# Networks, epidemics and vaccination: a review

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## 0. Epidemics on observable networks

Computerized age $\Longrightarrow$ data on large social networks

(Swedish) examples:

- Hospital data (relevant for MRSA): patient data
- Census data: ind. data on household, address and work
- Internet networks (dating sites, ...)

Networks are either static or dynamic

# Epidemic model on network

Define model as in uniform mixing populations

Example

1. Some pre-defined individuals are initially infectious

2. While individual $i$ is infectious (s)he spreads the disease to each friend independently at rate $\lambda$
(or at rates $\lambda w_{ij}$ in weighted network, perhaps added by "external" infectious force $\theta$)

3. Latent and infectious periods are i.i.d. $\sim F$ and $\sim G$ (or more general if heterogeneous population)

# What to do with model?

Probabilistic analysis? No

Statistical inference? Yes

**Additional data**: individual disease information

infected/not infected, show-of-symptom times, ...

**How to analyse data?**

Bayesian methods treating unobserved quantities (e.g. infection and removal times) as latent variables

**Output from analysis**:

Information about $\lambda$, $F$, $G$ and other model parameters, but also potential transmission routes, ...

# However

Many social networks are not observed!

$\Longrightarrow$ These can be analysed using random graphs (with some pre-defined properties) ...

# 1. Random graphs

$n$ nodes = individuals ($n$ assumed large)

Edges between nodes reflect social link: "friendship"

Simple undirected graph (no self-loops or multiple edges)

Simplest example: Erdös-Rényi: Edges between individuals are present independently with probability $\lambda/n$.

# Important properties of random graphs

1. **Degree distribution**: distribution of # friends $X$

How many friends do individuals have?

Erdös-Rényi: $X \sim Bin(n, \lambda/n) \approx Po(\lambda)$

2. **Clustering index**: $C$

Are friends of an individual friends themselves?

**Definition**: $C = \frac{3 \times \#\text{ triangles}}{\#\text{ connected triplets}}$

or corresponding expected proportion:

$P$(two friends of an individual are friends)

Erdös-Rényi: $C \approx \lambda/n \to 0$

3. **Assortative mixing**: Degree correlation $r$

Are friends of social individuals (anti-)social?

**Definition**:

$$r = \frac{1}{\text{\# friendships}} \sum_{i \sim j} (x_i - E(X))(x_j - E(X))$$

$r$ positive: assortative, $r$ negative: disassortative

Erdös-Rényi: $r \approx 0$

## Further generalisations not treated today

different types of individual

more structure on graph (e.g. households)

time dynamic

...

## Empirical social graphs/networks:

**Degree distribution**: heavy-tailed (e.g. power law)

**Clustering index**: C>0

**Degree correlation**: $r > 0$ (most often in social networks)

## General (unsolved) goal:

Given $X \sim F$, C and $r$, construct a random graph having these as degree distribution, clustering index and degree correlation $r$

In general not possible exactly, but maybe asymptotically?

**An example:**

$F$ arbitrary (finite second moment), $C = 0 = r$

Configuration model (Bollobás, e.g. 2001):

1. Draw $X_1, \ldots, X_n$ i.i.d from $F$ ($X_i = \#$ stubs from $i$)
2. If $\sum_i X_i$ odd redo.
3. Pair the stubs completely at random.
4. Remove all loops and merge multiple edges.

Resulting graph is simple. If $E(X) < \infty$ empirical degree distribution converges to $F$, i.e. a negligible fraction of edges are removed. (B,D,M-L-06)

# 2. Epidemic models

Short term outbreak

Given social graph, an infectious disease may spread on it

SIR: susceptible -> infectious -> removed (=immune)

## Model:

0. Initially, one randomly selected individual (the index case) externally infected. The rest are susceptible

1. An individual who gets infected becomes infectious for a duration $I$ (=infectious period) and is then removed.

2. During the infectious period an indivual infects his/her susceptible friends independently at rate $\lambda$.

The epidemic runs its course. Let $\mathcal{T}$ those ultimately infected and $T = |\mathcal{T}|$ be the final number infected.

$$\Longrightarrow p = P(\text{infect given susceptible}) = 1 - E(e^{-\lambda I})$$

If $I$ is constant then infections occur independently (This case is treated from now on!)

