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L8, 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

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

Exercise 8.1 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 $R_0 = \sum_i \alpha_i \gamma_i \nu \pi_i$

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Multitype epidemics

Exercise 8.2 Interpret α_i and γ_j

Exercise 8.3 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 assumpion. Is the answer surprising?

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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

$\Longrightarrow$ Important with models allowing for higher transmission within households

Households are small $\Longrightarrow$ randomness important

More about household epidemic models later in module

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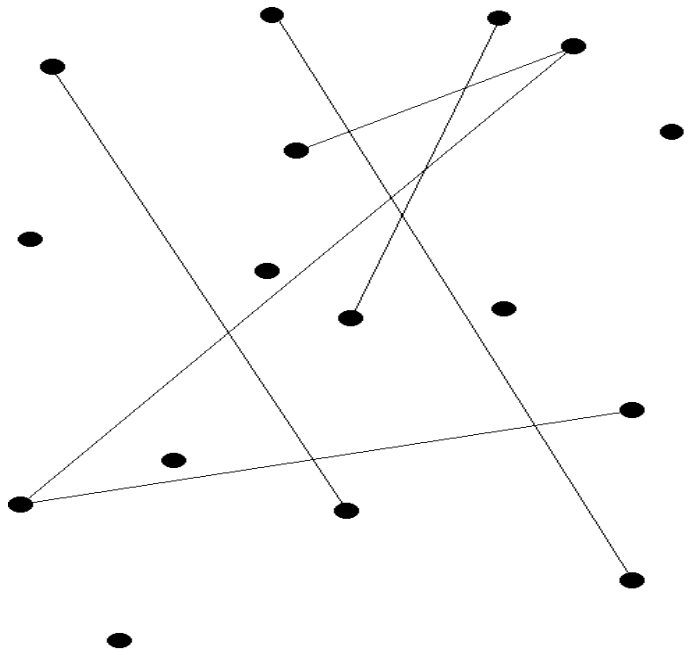
Networks

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")



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

Other features unobserved $\Longrightarrow$ Random network

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Stochastic epidemic model "on" network

Also spreading is uncertain $\Longrightarrow$ 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"

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Graph and its thinned version

Those connected to index case make up final outbreak

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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
- 1 randomly selected index case, $n-1$ susceptibles

What is R_0?

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- $R_0 = pE(D)$?

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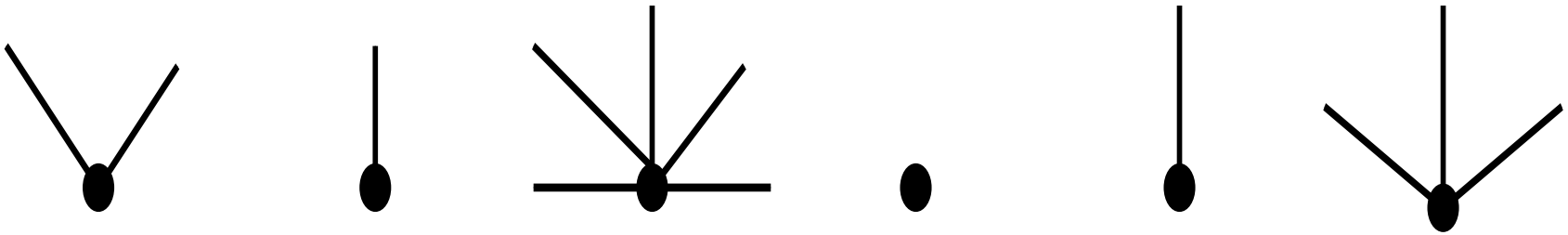
The basic reproduction number

