Generalized Contagion

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Principles of Complex Systems, Vols. 1 & 2
CSYS/MATH 300 and 303, 2021–2022| @pocsvox

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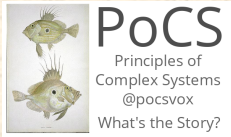
Computational Story Lab | Vermont Complex Systems Center
Vermont Advanced Computing Core | University of Vermont



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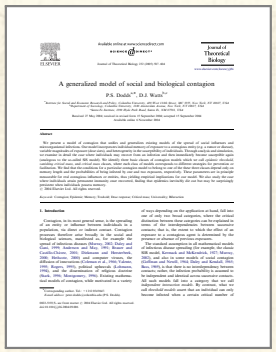
Outline

"Universal Behavior in a Generalized Model of Contagion"

Dodds and Watts,
Phys. Rev. Lett., **92**, 218701, 2004. [5]



"A generalized model of social and biological contagion"

Dodds and Watts,
J. Theor. Biol., **232**, 587–604, 2005. [6]

Generalized contagion model

Basic questions about contagion

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

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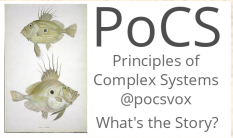
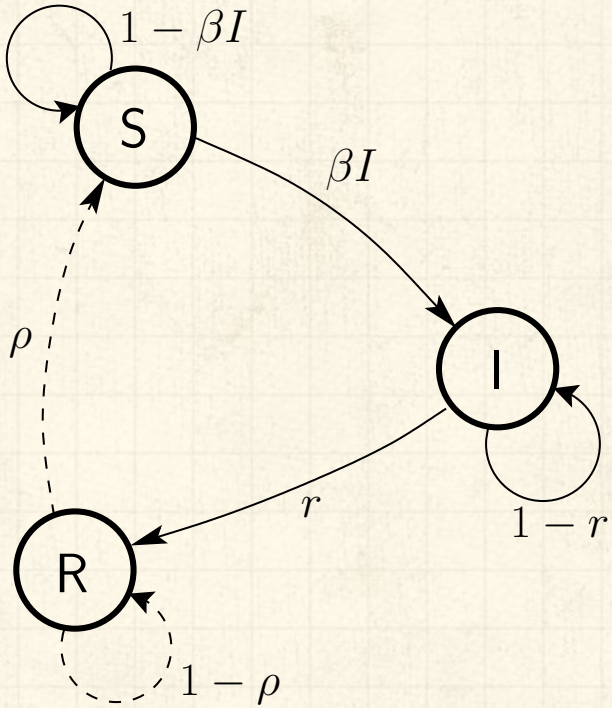
- Discrete and continuous time versions



Independent Interaction Models

Discrete time automata example:



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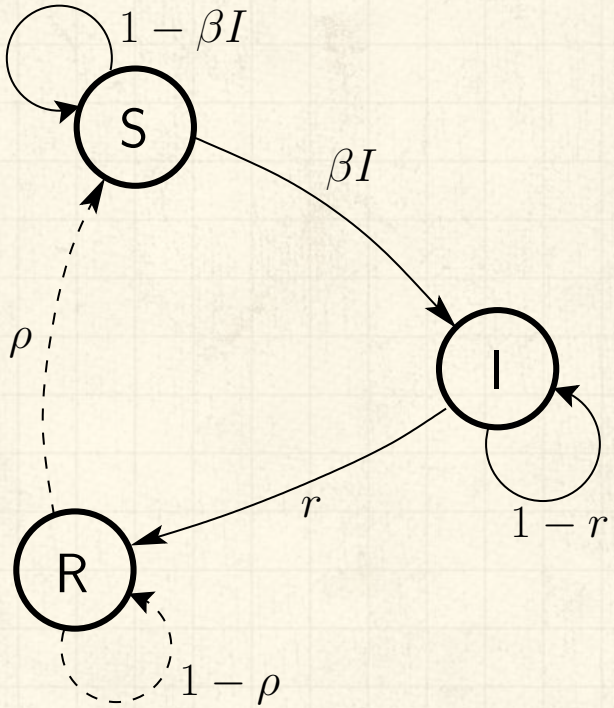

Transition Probabilities:

Independent Interaction Models

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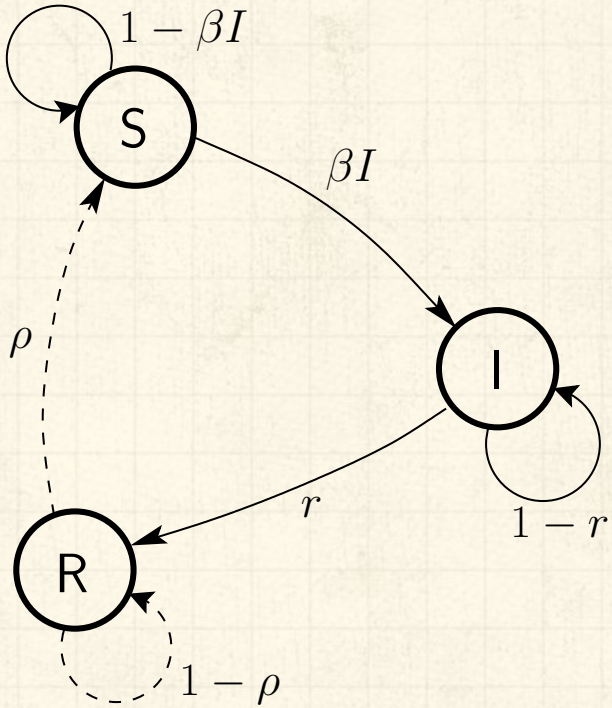

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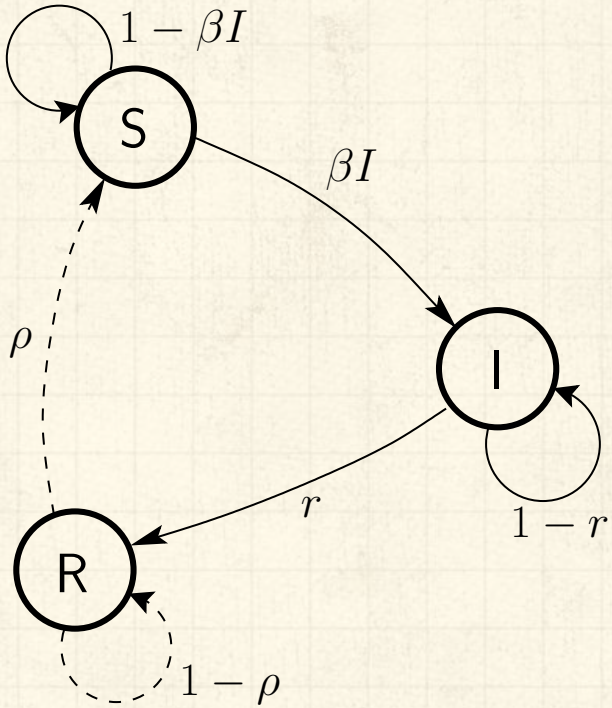

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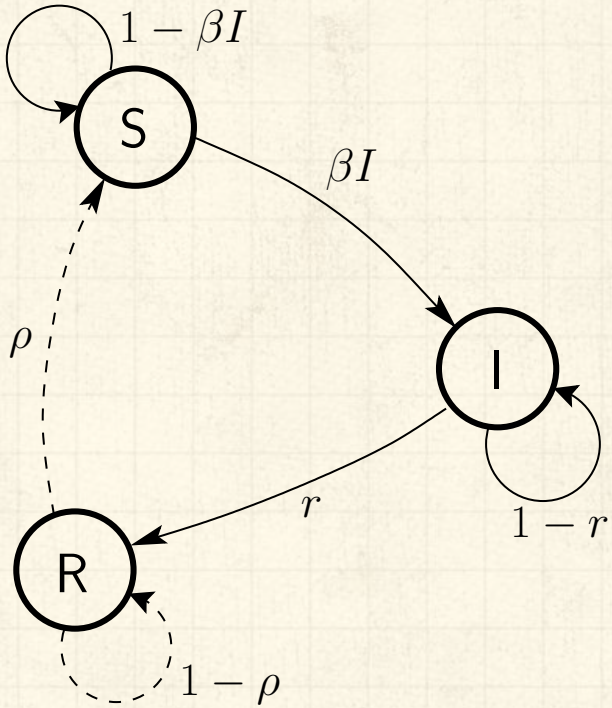

Transition Probabilities:

β for being infected given contact with infected
r for recovery
ρ for loss of immunity

Independent Interaction Models

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- 1920's/1930's: Kermack and McKendrick [8, 10, 9]

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- Coupled differential equations with a mass-action principle

Independent Interaction models

Differential equations for continuous model

$$\frac{\mathrm{d}}{\mathrm{d}t}S = -\beta IS + \rho R$$

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$$\frac{\mathrm{d}}{\mathrm{d}t}R = rI - \rho R$$

β, r, and ρ are now rates.

