Generalized Contagion
Principles of Complex Systems
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Outline

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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.
- \(\phi_t = \text{fraction infected at time } t\)
  \[
  = \text{probability of contact with infected individual}
  \]
- 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

\[ S \rightarrow I \]

- 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

\[ I \Rightarrow R \]
When \( D_{t,i} < d_i^* \), individual \( i \) recovers to state \( R \) with probability \( r \).

\[ R \Rightarrow S \]
Once in state \( R \), individuals become susceptible again with probability \( \rho \).
A visual explanation

(a) $\phi_t$ contact infective $p$ receive dose $d > 0$

$1 - \phi_t$ receive no dose

(b) $d_{t-T} \quad d_{t-T+1} \quad d_{t-1} \quad d_t \quad \Sigma \geq D_{t,i}$

(c) $S$

1 if $D_{t,i} < d_i^*$

$1 - \rho$ if $D_{t,i} < d_i^*$

$r(1 - \rho)$ if $D_{t,i} < d_i^*$

$1 - r$ if $D_{t,i} < d_i^*$

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

$I$

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

$R$

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

$1 - \rho$
Generalized model

Important quantities:

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

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

e.g.,

\( P_1 \) = Probability that \textbf{one dose} will exceed the threshold of a random individual

= Fraction of \textbf{most vulnerable} individuals.
Generalized model—heterogeneity, \( r = 1 \)

Fixed point equation:

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

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

\[ pP_1 T \geq 1 \]

\[ \Rightarrow \rho_c = 1/(TP_1) \]
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:** $P_1 > P_2/2$, $\rho_c = 1/(TP_1) < 1$
- **Vanishing critical mass:** $P_1 < P_2/2$, $\rho_c = 1/(TP_1) < 1$
- **Pure critical mass:** $P_1 < P_2/2$, $\rho_c = 1/(TP_1) > 1$
Calculations—Fixed points for $r < 1$, $d^* = 2$, and $T = 3$

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

$\Gamma(p, \phi^*; r) = (1 - r)(p\phi)^2(1 - p\phi)^2 + \sum_{m=1}^{\infty} (1 - r)^m (p\phi)^2 (1 - p\phi)^2 \times$

$[\chi_{m-1} + \chi_{m-2} + 2p\phi(1 - p\phi)\chi_{m-3} + p\phi(1 - p\phi)^2 \chi_{m-4}]$

where $\chi_m(p, \phi^*) = \sum_{k=0}^{[m/3]} \binom{m - 2k}{k} (1 - p\phi^*)^{m-k} (p\phi^*)^k$. 
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
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 ($T, r, \rho, P_1$, and/or $P_2$).
- To change behavior given model: ‘adjust’ probability of exposure ($\rho$) and/or initial number infected ($\phi_0$).
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

P. S. Dodds and D. J. Watts.
Universal behavior in a generalized model of contagion.

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