

Stochastic epidemic models with population structure

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

Many different heterogeneities: individual susceptibility, infectivity and social activity (multitype epidemics), household structure (macro individuals), spatial structure, **social networks**

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

Multitype epidemics

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?

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

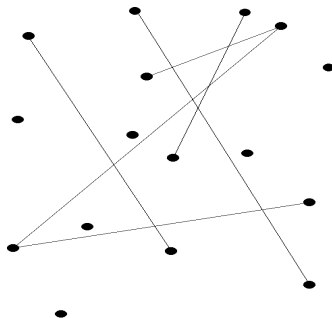
⇒ Important with models allowing for higher transmission within households

Households are small ⇒ randomness important

Networks

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

Common representation of social structure: network/graph with **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

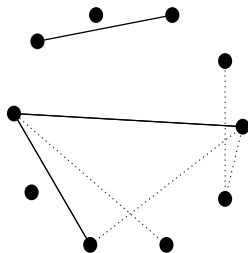
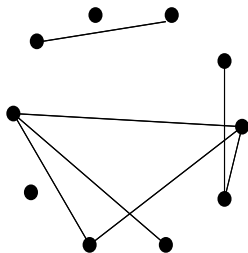
Also spreading is uncertain \implies stochastic epidemic model "on" the (random) network

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

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- $R_0 = p(E(D) - 1)$?

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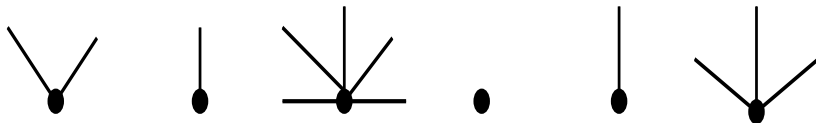
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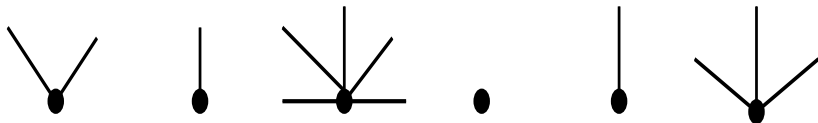
The basic reproduction number

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



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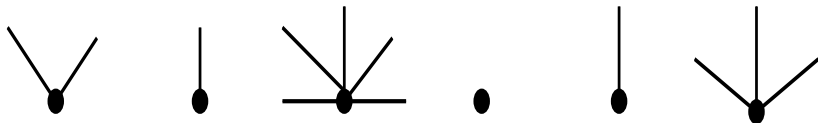
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Answer: $\{\tilde{p}_k; k \geq 1\}$, where $\tilde{p}_k = \text{const} \cdot kp_k = kp_k/E(D)$

The basic reproduction number

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



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 ...

Vaccination

Suppose a fraction v are vaccinated prior to outbreak

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Who are vaccinated?

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Who are vaccinated?

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!

Vaccination, cont'd

Can we do better than selecting vaccinees randomly?

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- Choose individuals at random

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

Britton, Janson & Martin-Löf (2007)

⇒ much more efficient

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

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

GRAPHS, EPIDEMICS AND VACCINATION STRATEGIES

17

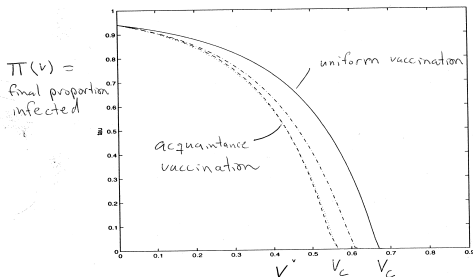


FIGURE 2. Final proportion infected τ as a function of the vaccination coverage v for four vaccination strategies: uni-

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

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

18

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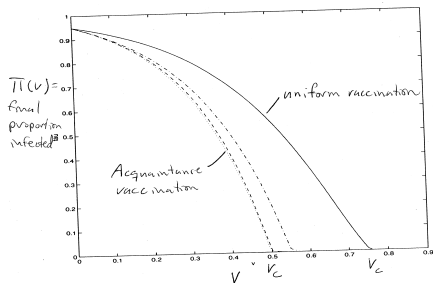


FIGURE 3. Final proportion infected as a function of the vaccination coverage for four vaccination strategies: uniform (—), acquaintance (···), E1 (---) and E2 (-·-·-). The degree distribution is heavy-tailed ($p_d \propto d^{-3.5}$) with mean

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.

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

Homogeneous vs Heterogeneous: qualitative results, cont'd

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?

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 deg 1 have a good chance to escape!

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!!!**

Individual prevention – Adaptive dynamics

Without preventive measures modelling predicts that some fraction $\tau(\theta)$ will get infected $\theta =$ model parameters

However, for severe diseases individuals will take precautions even without Public Health: isolation, distancing from infected, improved sanitation, using condom, ...