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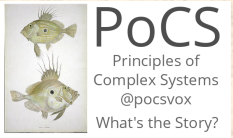
- Epidemic threshold: If $R_0 > 1$, 'epidemic' occurs.



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- At time $t = k$, single Infective remains infected with probability $(1 - r)^k$

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- Expected number infected by original Infective:

$$R_0 = \beta + (1-r)\beta + (1-r)^2\beta + (1-r)^3\beta + ...$$

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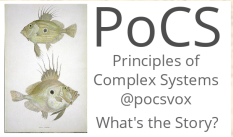
- Similar story for continuous model.



Independent Interaction models

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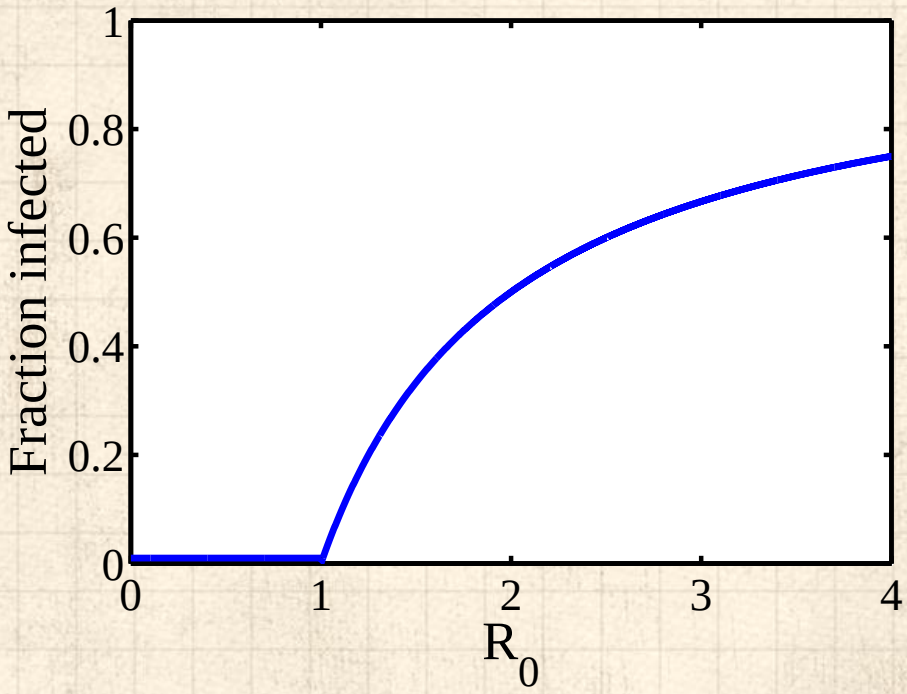

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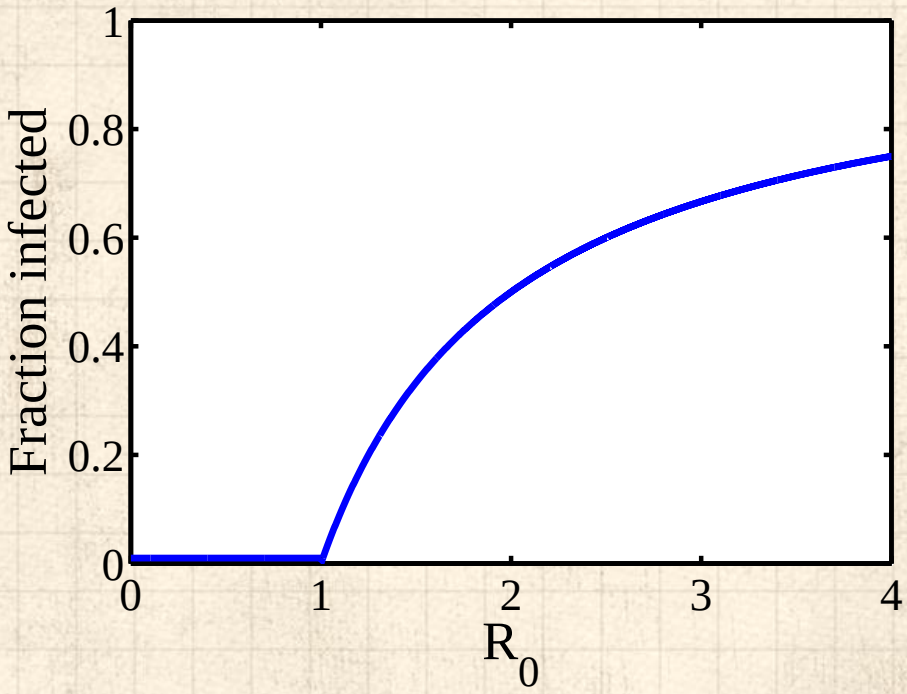

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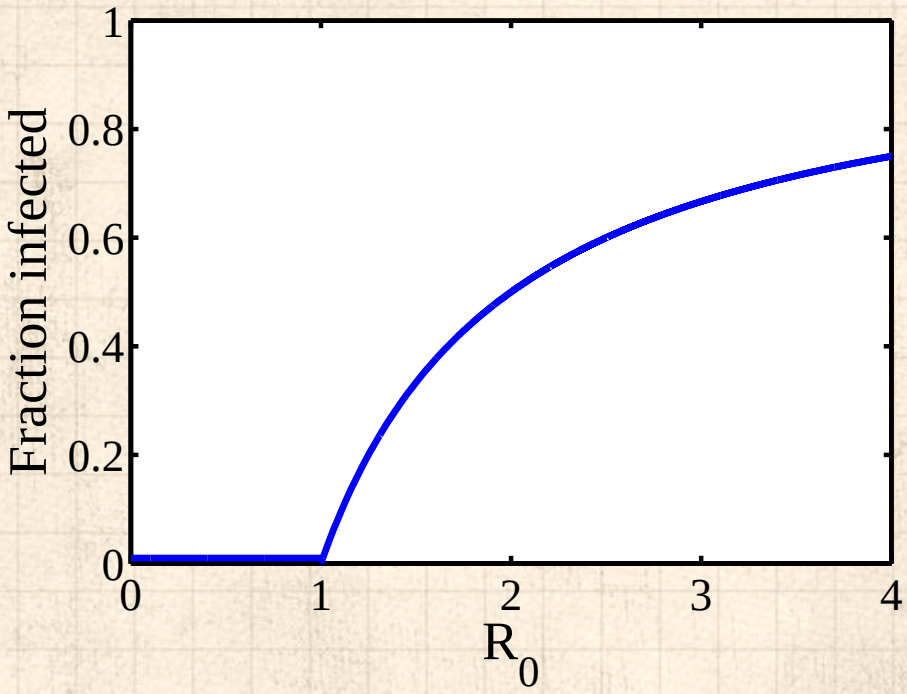

- Continuous phase transition.
- Fine idea from a simple model.

Simple disease spreading models

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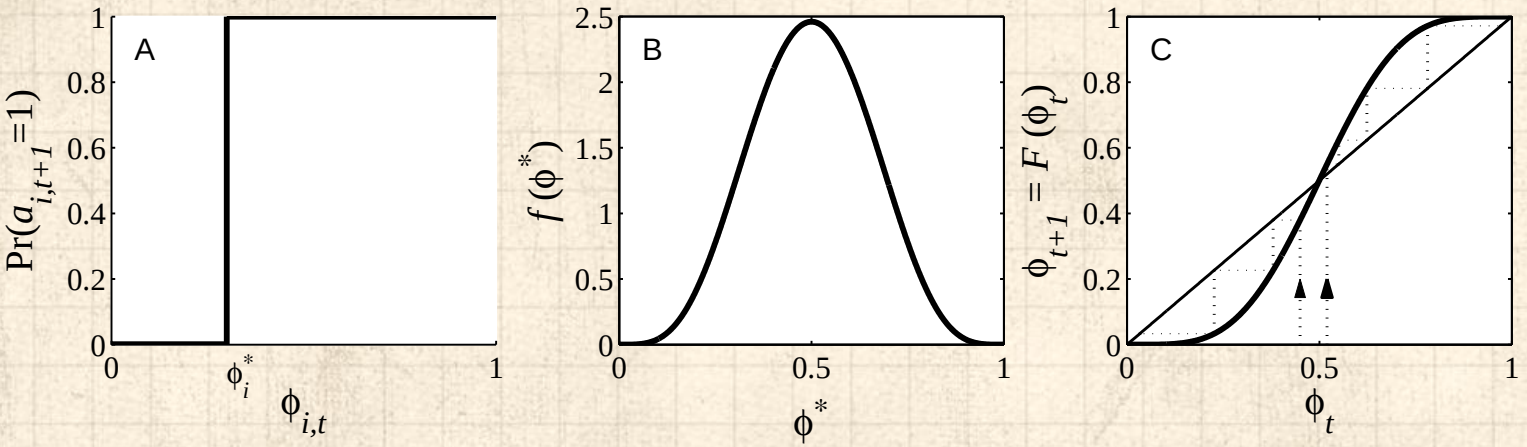
- Diffusion of innovations (Bass, 1969) [1]
- Spread of fanatical behavior (Castillo-Chávez & Song, 2003) [2]

Granovetter's model (recap of recap)

- Action based on perceived behavior of others.



