P(\text{two friends of an individual are friends})$ (*clustering*)
- $\rho = \text{correlation of degrees in a randomly selected friendship}$ (*degree correlation*)

Other features unobserved \implies Random network

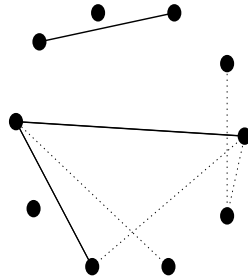
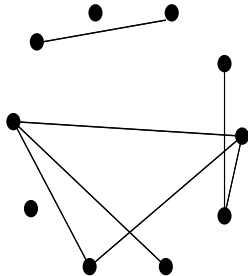
Also spreading is uncertain \implies stochastic epidemic model "on" the (random) network

Simplest model: an infected person infects each susceptible friend independently with prob p and then recovers (one index case)

Effect on graph: thinning – each **edge** is removed with prob $1 - p$

Interpretation: remaining edges reflect "potential spreading"

Graph and its thinned version



Those connected to index case make up final outbreak

Case study: Network epidemic model with arbitrary degree distribution $\{p_k\}$

- Social structure: Individuals have degree distribution $D \sim \{p_k\}$ and "friends" are chosen completely at random
- Epidemic model: each susc. friend is infected with prob p
- 1 randomly selected index case, $n - 1$ susceptibles

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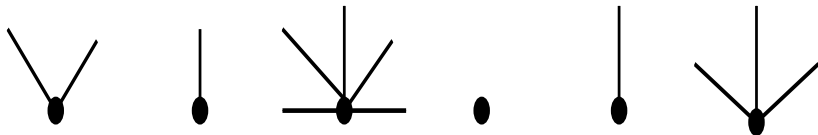
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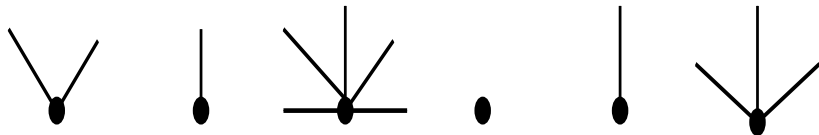
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What is the degree distribution of infectives (during early stages)?



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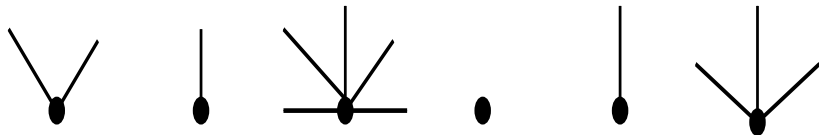
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Answer: $\{\tilde{p}_k; k \geq 1\}$, where $\tilde{p}_k = \text{const} \cdot kp_k = kp_k/E(D)$

The basic reproduction number

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Answer: $\{\tilde{p}_k; k \geq 1\}$, where $\tilde{p}_k = \text{const} \cdot kp_k = kp_k/E(D)$

$$\implies R_0 = p(E(\tilde{D}) - 1) = \dots = p \left(E(D) + \frac{V(D) - E(D)}{E(D)} \right)$$

Empirical networks have heavy-tailed degree distributions ...

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a) Randomly chosen individuals

$$\implies R_v = p(1 - v)(E(\tilde{D}) - 1) = (1 - v)R_0$$

$$\implies \text{if } v \geq 1 - 1/R_0 \text{ then } R_v \leq 1 \implies \text{no outbreak!}$$

- Critical vaccination coverage: $v_c = 1 - 1/R_0$

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- Critical vaccination coverage: $v_c = 1 - 1/R_0$
- **Problem:** If R_0 large (e.g. due to large $V(D)$), $v_c \approx 1 \implies$ impossible!

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Vaccinees will have degree distribution $\{\tilde{p}_k\}$ rather than $\{p_k\}$

\implies much more efficient

Proportion infected as function of v , $D \sim \text{Poisson}$

$$\left. \begin{array}{l} D \sim P_0(6) \\ p = \frac{1}{2} \end{array} \right\} \Rightarrow R_0 = 3$$

GRAPHS, EPIDEMICS AND VACCINATION STRATEGIES

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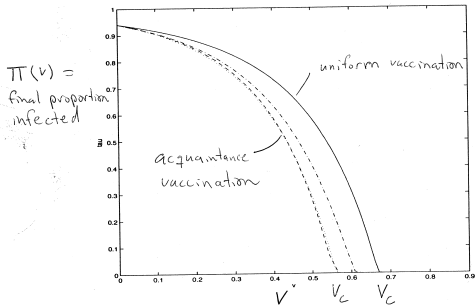


FIGURE 2. Final proportion infected τ as a function of the vaccination coverage v for four vaccination strategies: uni-

Proportion infected as function of v , $D \sim$ heavy-tailed

$$D \sim \text{Heavy tail } (E(D)=6)$$
$$p = 0.5$$

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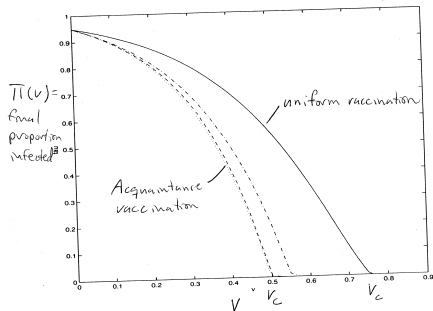


FIGURE 3. Final proportion infected as a function of the vaccination coverage for four vaccination strategies: uniform (—), acquaintance (···), E1 (---) and E2 (- · - · -). The degree distribution is heavy-tailed ($p_d \propto d^{-3.5}$) with mean

Main conclusion:

- Not only mean number of partners but also variance important!
- Core-groups play important roll
- Large variance of degree distribution imply large R_0 (but not necessarily large outbreak)

Important extensions: time-dynamic network, clustering, varying/dependent transmission probabilities, degree correlation

Exercise 24. Suppose the mean degree equals $E(D) = 3$ and the transmission probability per relationship equals $p = 0.25$. Compute R_0 and v_c (assuming uniform vaccination) assuming the standard deviation $\sqrt{V(D)}$ of number of partners equal 0, 1, 3, 10.