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



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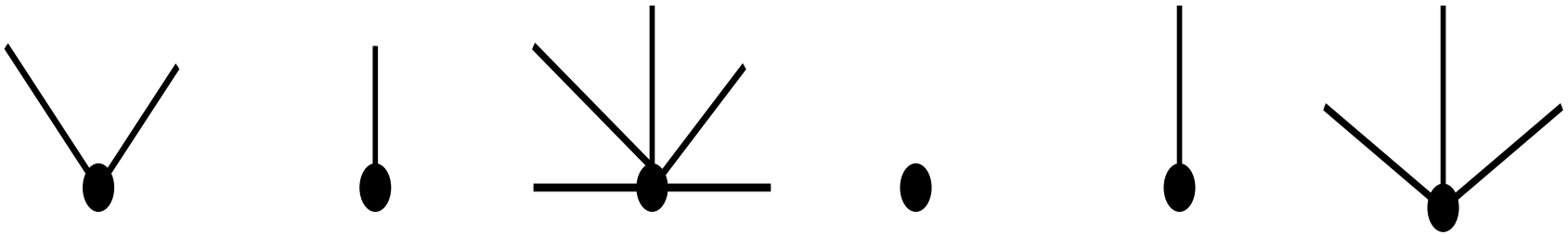

Answer: $\{\tilde{p}_k; k \geq 1\}$, where $\tilde{p}_k = const \cdot kp_k = kp_k/E(D)$

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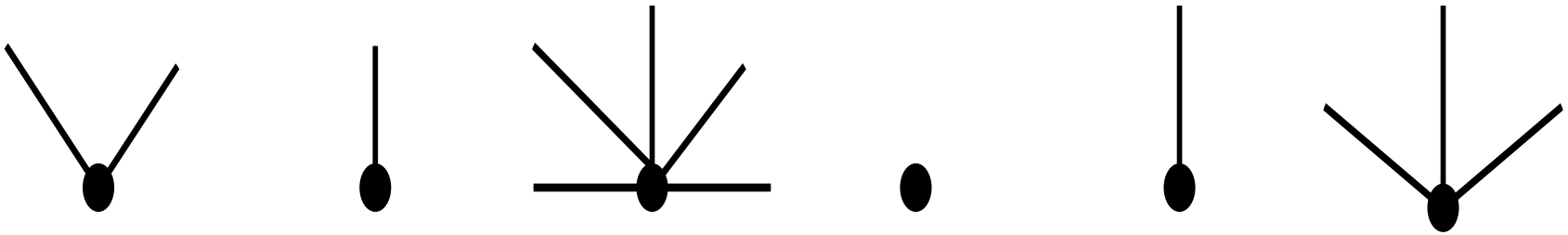

Answer: $\{\tilde{p}_k; k \geq 1\}$, where $\tilde{p}_k = const \cdot kp_k = kp_k/E(D)$

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

Empirical networks have heavy-tailed degree distributions ...

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Vaccination

Suppose a fraction v are vaccinated prior to outbreak

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Who are vaccinated?

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Vaccination

Suppose a fraction v are vaccinated prior to outbreak

Who are vaccinated?

a) Randomly chosen individuals

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

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

- 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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Vaccination, cont'd

Can we do better than selecting vaccinees randomly?

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Yes! Vaccinate social people

But social network usually not observed ...

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Vaccination, cont'd

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Yes! Vaccinate social people

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b) Acquaintance vaccination strategy

- Choose individuals at random
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Vaccinees will have degree distribution $\{\tilde{p}_k\}$ rather than $\{p_k\}$