- Two states: S and I.
- Recovery now possible (SIS).
- ϕ = fraction of contacts 'on' (e.g., rioting).
- Discrete time, synchronous update.
- This is a Critical mass model.
- Interdependent interaction model.

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- Mean-field models neglect network structure
- Network effects only part of story: media, advertising, direct marketing.

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- If exposed, individual receives a dose of size d drawn from distribution f. Otherwise $d = 0$.

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

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

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I ⇒ R

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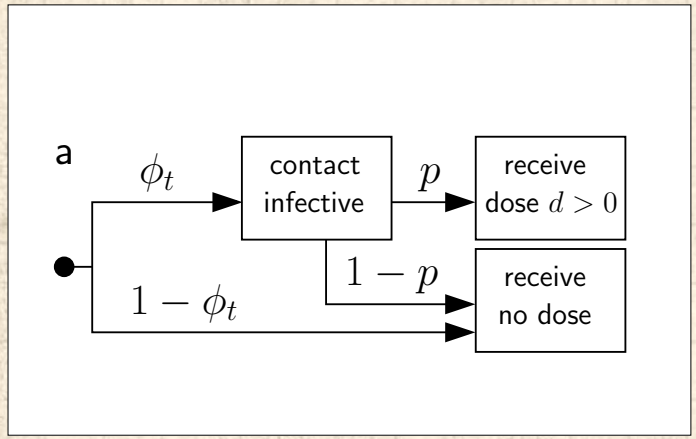
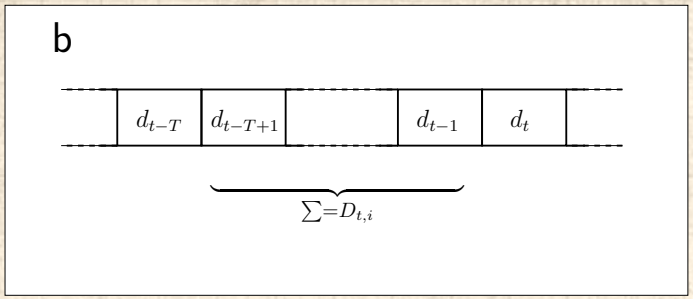
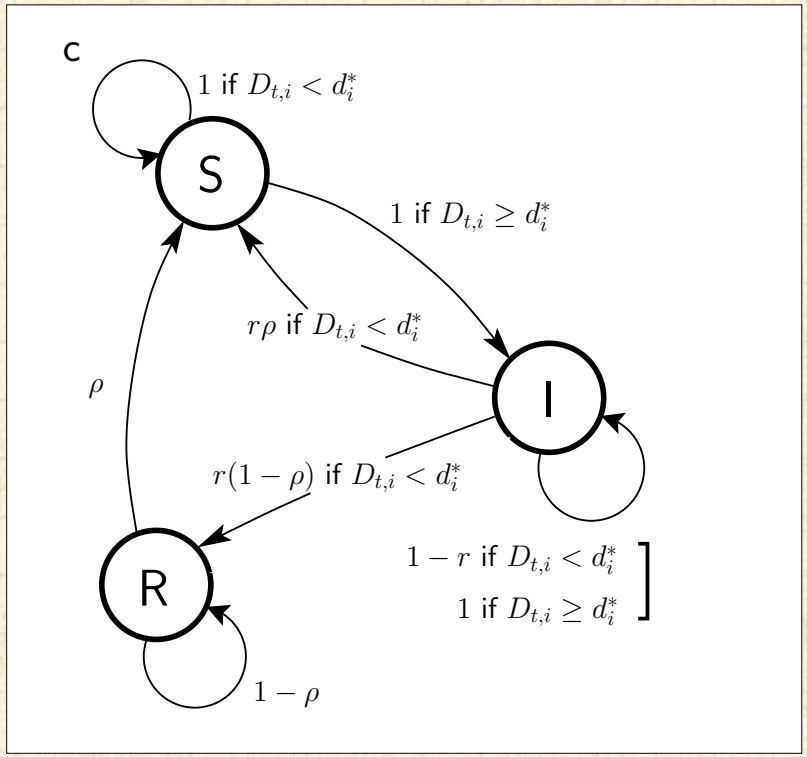
R ⇒ S

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

A visual explanation







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- All dose sizes are equal: $d = 1$

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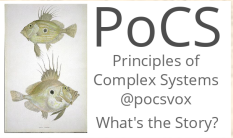

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b: Probability of being infected and not being reinfected.

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b: Probability of being infected and not being reinfected.
c: Probability of not recovering.

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- Goodness: Matches $R_o = \beta/\gamma > 1$ condition.

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- Note: we can solve for p but not ϕ^*:

$$p = (\phi^*)^{-1}[1 - (1 - \phi^*)^{1/T}].$$

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- With history H_1, probability of being infected (not recovering in one time step) is $1 - r$.

Homogeneous, one hit models:

Fixed points for $r \leq 1$, $d^* = 1$, and $T \geq 1$

- In general, relevant dose histories are:

$$H_{m+1} = \{\ldots, d_{t-T-m-1}, 1, \underbrace{0, 0, \ldots, 0, 0}_{m\ 0\text{'s}}, \underbrace{0, 0, \ldots, 0, 0}_{T\ 0\text{'s}}\}.$$

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c: Pr(no recovery in m chances)

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- Using the probability of not recovering, we end up with a fixed point equation:

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- $$\Rightarrow \quad p_c = \frac{1}{T + 1/r - 1} = \frac{1}{T + \tau}.$$

  where τ = mean recovery time for simple relaxation process.
- Decreasing r keeps individuals infected for longer and decreases p_c.

Epidemic threshold:

Fixed points for $d^* = 1$, $r \leq 1$, and $T \geq 1$

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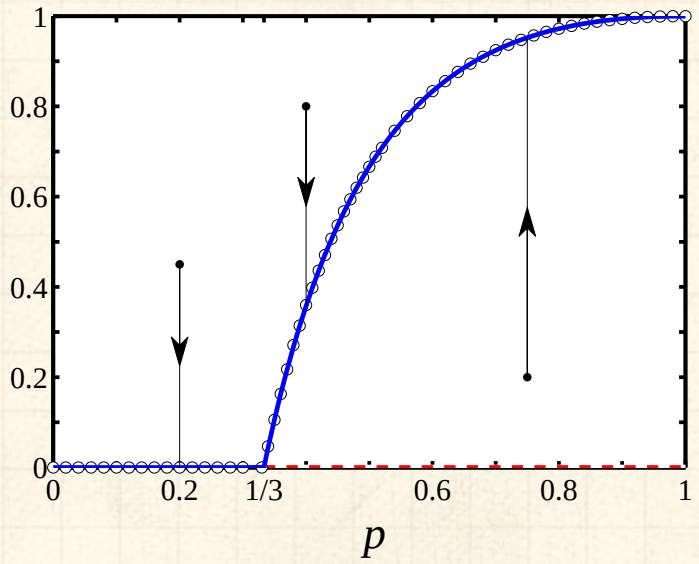

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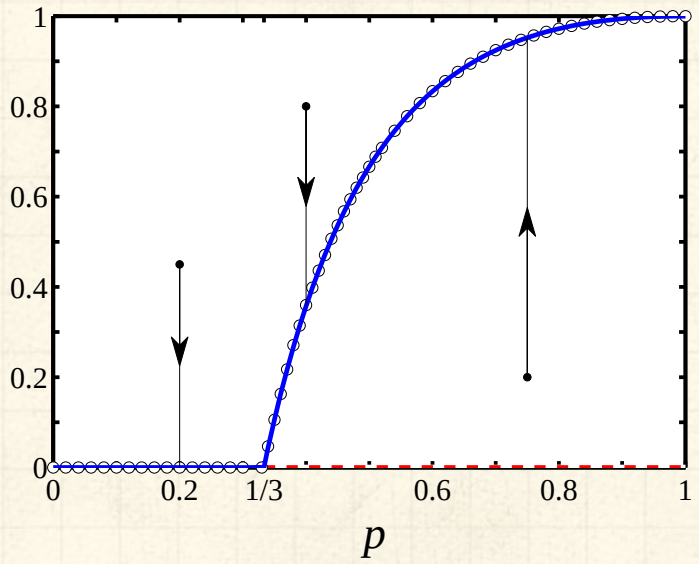

