

# L5, Modeling using networks and other heterogeneities

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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  $\beta_{ij}/n$  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  $R_0 = \sum_i \alpha_i \gamma_i \nu \pi_i$

# Multitype epidemics

**Exercise 22** Interpret  $\alpha_i$  and  $\gamma_j$

**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?

# Household epidemics

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

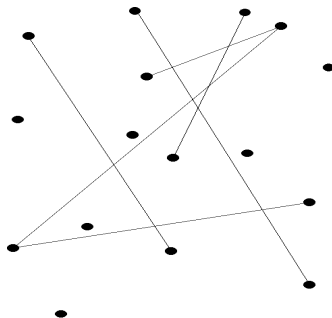
Households are small ⇒ randomness important

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”)



# Random networks

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*)
- $\rho =$  correlation of degrees in a randomly selected friendship (*degree correlation*)

Other features unobserved  $\implies$  Random network



## Stochastic epidemic model "on" network

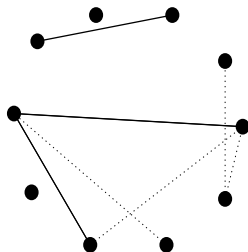
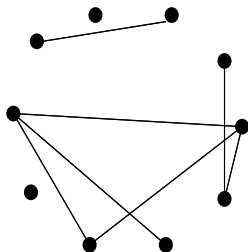
Also spreading is uncertain  $\implies$  stochastic epidemic model "on" the (random) network

**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

# The degree distribution and its effect on $R_0$

**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  $p$
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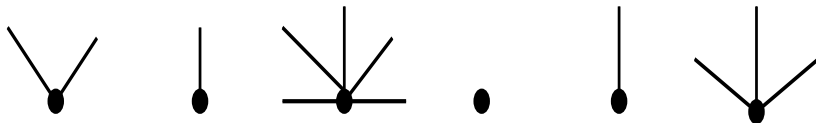
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# The basic reproduction number

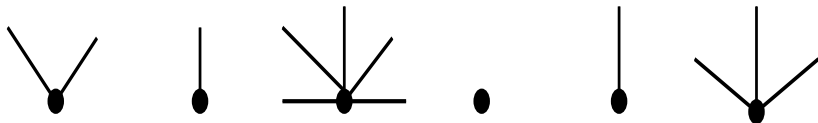
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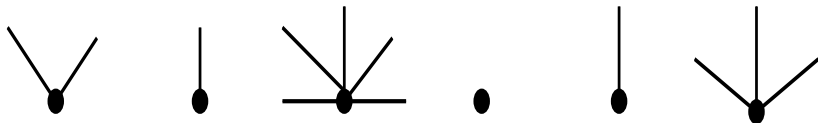
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$$\implies R_0 = p(E(\tilde{D}) - 1) = \dots = p \left( E(D) + \frac{V(D) - E(D)}{E(D)} \right)$$

Empirical networks have heavy-tailed degree distributions ...

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

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

- 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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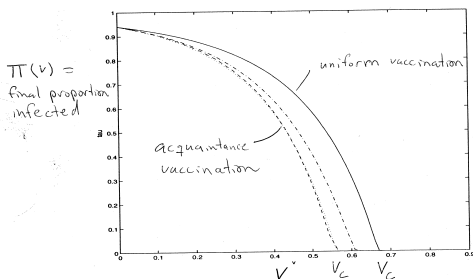


FIGURE 2. Final proportion infected  $\tau$  as a function of the vaccination coverage  $v$  for four vaccination strategies: uni-

# 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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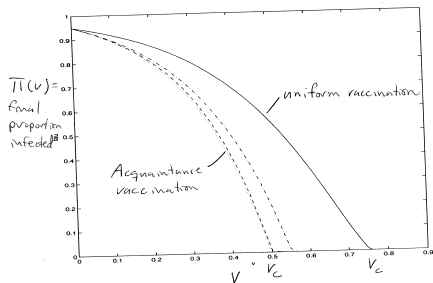


FIGURE 3. Final proportion infected as a function of the vaccination coverage for four vaccination strategies: uniform (—), acquaintance (···), E1 (---) and E2 (-·-·-). The degree distribution is heavy-tailed ( $p_d \propto d^{-3.5}$ ) with mean

# Network epidemics: summary and exercise

## 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)
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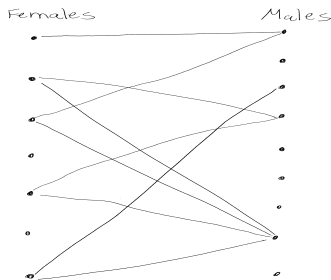
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It can be shown that

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

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Similar to before:

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

promiscuous people (super-spreaders) play an important role

# Improved analysis

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- $P(\text{transmission})$  depends on # sex-acts in relationship
- Promiscuous individuals tend to have fewer sex-acts *per partner*
- This should reduce  $R_0$ !

## Improved analysis: continued

**Extended model:** short and long term relationships



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**Extended model:** short and long term relationships

⇒ two types of edges (with different trans prob)

New (complicated) expression for  $R_0$

The effect of different transmission probabilities depends on calibration

# Calibration using survey on sexual habits

## Data:

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

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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

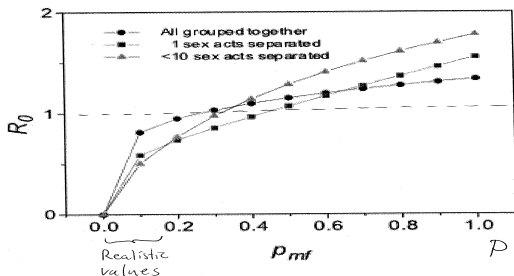
# $R_0$ as function of $p$ (fitted to Gotland data)

$R_0$  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  $R_0$
2. Acknowledging short and long-term relationships **reduces** this effect
3. Endemicity not possible (for realistic  $p$ 's)

## Conclusions:

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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  $E(D) = 4$

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

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

Consider **two diseases**: 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



## Homogeneous vs Heterogeneous: qualitative results, cont'd

Disease 2:  $p=0.75$

Network 1:  $R_0 = 3 \cdot 0.75 = 2.25$ , Network 2:

$R_0 = 5.25 \cdot 0.75 = 3.93$

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Which outbreak will be bigger?

## Homogeneous vs Heterogeneous: qualitative results, cont'd

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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!!!**