Generalized Contagion

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Outline

Generalized contagion model

Basic questions about contagion

- How many types of contagion are there?
- How can we categorize real-world contagions?
- Can we connect models of disease-like and social contagion?

Some (of many) issues

- Disease models assume independence of infectious events.
- Threshold models only involve proportions: $3/10 \equiv 30/100$.
- Threshold models ignore exact sequence of influences
- Threshold models assume immediate polling.
- Mean-field models neglect network structure
- Network effects only part of story: media, advertising, direct marketing.

Generalized model—ingredients

- Incorporate memory of a contagious element [1, 2]
- Population of N individuals, each in state S, I, or R.
- Each individual randomly contacts another at each time step.
- ϕ_t = fraction infected at time t
  = probability of contact with infected individual
- With probability p, contact with infective leads to an exposure.
- If exposed, individual receives a dose of size d drawn from distribution f. Otherwise $d = 0$.

Generalized model—ingredients

$\boxed{S \Rightarrow I}$

- Individuals 'remember' last T contacts:

$$D_{t,i} = \sum_{t'=t-T+1}^{t} d_i(t')$$

- Infection occurs if individual i's 'threshold' is exceeded:

$$D_{t,i} \geq d_i^*$$

- Threshold d_i^* drawn from arbitrary distribution g at $t = 0$.

Generalized model—ingredients

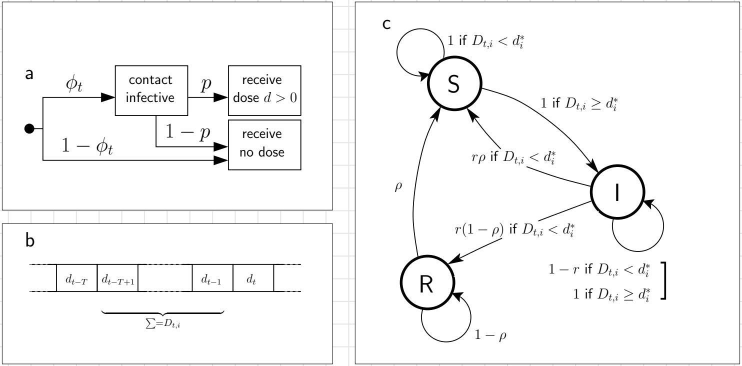
$\mathrm{I} \Rightarrow \mathrm{R}$

When $D_{t,i} < d_i^*$,
individual i recovers to state R with probability r.

$\mathrm{R} \Rightarrow \mathrm{S}$

Once in state R, individuals become susceptible again with probability ρ.

A visual explanation



Generalized model

Important quantities:

$$P_k = \int_0^{\infty} \mathrm{d}d^* \, g(d^*) P\left(\sum_{j=1}^{k} d_j \geq d^*\right) \text{ where } 1 \leq k \leq T.$$

P_k = Probability that the threshold of a randomly selected individual will be exceeded by k doses.

e.g.,
P_1 = Probability that one dose will exceed the threshold of a random individual
= Fraction of most vulnerable individuals.

Generalized model—heterogeneity, $r = 1$

Fixed point equation:

$$\phi^* = \sum_{k=1}^{T} \binom{T}{k} (p\phi^*)^k (1 - p\phi^*)^{T-k} \underline{P_k}$$

Expand around $\phi^* = 0$ to find Spread from single seed if

$$pP_1 T \geq 1$$

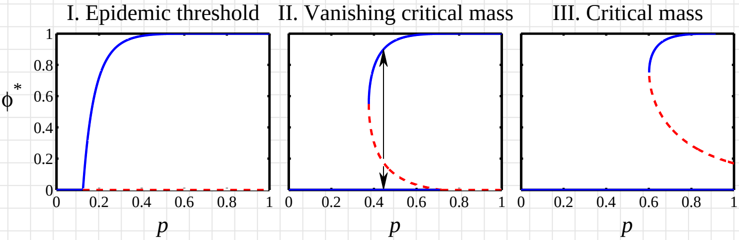
$$\Rightarrow p_c = 1/(TP_1)$$

Heterogeneous case

Example configuration:

- Dose sizes are lognormally distributed with mean 1 and variance 0.433.
- Memory span: $T = 10$.
- Thresholds are uniformly set at
  1. $d_* = 0.5$
  2. $d_* = 1.6$
  3. $d_* = 3$
- Spread of dose sizes matters, details are not important.