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- Phase transition can be seen as a transcritical bifurcation. [12]

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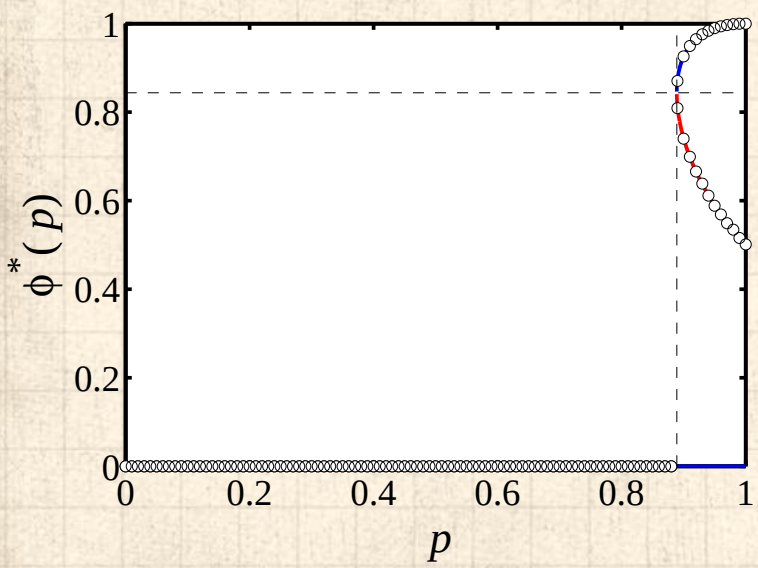

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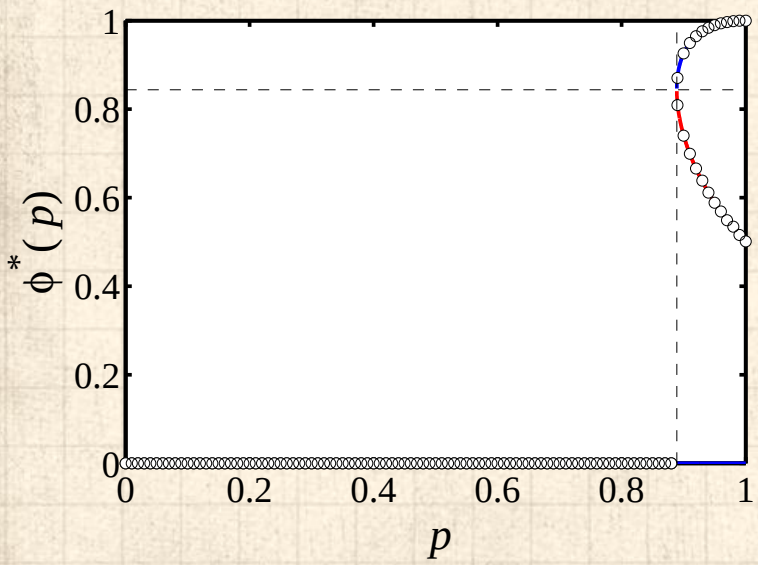

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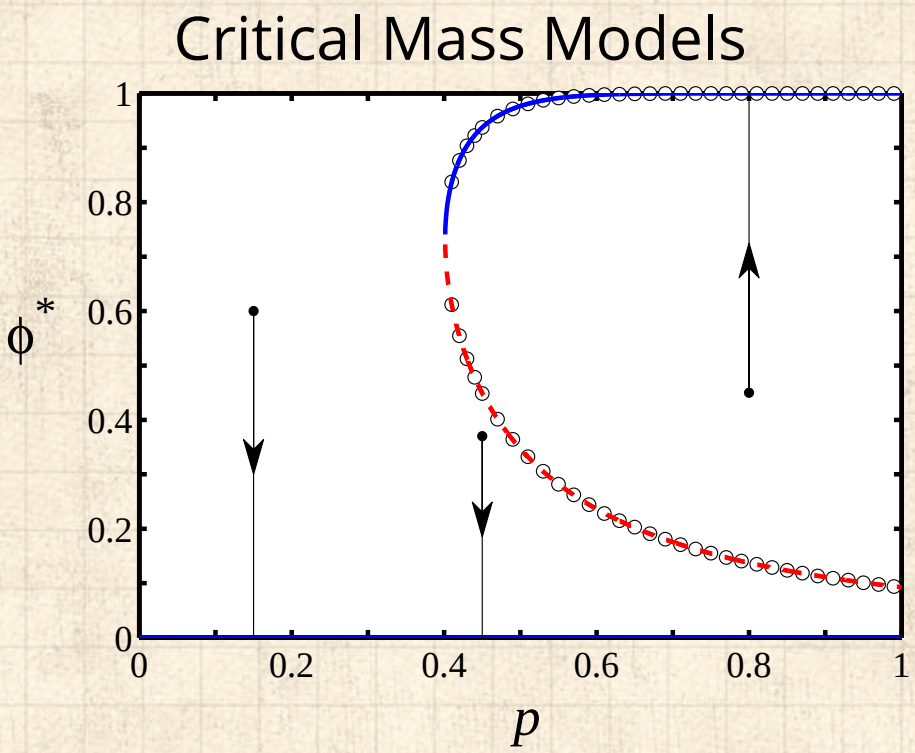
- Behavior akin to output of Granovetter's threshold model.

Homogeneous, multi-hit models:

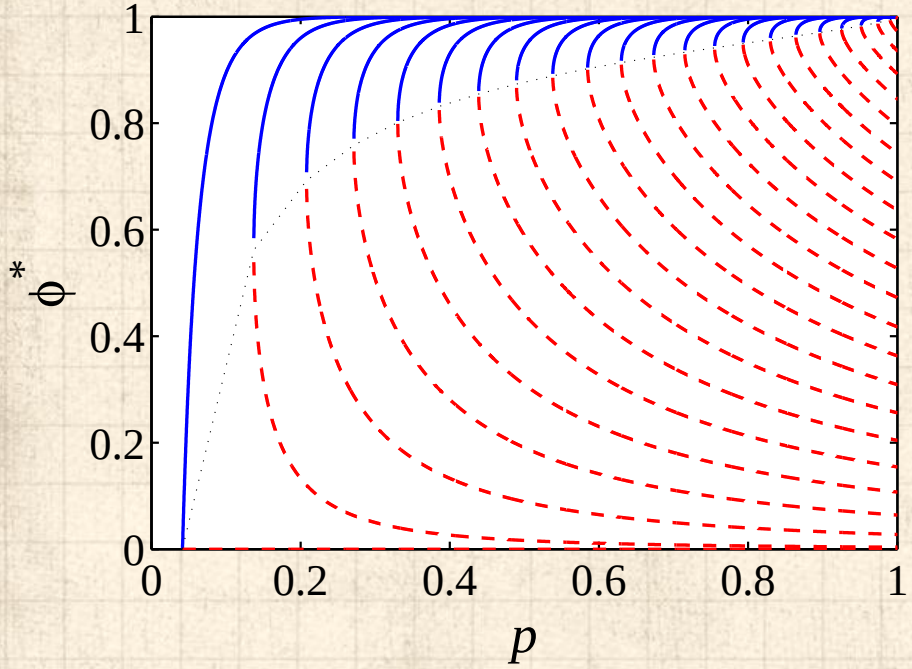
- Another example:



- $r = 1, d^* = 3, T = 12$ Saddle-node bifurcation.

Fixed points for $r = 1$, $d^* > 1$, and $T \geq 1$

- $T = 24$, d^* = 1, 2, ...23.