$\Longrightarrow$ much more efficient

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

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

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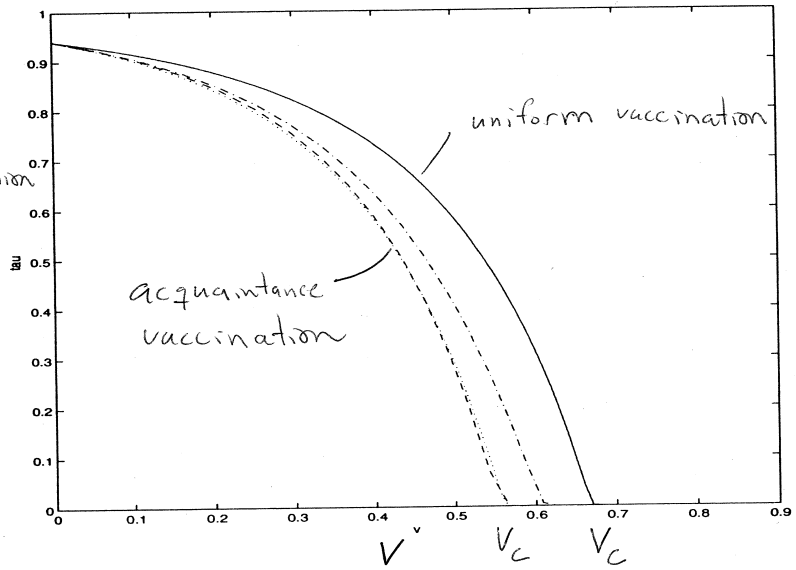

$\pi(v)$ = final proportion infected

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

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

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

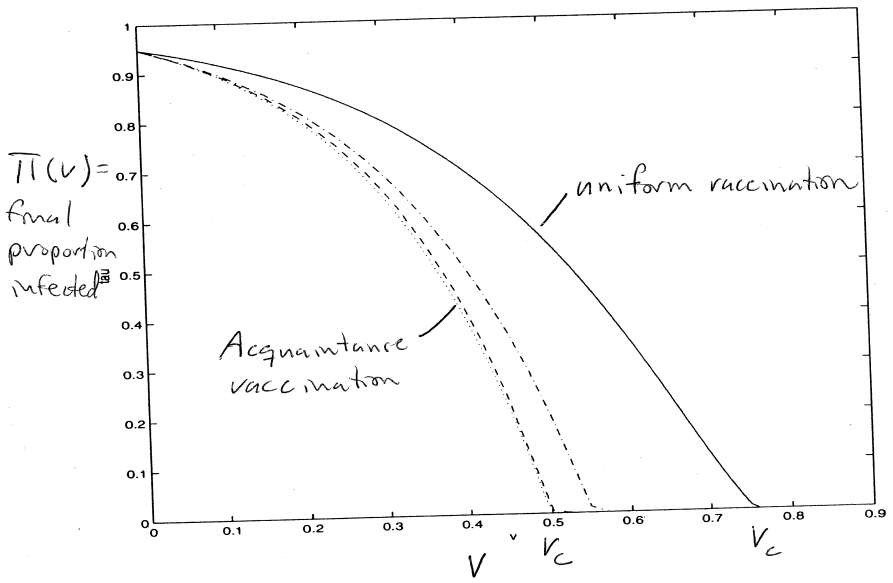

FIGURE 3. Final proportion infected as a function of the vaccination coverage for four vaccination strategies: uniform (—), acquaintance (· · ·), E1 (- - -) and E2 (— · — · —.) The degree distribution is heavy-tailed ($p_d \propto d^{-3.5}$) with mean

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 8.4. 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.

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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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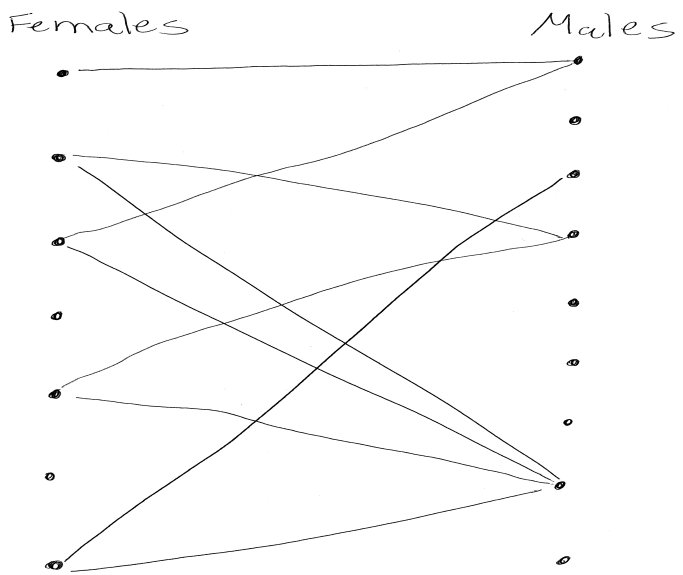