Heterogeneous case—Three universal classes



- Epidemic threshold: $P_1 > P_2/2$, $p_c = 1/(TP_1) < 1$
- Vanishing critical mass: $P_1 < P_2/2$, $p_c = 1/(TP_1) < 1$
- Pure critical mass: $P_1 < P_2/2$, $p_c = 1/(TP_1) > 1$

Calculations—Fixed points for $r < 1$, $d^* = 2$, and $T = 3$

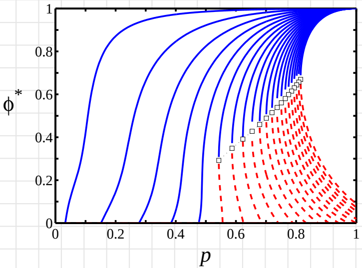
$$\text{F.P. Eq:}\quad \phi^* = \Gamma(p, \phi^*; r) + \sum_{i=d^*}^{T} \binom{T}{i} (p\phi^*)^i (1 - p\phi^*)^{T-i}.$$

$$\Gamma(p, \phi^*; r) = (1-r)(p\phi)^2(1-p\phi)^2 + \sum_{m=1}^{\infty} (1-r)^m (p\phi)^2 (1-p\phi)^2 \times \left[\chi_{m-1} + \chi_{m-2} + 2p\phi(1-p\phi)\chi_{m-3} + p\phi(1-p\phi)^2\chi_{m-4}\right]$$

$$\text{where}\quad \chi_m(p, \phi^*) = \sum_{k=0}^{[m/3]} \binom{m-2k}{k} (1 - p\phi^*)^{m-k} (p\phi^*)^k.$$

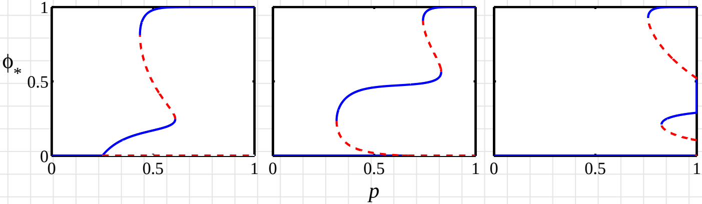
SIS model

Now allow $r < 1$:



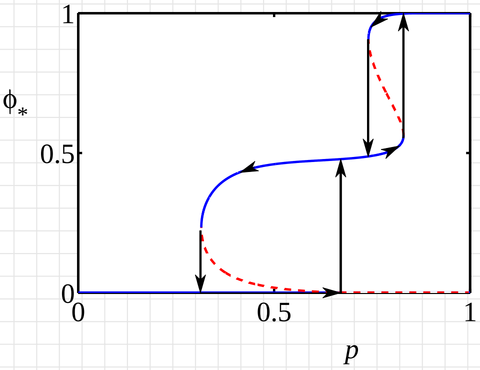
II-III transition generalizes: $p_c = 1/[P_1(T + \tau)]$
(I-II transition less pleasant analytically)

More complicated models



- Due to heterogeneity in individual thresholds.
- Same model classification holds: I, II, and III.

Hysteresis in vanishing critical mass models



Generalized model—heterogeneity, $r \leq 1$

II-III transition generalizes:

$$p_c = 1/[P_1(T + \tau)]$$

where $\tau = 1/r =$ expected recovery time

Discussion

- Memory is crucial ingredient.
- Three universal classes of contagion processes:
  - I. Epidemic Threshold
  - II. Vanishing Critical Mass
  - III. Critical Mass
- Dramatic changes in behavior possible.
- To change kind of model: ‘adjust’ memory, recovery, fraction of vulnerable individuals (T, r, ρ, P_1, and/or P_2).
- To change behavior given model: ‘adjust’ probability of exposure (p) and/or initial number infected (ϕ_0).

Discussion

- If $pP_1(T+\tau) \geq 1$, contagion can spread from single seed.
- Key quantity: $p_c = 1/[P_1(T+\tau)]$
- Depends only on:
  1. System Memory $(T+\tau)$.
  2. Fraction of highly vulnerable individuals (P_1).
- Details unimportant (Universality): Many threshold and dose distributions give same P_k.
- Most vulnerable/gullible population may be more important than small group of super-spreaders or influentials.

Future work/questions

- Do any real diseases work like this?
- Examine model's behavior on networks
- Media/advertising + social networks model
- Classify real-world contagions

References I

[1] P. S. Dodds and D. J. Watts.
Universal behavior in a generalized model of contagion.
Phys. Rev. Lett., 92:218701, 2004. pdf (⊞)

[2] P. S. Dodds and D. J. Watts.
A generalized model of social and biological contagion.
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