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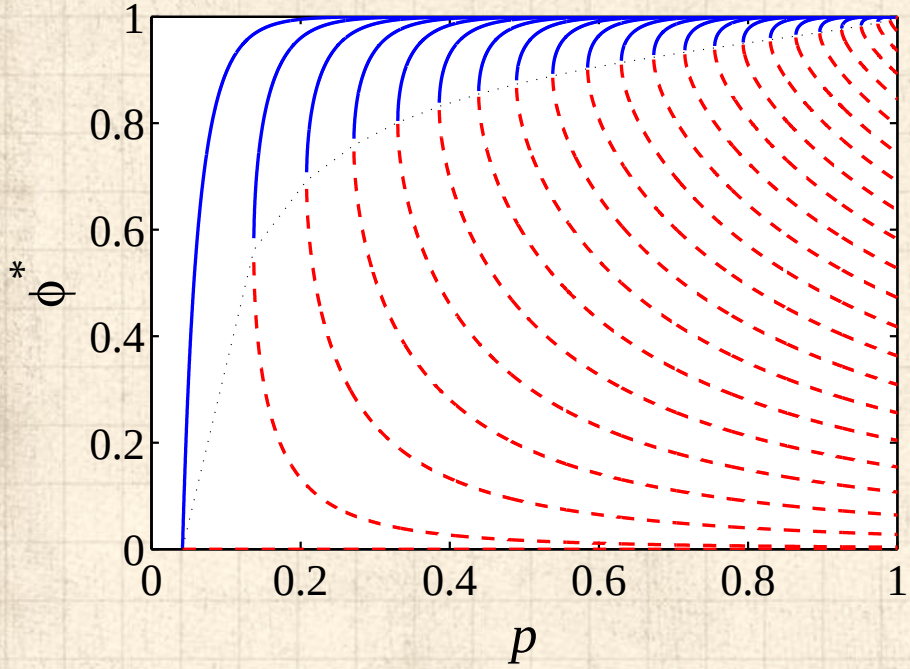

- $d^* = 1 \to d^* > 1$: jump between continuous phase transition and pure critical mass model.
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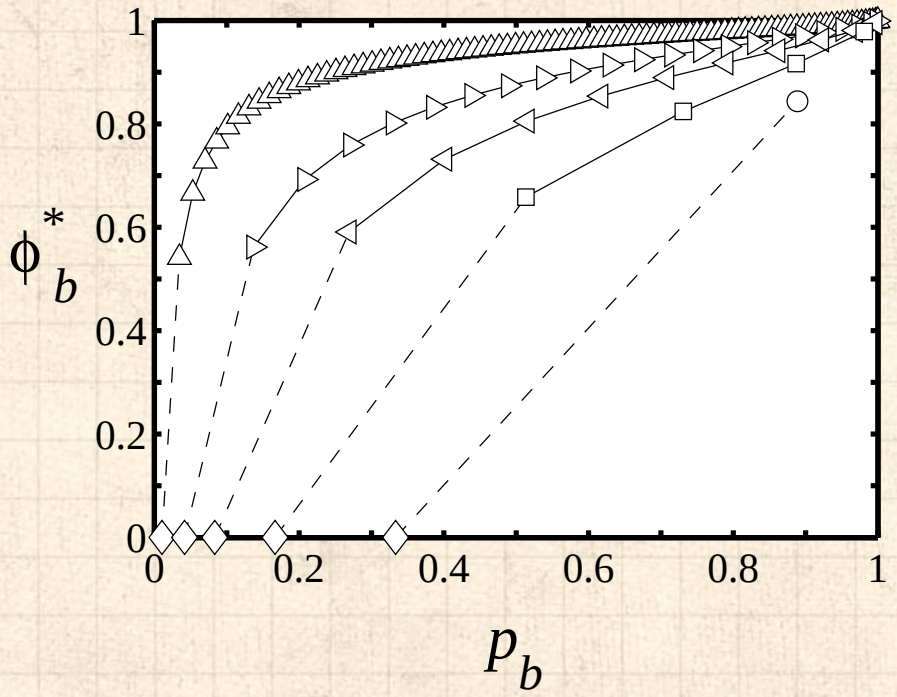
- See either simple phase transition or saddle-node bifurcation, nothing in between.

Fixed points for $r = 1$, $d^* > 1$, and $T \geq 1$

- Bifurcation points for example fixed T, varying d^*:



- $T = 96$ ( ).
- $T = 24$ (▷),
- $T = 12$ (◁),
- $T = 6$ (□),
- $T = 3$ (○),

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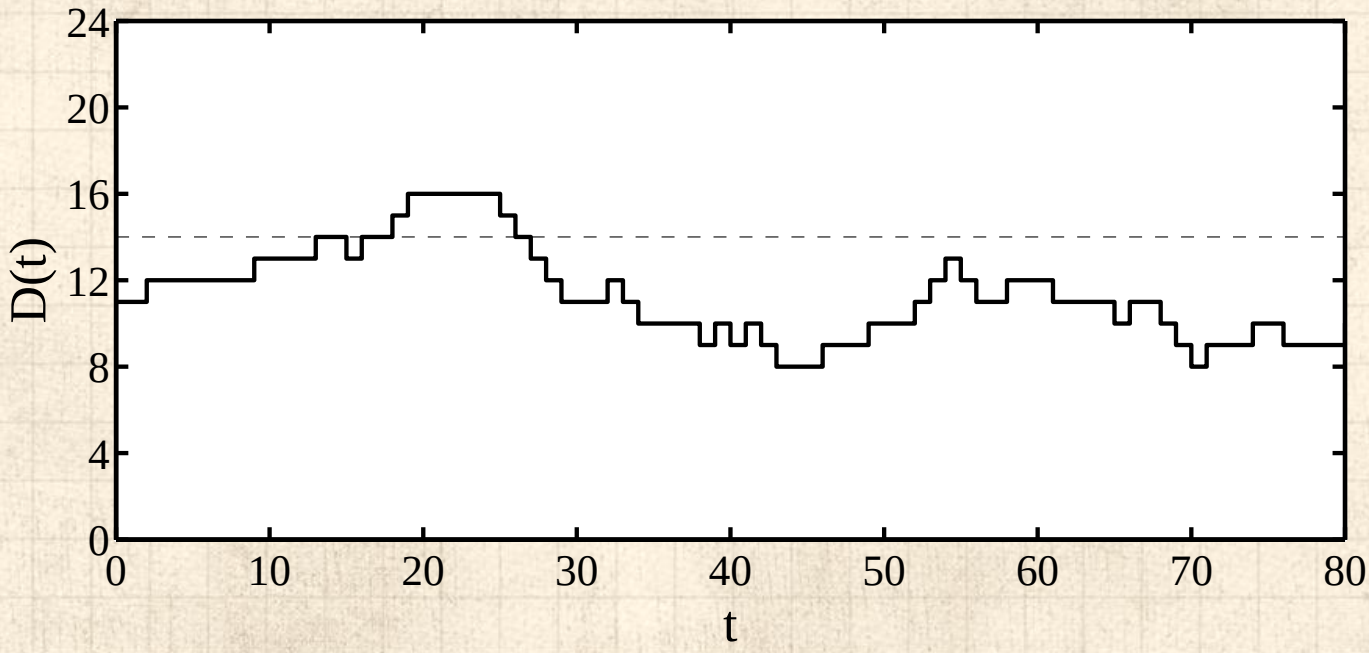

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$$\phi^* = \Gamma(p, \phi^*; r) + \sum_{i=d^*}^{T} \binom{T}{i} (p\phi^*)^i (1 - p\phi^*)^{T-i}.$$

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- Note: second sequence includes an extra 0 since this is necessary to stay below $d^* = 2$.
- To stay below threshold, observe acceptable following sequences may be composed of any combination of two subsequences:

$$a = \{0\} \quad \text{and} \quad b = \{1, 0, 0\}.$$

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- Corresponding possible values for N_a:

$$m, m-3, m-6, \ldots, m-3\left\lfloor \frac{m}{3} \right\rfloor.$$

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- Choose positions of either a's or b's:

$$\binom{N_a + N_b}{N_a} = \binom{N_a + N_b}{N_b}.$$

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- Total number of allowable sequences of length m:

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- Notation: Write a randomly chosen sequence of a's and b's of length m as $D_m^{a,b}$.

Fixed points for $r < 1$, $d^* > 1$, and $T \geq 1$

- Nearly there ...must account for details of sequence endings.
- Three endings $\Rightarrow$ Six possible sequences:

$$D_1 = \{1, 1, 0, 0, D^{a,b}_{m-1}\}$$

$$D_2 = \{1, 1, 0, 0, D^{a,b}_{m-2}, 1\}$$

$$D_3 = \{1, 1, 0, 0, D^{a,b}_{m-3}, 1, 0\}$$

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PoCS
Principles of Complex Systems
@pocsvox
What's the Story?

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

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

where $\Gamma(p, \phi^*; r) =$

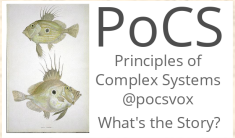
$$(1-r)(p\phi)^2(1-p\phi)^2 + \sum_{m=1}^{\infty} (1-r)^m (p\phi)^2(1-p\phi)^2 \times$$

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

and

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

Note: $(1-r)(p\phi)^2(1-p\phi)^2$ accounts for $\{1, 0, 1, 0\}$ sequence.



