

# Generalized Contagion

## Principles of Complex Systems

### Course 300, Fall, 2008

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# Outline

Generalized  
Contagion

Generalized Model  
of Contagion

References

Generalized Model of Contagion

References

Frame 2/21



## Basic questions about contagion

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# 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:  
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# Generalized model—ingredients

- ▶ Incorporate memory of a contagious element<sup>[1, 2]</sup>
- ▶ Population of  $N$  individuals, each in state S, I, or R.
- ▶ Each individual randomly contacts another at each time step.
- ▶  $\phi_t$  = 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  $d = 0$ .

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- ▶ 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:

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

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$I \Rightarrow R$

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

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Once in state R, individuals become susceptible again  
with probability  $\rho$ .

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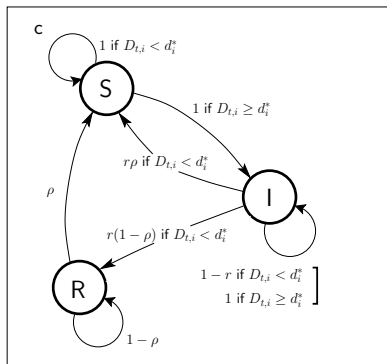
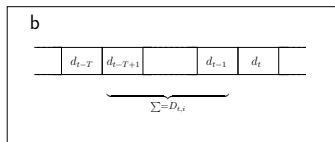
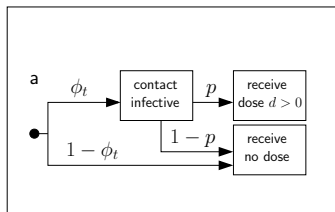
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# A visual explanation



Important quantities:

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

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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:

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

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

## 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.



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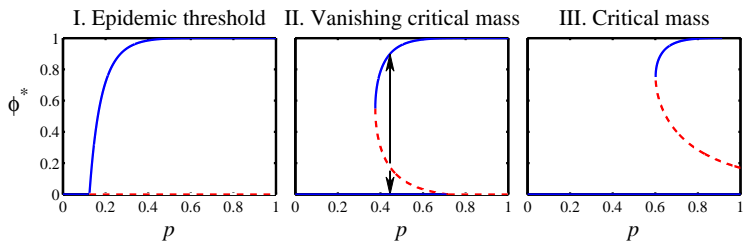
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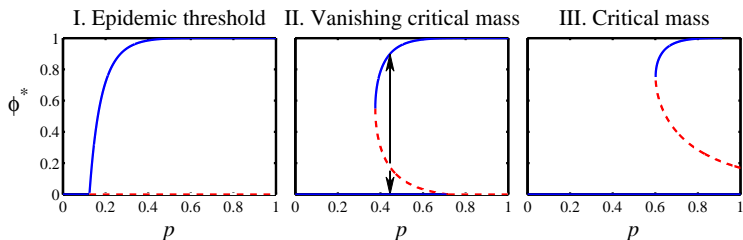
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# Heterogeneous case—Three universal classes



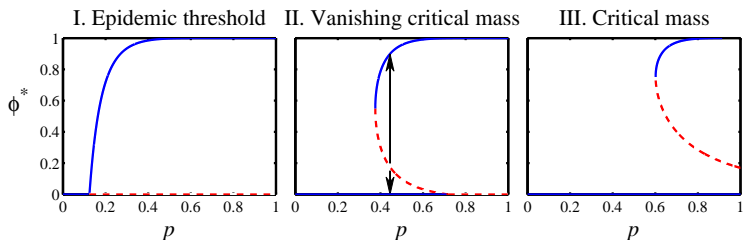
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- ▶ Vanishing critical mass:  $P_1 < P_2/2, p_c = 1/(TP_1) < 1$
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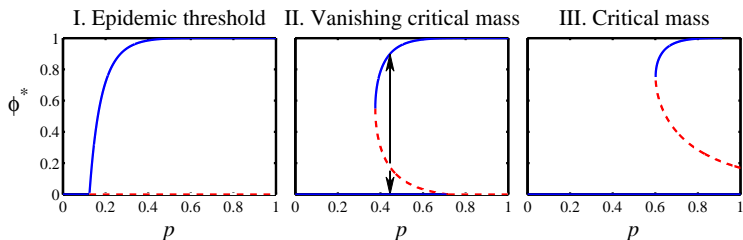
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# Calculations—Fixed points for $r < 1$ , $d^* = 2$ , and $T = 3$

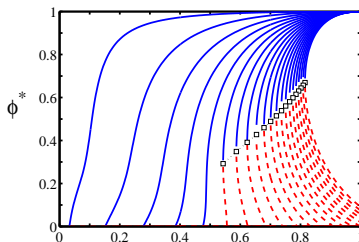
$$\text{F.P. Eq: } \phi^* = \Gamma(p, \phi^*; r) + \sum_{i=d^*}^T \binom{T}{i} (p\phi^*)^i (1 - p\phi^*)^{T-i}.$$

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

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

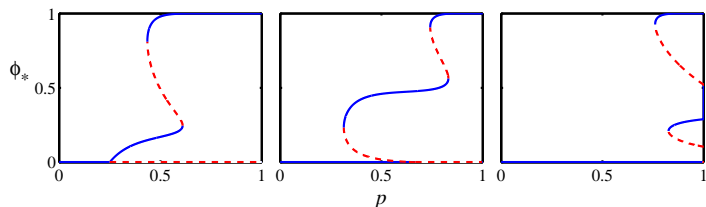


Now allow  $r < 1$ :



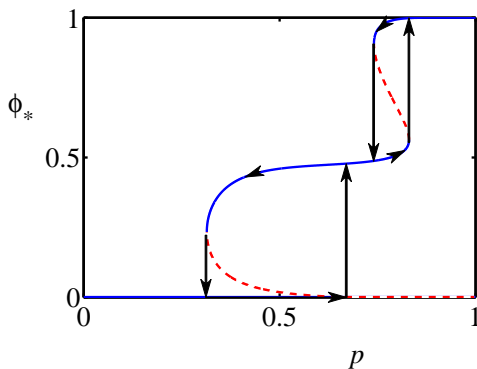
II-III transition generalizes:  $p_c = 1/[P_1(T + \tau)]$   
(I-II transition less pleasant analytically)

# 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

- ▶ **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 ( $p$ ) and/or initial number infected ( $\phi_0$ ).

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- ▶ 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.

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