It can be shown that

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

Similar to before:

A heavy-tailed degree distribution makes R_0 large.

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

Similar to before:

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

promiscuous people (super-spreaders) play an important role

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Improved analysis

However:

- P(transmission) depends on # sex-acts in relationship

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However:

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

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Improved analysis: continued

Extended model: short and long term relationships

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Improved analysis: continued

Extended model: short and long term relationships

$\Longrightarrow$ 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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$P(\text{transmission}|p)$ 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

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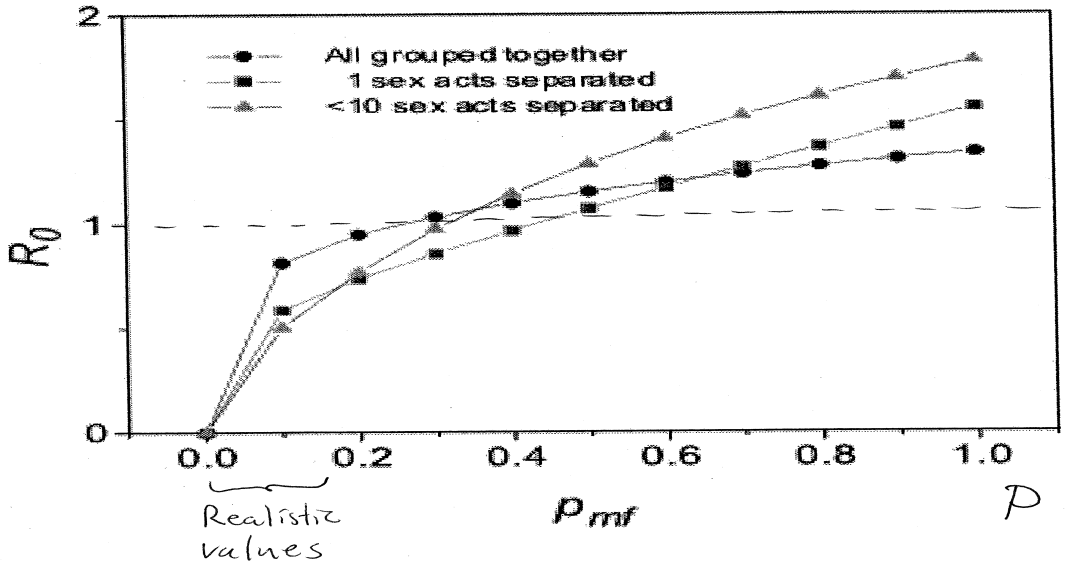
R_0 as function of p (fitted to Gotland data)

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

$P_{longterm}$, $P_{short\ term}$ } = 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:

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 ...

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Homogeneous vs Heterogeneous: qualitative results

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

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

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

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

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

Consider **two diseases**: Disease 1: $p = 0.25$

Network 1: $R_0 = 3/4 = 0.75$, Network 2: $R_0 = 5.25/4 = 1.31$

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

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Homogeneous vs Heterogeneous: qualitative results, cont'd

Disease 2: p=0.75

Network 1: $R_0 = 3 \cdot 0.75 = 2.25$, Network 2:
$R_0 = 5.25 \cdot 0.75 = 3.93$

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

Which outbreak will be bigger?

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Homogeneous vs Heterogeneous: qualitative results, cont'd

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$\Longrightarrow$ 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**!!!