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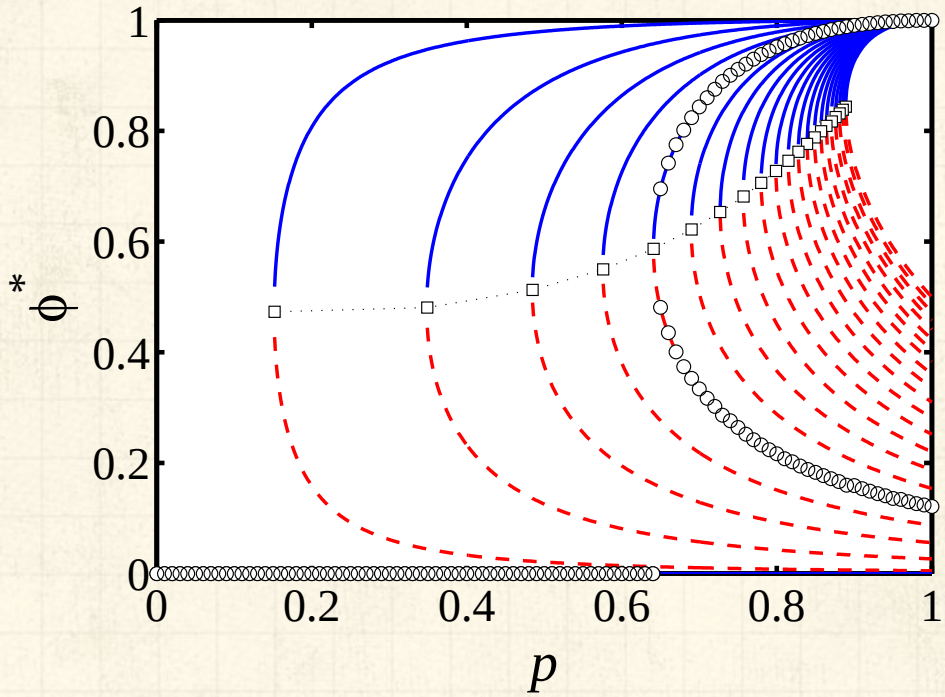

$r = 0.01, 0.05, 0.10, 0.15, 0.20, \ldots, 1.00.$

Fixed points for $r < 1$, $d^* > 1$, and $T \geq 1$

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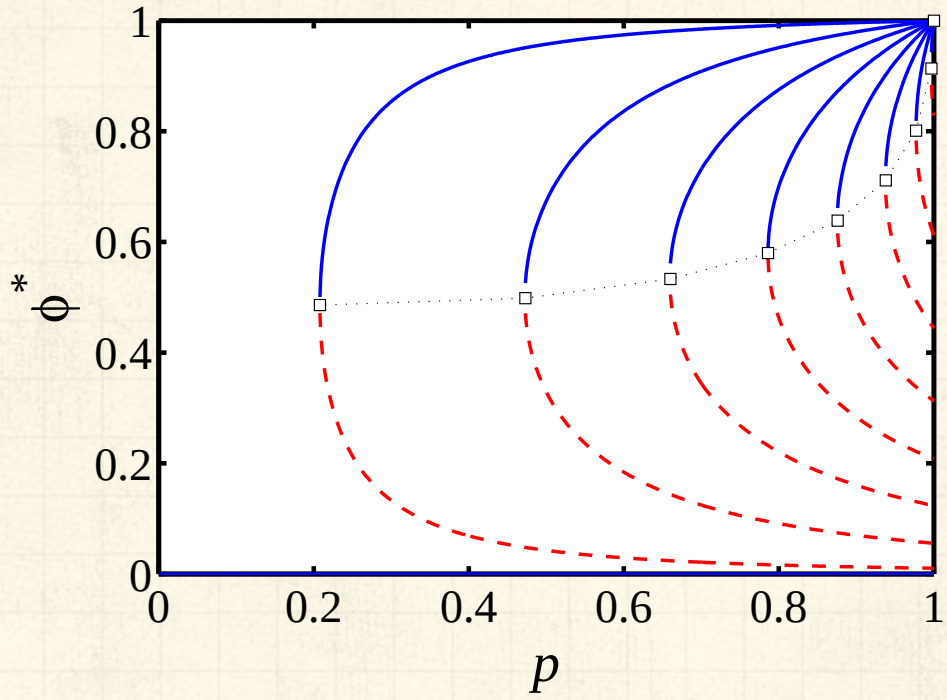

$r = 0.01, 0.05, 0.10, \ldots, 0.3820 \pm 0.0001.$

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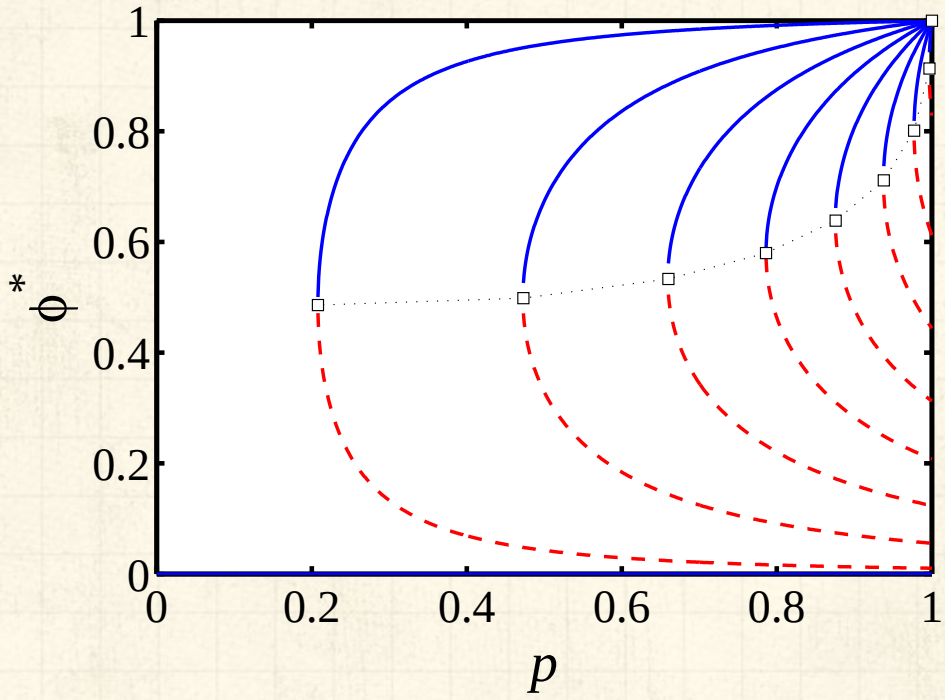

- $r = 0.01, 0.05, 0.10, \ldots, 0.3820 \pm 0.0001.$
- No spreading for $r \gtrsim 0.382$.

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- Are other behaviors possible?

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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, $r = 1$

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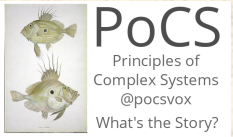
  2. pP_1T is $\therefore$ the expected number of successful infections (equivalent to R_0).
- Observe: p_c may exceed 1 meaning no spreading from a small seed.



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- Now find three basic universal classes of contagion models ...

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- Dose sizes are lognormally distributed with mean 1 and variance 0.433.

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Heterogeneous case

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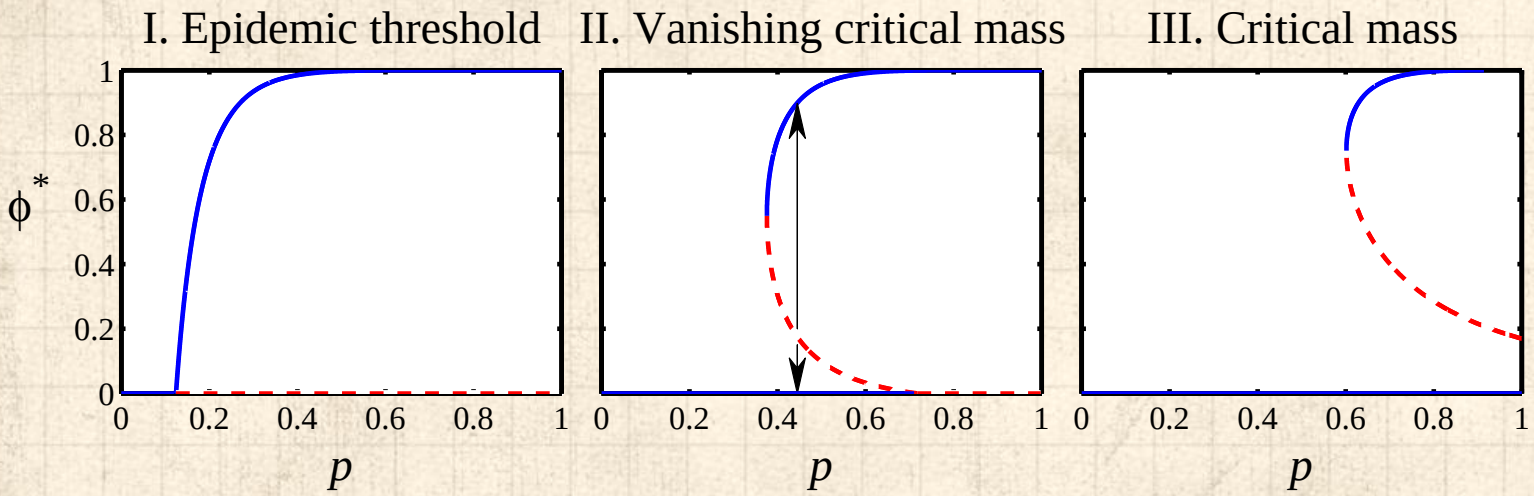
- Dose sizes are lognormally distributed with mean 1 and variance 0.433.
- Memory span: $T = 10$.
- Thresholds are uniformly set at
  1. $d_* = 0.5$
  2. $d_* = 1.6$
  3. $d_* = 3$

