Stochastic epidemic models with population structure

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Juin, 2024
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 $\pi_j = \text{community fraction of type } j$, $j = 1, \ldots, k$
- 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 \( R_0 = \sum \alpha_i \gamma_i \nu \pi_i \)
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
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”)

![Network Diagram]
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)
- \( \rho = \text{correlation of degrees in a randomly selected friendship} \) (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
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 $R_0$?
The degree distribution and its effect on $R_0$

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- $R_0 = pE(D)$?
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What is the degree distribution of infectives (during early stages)?
The basic reproduction number

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

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

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

Empirical networks have heavy-tailed degree distributions ...
Vaccination

Suppose a fraction $\nu$ are vaccinated prior to outbreak
Vaccination

Suppose a fraction $v$ are vaccinated prior to outbreak

Who are vaccinated?
Vaccination

Suppose a fraction $\nu$ are vaccinated prior to outbreak

Who are vaccinated?

a) Randomly chosen individuals

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

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

Critical vaccination coverage: $\nu_c = 1 - 1/R_0$
Vaccination

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Who are vaccinated?

a) Randomly chosen individuals

$$ R_{\nu} = p(1 - \nu)(E(\tilde{D}) - 1) = (1 - \nu)R_0 $$

if $\nu \geq 1 - 1/R_0$ then $R_{\nu} \leq 1 \implies$ no outbreak!

- Critical vaccination coverage: $\nu_c = 1 - 1/R_0$

- **Problem**: If $R_0$ large (e.g. due to large $V(D)$), $\nu_c \approx 1 \implies$ impossible!
Vaccination, cont’d

Can we do better than selecting vaccinees randomly?
Vaccination, cont’d

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Yes! Vaccinate social people

But social network usually not observed ...
Vaccination, cont’d

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b) Acquaintance vaccination strategy
- Choose individuals at random
Vaccination, cont’d

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- Choose individuals at random
- Vaccinate one of their friends
Vaccination, cont’d

Can we do better than selecting vaccinees randomly?
Yes! Vaccinate social people

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b) Acquaintance vaccination strategy

- Choose individuals at random
- Vaccinate one of their friends

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

Britton, Janson & Martin-Löf (2007)

\[ \rightarrow \] much more efficient
Proportion infected as function of \( \nu \), \( D \sim \text{Poisson} \)

\[
D \sim P_0(6), \quad P = \frac{1}{2} \Rightarrow R_0 = 3
\]

**Figure 2.** Final proportion infected \( \tau \) as a function of the vaccination coverage \( \nu \) for four vaccination strategies: uniform vaccination and acquaintance vaccination.
Proportion infected as function of $v$, $D \sim$ heavy-tailed

\[ D \sim \text{Heavy tail} \quad (E(D) = 6) \]

\[ p = 0.5 \]

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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 ($p_d \propto d^{-2.5}$) 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 $\nu_c$ (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)

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 $E(D) + \frac{V(D) - E(D)}{E(D)} = 5.25$

Infectious Disease 1: $p = 0.25$

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

$\Rightarrow R_0$ 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: \( R_0 = 5.25 \cdot 0.75 = 3.93 \)

\( \Rightarrow R_0 \) larger for Network 2. Outbreak possible in both networks

Which outbreak will be bigger?
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? 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 $\theta = \text{model parameters}$

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 $\lambda$, and infectious individuals recover and become immune at rate $\gamma$

**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: $\lambda$ (=transmission rate), $\gamma$ (=recovery rate), $\omega$ (=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 $\alpha$ 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 $\lambda$ and decreases $\gamma$ and $\omega$ (as expected).

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

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Stochastic epidemic models with population structure
Final size \( \tau \): Dropping model \((\alpha = 0)\)

**Equivalent Def of Dropping model:** infectious individuals "inform" each susceptible neighbour, **independently**, at rate \( \omega \) (when informed, the connection is dropped)
Final size $\tau$: Dropping model ($\alpha = 0$)

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

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

In Modified model all edges (with transmission potential) from infective are dropped at the same time
Final size $\tau$: Dropping model ($\alpha = 0$)

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

Related Modified model: infectious individual inform all neighbours at the same time (still having rate $\omega$)

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

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

$\Rightarrow \tau = \tau(\omega)$ decreases with $\omega$ (as expected)

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

Much harder to analyse

As a function of rewiring/dropping rate $\omega$

**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 $\omega$

($\implies$ **Bigger** outbreak with social distancing!)
Final size $\tau$: General model

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As a function of rewiring/dropping rate $\omega$

**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 $\omega$ ($\implies$ **Bigger** outbreak with social distancing!)

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

A

B

Stochastic epidemic models with population structure
Final size $\tau = \tau(\lambda)$ as a function of transmission rate $\lambda$

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

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

Set $\lambda_c = (\gamma + \omega)/(\mu - 1)$ ($\iff R_0(\lambda_c) = 1$ 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!!!
- ...

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