**Elegant observation** (Mollison?)

Thin the original graph by removing each edge with probability $1-p$

Let $\mathcal{C}$ be the connected component of the index case and $C = |\mathcal{C}|$

**Theorem**: $\mathcal{C} = \mathcal{T}$ and $C = T$

Why? An edge (friendship) will be used at most in one direction for transmission. Whether such a contact will result in transmission can be generated in advance.

**Important questions**

1. Given $F$, $C$ and $r$: Can a big outbreak occur?

Equiv: Is there a giant component in thinned graph?

2. (If yes on 1) What is the probability of a major outbreak and how big will it be?

Equivalently: How big is the giant component?

**Elegant observation**: Index case randomly selected

$\Longrightarrow P$(index belongs to giant) = relative size of giant

$P$(outbreak)=relative size of giant component = relative size of outbreak

Random graph theory: There is only one giant $O(n)$ component (B,J,R-07)

$P$(outbreak) easier to derive (using branching process theory)

**An example** (continued)
Main idea: During early stages of an epidemic in a large community, all friends of an infected (except the one (s)he was infected by!) will be susceptible

**Q**: What is degree distribution $\{\tilde{p}_k\}$ of infected during early stages?

**A**: $\tilde{p}_k \propto kp_k \quad (=kp_k/E(X))$

Given $\tilde{X} = k$ the infected will infect $Bin(k-1, p)$

$\Longrightarrow$ Off-spring distribution $Y \sim MixBin(\tilde{X} - 1, p)$

From theory for branching processes

a) If $E(Y) = R_0 = E(\tilde{X} - 1)p \leq 1$ (subcritical)

then br-pr will die out (minor epidemic) with prob 1

$R_0 = p \sum_k (k-1) k p_k / E(X) = p(E(X) - \frac{V(X) - E(X)}{E(X)})$

b) If $R_0 > 1$ br-pr takes off (major outbreak) with prob $1 - q$

where $q = P(\text{br-pr dies out})$ smallest positive solution to

$q = \sum_j P(\text{br-pr dies out}|j \text{ off-spring }) P(Y = j) = \sum_j q^j P(Y = j)$

$q$ solves $q = \phi(q)$ where $\phi(s) = E(s^Y)$

$1 - q$ is also size of major outbreak (C,H,b-A-03)

# 3. Vaccination

Suppose a vaccine giving 100% immunity is available

Suppose individuals are vaccinated prior to outbreak

**Q**: Who and how many should be vaccinated such that $P$(outbreak)=0? ("Herd immunity")

**Q'**: Given a specific vaccination strategy $v$, what is induced reproduction number $R_v$ (and $P$(outbreak) and size of outbreak if $R_v > 1$)?

Answer depends on how vaccinees are selected

Intuition: Better to vaccinate "social" individuals

Effect on graph: thinning of nodes (vaccinated nodes and edges connecting to them are removed)

## An example

Uniform vaccination: a proportion $v$ of randomly selected individuals are vaccinated

Effect on br-pr approximation:

a) Infectious individuals have same degree distribution $\tilde{X}$.

b) Given degree $k$ the individual will infect $Bin(k-1, p(1-v))$ individuals

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

$\Longrightarrow$ Critical vaccination coverage $v_c = 1 - 1/R_0$

same as "classical" $v_c$ (P-S, V-01)

If $R_v > 1$ $P$(outbreak) and outbreak size can also be determined using identical methods

## Another example

Acquaintance vaccination: Individuals are selected randomly. A randomly selected friend of each individual is vaccinated (if it isn't yet vaccinated), until a proportion $v$ are vaccinated.

This strategy is more effective because vaccinated individuals will have degree distribution $\tilde{X}$

Effect on br-pr approximation and final size:

Much harder problem (C,H,b-A-03 + B,J,M-L-07)

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