Heterogeneous case

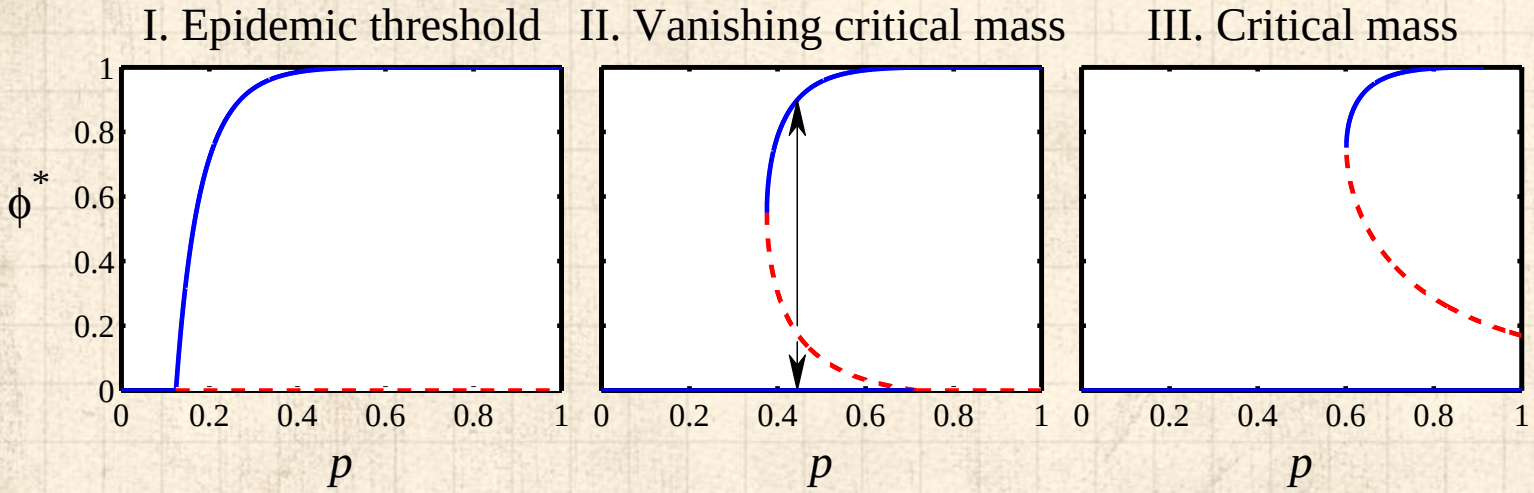
Example configuration:

- 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.

Three universal classes



Three universal classes



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

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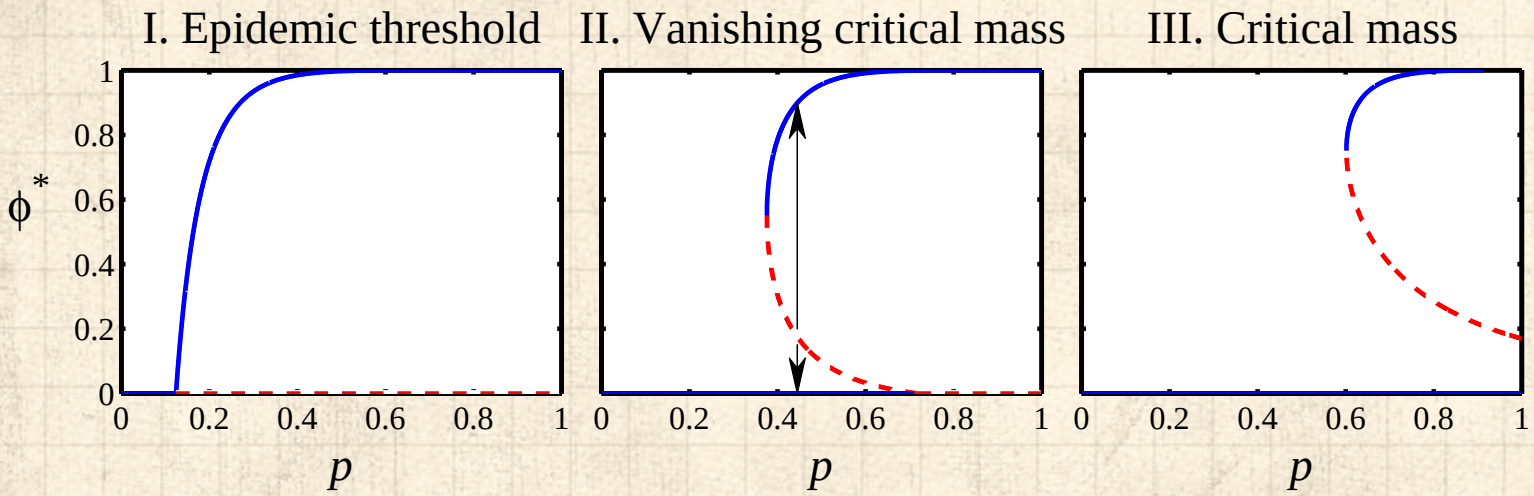

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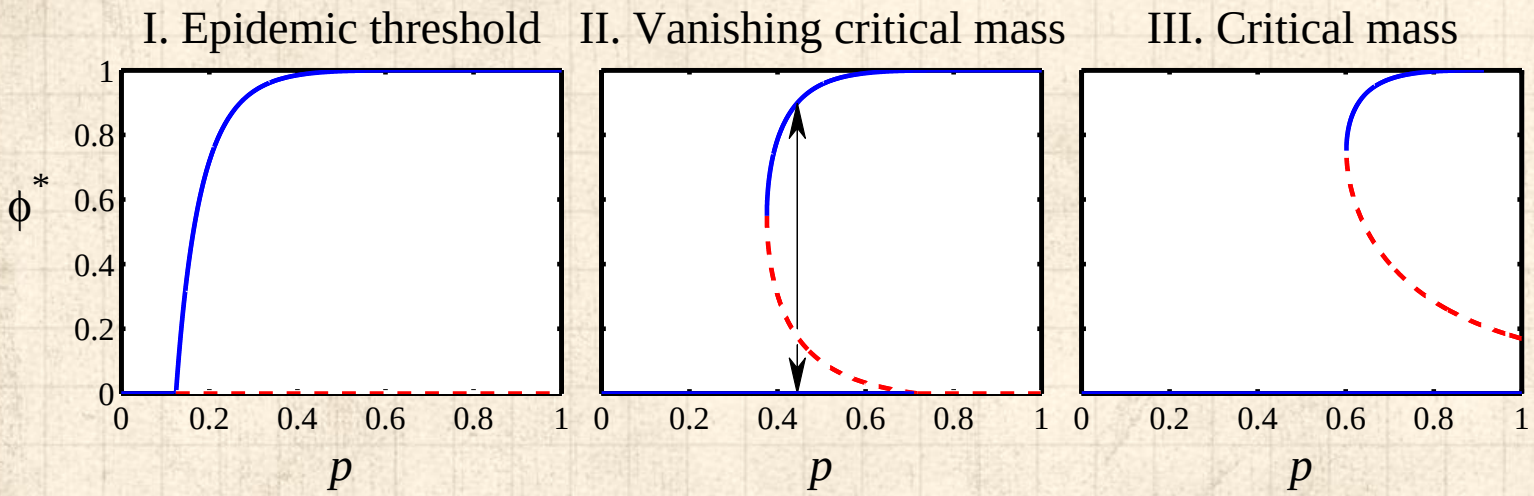