Empirical evidence (e.g. Ebola): spreading drops over time more than predicted by models, and final size often $\ll \tau(\theta)$

Adaptive dynamics: models where individuals change behaviour as an effect of the (epidemic) process

Our focus: Analyse the effect of social distancing from neighbouring infectives in an epidemic model on a social network

Network SIR Epidemic model with Social Distancing

Leung et al. (2018), Ball et al (2019), Ball & B (2021)

Consider a large fixed community of size n . Continuous time

Network model:

Configuration model: nodes have i.i.d. degrees $D \sim \{p_k\}$
($\mu := E(D)$) and edge-stubs are connected pairwise at random.

N.B.: network of friendships is static in absence of epidemic!

Transmission model (SIR): infectious individuals transmit to each susceptible neighbour at rate λ , and infectious individuals recover and become immune at rate γ

Social distancing: Susceptibles having infectious neighbours ...
... *rewires* such edges (to a uniformly chosen individual) at rate $\omega\alpha$
... *drops* such edges at rate $\omega(1 - \alpha)$

Comments on model

Model parameters: λ (=transmission rate), γ (=recovery rate), ω (=dropping/rewiring rate), $\alpha = P(\text{rewiring})$, and D degree distribution ($\mu = E(D)$)

Simplifying assumptions: No latent period, constant infectivity during infectious period, Markov assumption, ...

The case $\omega = 0$: well understood (e.g. Ball and others)

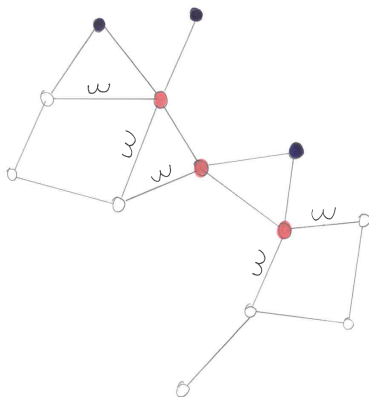
Dropping model ($\alpha = 0$) quite hard to analyse,
General model ($\alpha > 0$) very hard to analyse

Complication reason: the probability to get infected from neighbours now changes over course of epidemic

Easy result: Rewiring/dropping is rational from individual perspective: the probability to get infected *decreases* with rate at which (s)he drops/rewires!

Illustration of dropping/rewiring

Rewiring/Dropping possibilities



- = Susceptible
- = Infective
- = Recovered (=immune)

Beginning of epidemic

In beginning of epidemic (when fraction infected still small) the model can be approximated by a branching process

Rewiring or dropping doesn't matter (so α irrelevant): during early stages all rewirings are to susceptibles and have no effect

B-P: An individual who gets infected during early stages has size-biased degree distr $\tilde{D} \sim \{kp_k/\mu\}$ (where $\mu = E(D)$)

Its infector is infected, all other $\tilde{D} - 1$ are susceptible, \implies

$$R_0 = E(\tilde{D} - 1)P(\text{infect neighbour}) = \left(\frac{E(D^2)}{E(D)} - 1 \right) \frac{\lambda}{\lambda + \gamma + \omega}$$

So R_0 **increases** in λ and **decreases** γ and ω (as expected)

No major outbreaks for large ω , ($R_0 = R_0(\omega) < 1$ for large enough ω)

Final size τ : Dropping model ($\alpha = 0$)

Equivalent Def of Dropping model: infectious individuals "inform" each susceptible neighbour, **independently**, at rate ω (when informed, the connection is dropped)

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Related **Modified model:** infectious individual inform **all neighbours at the same time** (still having rate ω)

In Modified model all edges (with transmission potential) from infective are dropped at the same time

\implies Modified model is equivalent to model without rewiring: $\omega = 0$, and $\gamma \rightarrow \gamma + \omega$ for which results are available

$\implies \tau = \tau(\omega)$ decreases with ω (as expected)

Result for Dropping model: Initial phase as described above. Final LLN fraction infected τ same as model without dropping but increased recovery rate $\gamma + \omega$ (CLT different but available)

Final size τ : General model

Much harder to analyse

As a function of rewiring/dropping rate ω

Theorem: There exists degree distribution D and $(\lambda_0, \gamma_0, \alpha_0)$ for which $\tau = \tau(\omega)$ initially **increases**, i.e. $\tau(\omega) > \tau(0)$ for small ω
(\implies **Bigger** outbreak with social distancing!)