A model for an STI in a heterosexual community

The model (Britton, Nordvik and Liljeros, 2007)

- $D = \#$ sex-partners (e.g. during a year)
- $p = P(\text{transmission in a relationship})$

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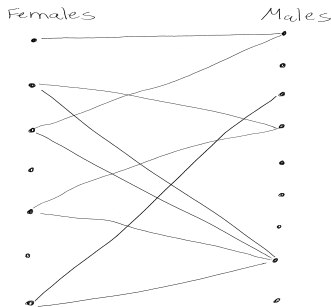
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It can be shown that

$$R_0 = \sqrt{p_f \left(E(D_f) + \frac{V(D_f) - E(D_f)}{E(D_f)} \right)} \\ \times \sqrt{p_m \left(E(D_m) + \frac{V(D_m) - E(D_m)}{E(D_m)} \right)}$$

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A heavy-tailed degree distribution makes R_0 large.

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Similar to before:

A heavy-tailed degree distribution makes R_0 large. \implies

promiscuous people (super-spreaders) play an important role

However:

- $P(\text{transmission})$ depends on # sex-acts in relationship

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- Promiscuous individuals tend to have fewer sex-acts *per partner*
- This should reduce R_0 !

Extended model: short and long term relationships

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⇒ two types of edges (with different trans prob)

New (complicated) expression for R_0

The effect of different transmission probabilities depends on calibration

Data:

- (Anonymous) study of sexual habits in Gotland
- ≈ 800 people (17-28 yrs)
- Among other things: How many sex-partners during last year and how many sex-acts in each relationship

Calibration using survey on sexual habits

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$P(\text{transmission}|p)$ for short/long relationship estimated as cohort mean of:

$$P(\text{transmission}) = 1 - (1 - p)^{\# \text{ sex-acts}}, \quad p = \text{per sex-act trans prob}$$

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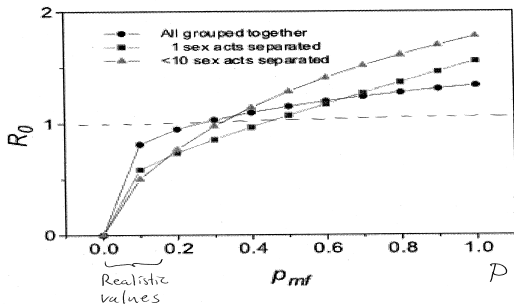
R_0 fitted to data and computed as a function of p : for one type of relationship, and two separations of short vs long

R_0 as function of p (fitted to Gotland data)

R_0 as function of $p = P(\text{transmission per contact})$

$P_{\text{long term}}$
 $P_{\text{short term}}$ } = mean values of $1 - (1-p)^{\# \text{sex-acts}}$

Assumption $P_m = P_f = P$



Conclusions:

1. Heavy-tailed degree distribution (promiscuity) increases R_0
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1. Heavy-tailed degree distribution (promiscuity) increases R_0
2. Acknowledging short and long-term relationships **reduces** this effect
3. Endemicity not possible (for realistic p 's) but maybe in sub-communities ...

Homogeneous vs Heterogeneous: qualitative results

We now illustrate a general conclusion with an example (from the network model defined earlier)

$$\text{Recall that } R_0 = p \left(E(D) + \frac{V(D) - E(D)}{E(D)} \right)$$

Consider **two networks** with the same mean degree $E(D) = 4$

$$\text{Network 1: } D \equiv 4, \text{ so } V(D) = 0 \text{ and } E(D) + \frac{V(D) - E(D)}{E(D)} = 3$$

$$\text{Network 2: } P(D = 1) = P(D = 7) = 0.5, \text{ so } V(D) = 9 \text{ and } E(D) + \frac{V(D) - E(D)}{E(D)} = 5.25$$

Infectious Disease 1: $p = 0.25$

$$\text{Network 1: } R_0 = 3/4 = 0.75, \text{ Network 2: } R_0 = 5.25/4 = 1.31$$

$\implies R_0$ larger for Network 2. Outbreak not possible in Network 1 but possible for Network 2

Infectious Disease 2: $p=0.75$

Network 1: $R_0 = 3 \cdot 0.75 = 2.25$,

Network 2: $R_0 = 5.25 \cdot 0.75 = 3.93$

$\implies R_0$ larger for Network 2. Outbreak possible in both networks

Which outbreak will be bigger?

Infectious Disease 2: $p=0.75$

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$\implies R_0$ larger for Network 2. Outbreak possible in both networks

Which outbreak will be bigger? Outbreak in Network 1 since in Network 2 individuals with degree 1 have a good chance of escaping!

General conclusion. (Starting with a homogeneous situation):

- Heterogenizing *always* increases R_0
- If original (=homogeneous case) R_0 is small, then outbreak will be bigger in heterogeneous case
- But if original R_0 is large, then heterogenizing makes outbreak **smaller!!!**