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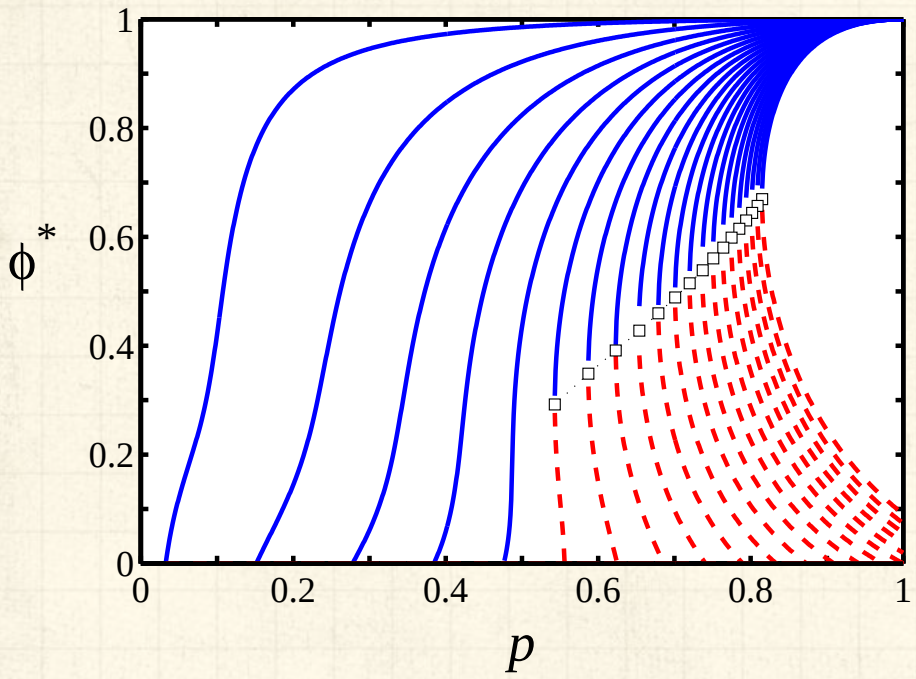
- Vanishing critical mass: $P_1 < P_2/2$, $p_c = 1/(TP_1) < 1$
- Pure critical mass: $P_1 < P_2/2$, $p_c = 1/(TP_1) > 1$

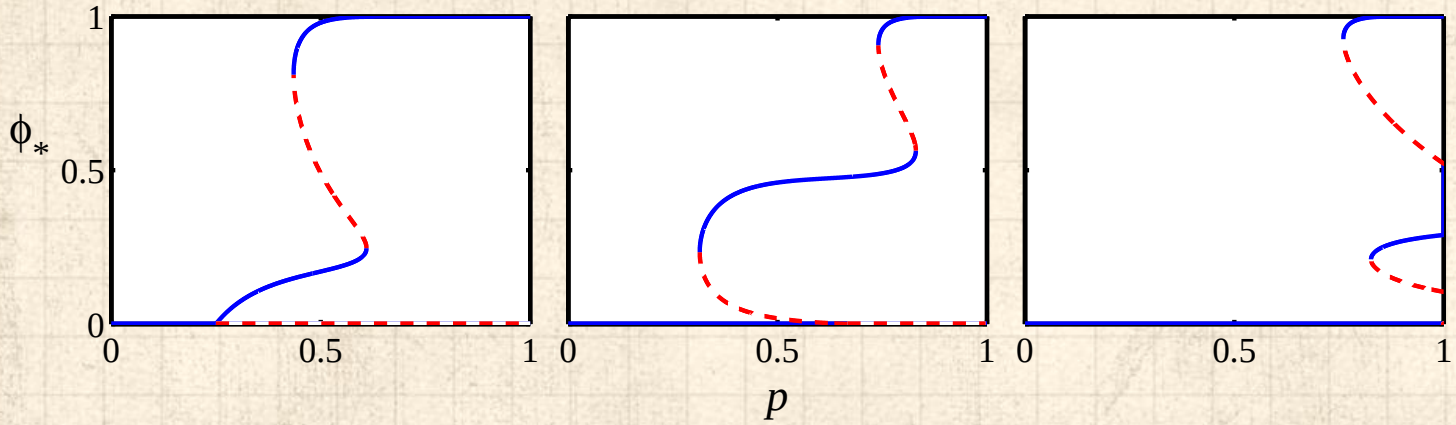
Heterogeneous case

Now allow $r < 1$:



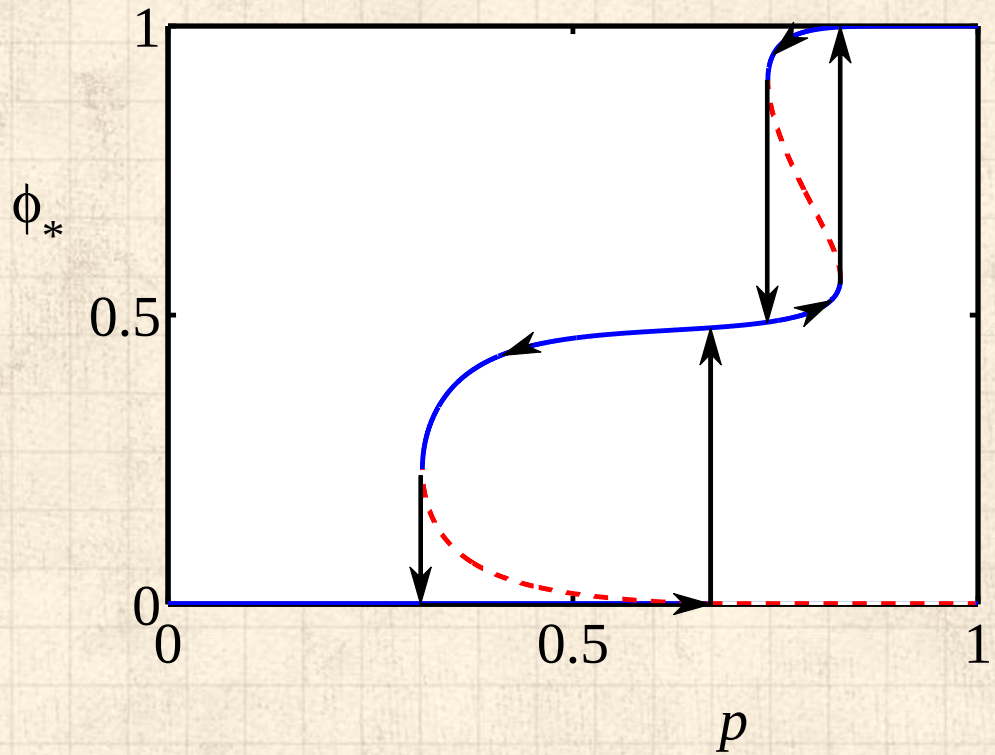
- II-III transition generalizes: $p_c = 1/[P_1(T+\tau)]$ where $\tau = 1/r - 1 =$ expected recovery time
- I-II transition less pleasant analytically.

More complicated models



- Due to heterogeneity in individual thresholds.
- Three classes based on behavior for small seeds.
- Same model classification holds: I, II, and III.

Hysteresis in vanishing critical mass models



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- To change behavior given model: 'adjust' probability of exposure (p) and/or initial number infected (ϕ_0).

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- Details unimportant: Many threshold and dose distributions give same P_k.
- Another example of a model where vulnerable/gullible population may be more important than a small group of super-spreaders or influentials.

Appendix: Details for Class I-II transition:

$$\begin{aligned}
\phi^* &= \sum_{k=1}^{T} \binom{T}{k} P_k (p\phi^*)^k (1-p\phi^*)^{T-k}, \\
&= \sum_{k=1}^{T} \binom{T}{k} P_k (p\phi^*)^k \sum_{j=0}^{T-k} \binom{T-k}{j} (-p\phi^*)^j, \\
&= \sum_{k=1}^{T} \sum_{j=0}^{T-k} \binom{T}{k} \binom{T-k}{j} P_k (-1)^j (p\phi^*)^{k+j}, \\
&= \sum_{m=1}^{T} \sum_{k=1}^{m} \binom{T}{k} \binom{T-k}{m-k} P_k (-1)^{m-k} (p\phi^*)^m, \\
&= \sum_{m=1}^{T} C_m (p\phi^*)^m
\end{aligned}$$

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$$C_m = (-1)^m \binom{T}{m} \sum_{k=1}^{m} (-1)^k \binom{m}{k} P_k,$$

since

$$\begin{aligned}
\binom{T}{k}\binom{T-k}{m-k} &= \frac{T!}{k!(T-k)!}\frac{(T-k)!}{(m-k)!(T-m)!} \\
&= \frac{T!}{m!(T-m)!}\frac{m!}{k!(m-k)!} \\
&= \binom{T}{m}\binom{m}{k}.
\end{aligned}$$

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- Linearization gives

$$\phi^* \simeq C_1 p \phi^* + C_2 p_c^2 {\phi^*}^2.$$

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- Sign of derivative governed by $P_1 - P_2/2$.

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