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Heuristic explanation:

- An individual with high degree will most likely get infected even if rewiring at small rate
 - After such rewiring events the individual may get connected to individuals who previously had low degree and would likely have avoided infection
- \implies reduced infection risk *more than* compensated by increased possibility to infect low degree individuals

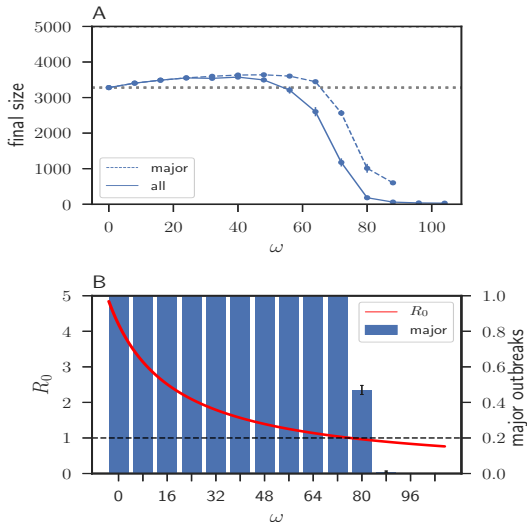
$\tau(\omega)$

$\tau(\omega)$ increasing seem to happen when:

- R_0 is large, and
- Many individuals with low degree, and a few with high

Result would be more pronounced if rewiring was focused towards low degree individuals (which is better from an individual's perspective)

Illustration $\tau(\omega)$: $p_k = c/(k+1), k = 0, \dots, 10, n = 5000$



Simulations and empirical networks

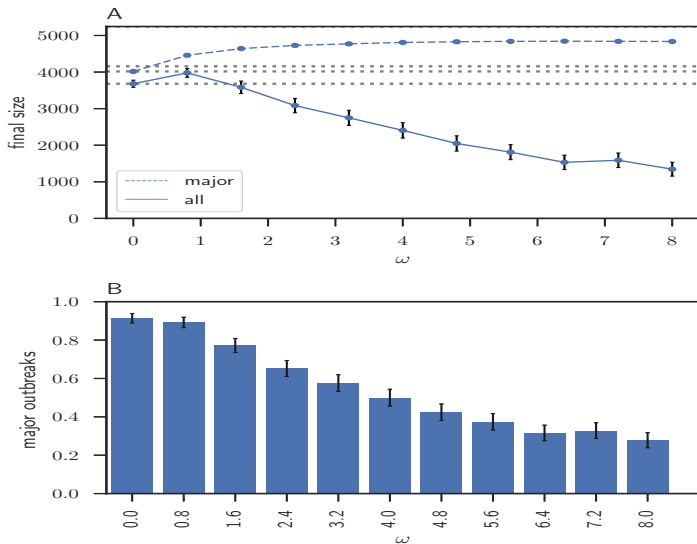
So $\tau(\omega)$ can increase in semi-realistic degree distributions

How about empirical networks?

We simulated our SIR epidemic model with rewiring on 10-15
empirical networks in the Stanford network data base

We observed $\tau(\omega)$ initially growing in 2 of them: Social circles on Facebook, and Collaboration network of ArXiv on general relativity

Empirical networks: Collaboration network



$\tau(\lambda)$: General model (Ball & Britton, 2021)

Final size $\tau = \tau(\lambda)$ as a function of transmission rate λ

Consider E-R network ($D \sim Po(\mu)$)

Fix $\mu > 1, \gamma, \omega$ and $\alpha > 0$.

Set $\lambda_c = (\gamma + \omega)/(\mu - 1)$ ($\implies R_0(\lambda_c) = 1$ and $\tau(\lambda_c) = 0$)

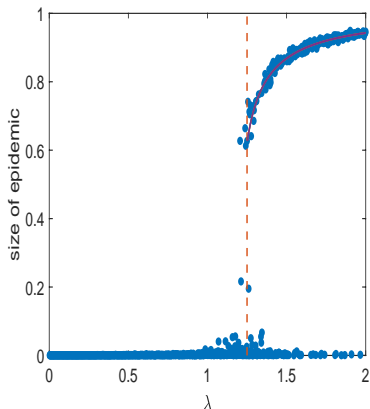
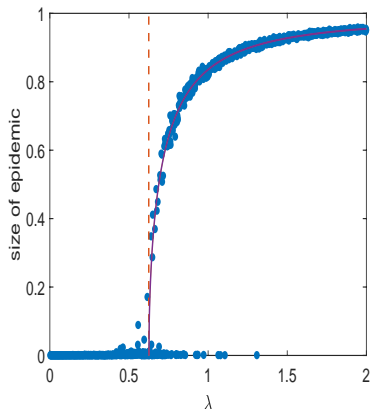
Theorem: If $\gamma < \omega(2\alpha - 1)$ and $\mu > 2\alpha\omega/(\omega(2\alpha - 1) - \gamma)$, then

$$\lim_{\lambda \downarrow \lambda_c} \tau(\lambda) > 0$$

Illustration $\tau(\lambda)$: $\mu = 5$, $\gamma = 1$, $\alpha = 1$, $n = 10000$

Left panel: $\omega = 1.5$ (continuous)

Right panel: $\omega = 4$ (discont)



Extensions and Open problems

Many solved as well as open problems for various extensions

- Considering different types of individual (Multitype epidemic)
- Including other preventive measures
- Including social structures: network epidemics, household epidemics, ...
- SEIR, SIRS, ...
- Dynamic population and dynamic behaviour
- Spatial aspects and mobility
- Virus evolution and immunity waning
- Estimation!!!
- ...