Generalized Contagion

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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 socia contagion?
 - Focus: mean field models

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The standard SIR model [10]

S = Susceptible
 I = Infective/Infectious
 R = Recovered or Removed or Refracto

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 Presumes random interactions (mass-action principle)

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- Discrete and continuous time versions

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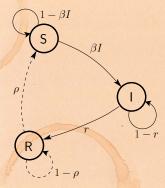
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Discrete time automata example:



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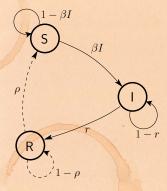
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Transition Probabilities:

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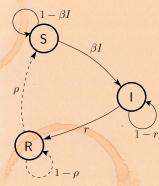
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Discrete time automata example:



Transition Probabilities:

 β for being infected given contact with infected

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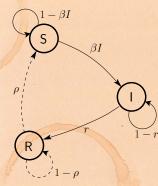
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β for being infected given contact with infected r for recovery

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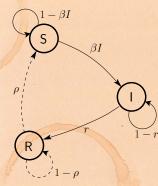
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Discrete time automata example:



Transition Probabilities:

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

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Original models attributed to

- 1920's: Reed and Frost
- 1920's/1930's: Kermack and McKendrick^{17, 9, 8}
- Coupled differential equations with a mass-actio

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Differential equations for continuous model

$$\frac{d}{dt}S = -\beta IS + \rho R$$
$$\frac{d}{dt}I = \beta IS - rI$$
$$\frac{d}{dt}R = rI - \rho R$$

- β , *r*, and ρ are now rates.
- Reproduction Number R₀:

*R*₀ = expected number of infected individuals resulting from a single initial infective
 Epidemic threshold: If *R*₀ > 1, 'epidemic' occursion

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Discrete version:

 Set up: One Infective in a randomly mixing population of Susceptibles

 Probability of transmission = 0
 At time t = 1, single infective remains infected wit corebability 1 = t

At time *t* = h, single infective remains infected wi

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Discrete version:

- Set up: One Infective in a randomly mixing population of Susceptibles
- At time t = 0, single infective random bumps into a Susceptible

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Discrete version:

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- Probability of transmission = β

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- Probability of transmission = β
- At time t = 1, single Infective remains infected with probability 1 − r
- At time t = k, single Infective remains infected with probability $(1 r)^k$

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Discrete version:

Expected number infected by original Infective:

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

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Discrete version:

Expected number infected by original Infective:

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

$$=\beta\left(1+(1-r)+(1-r)^{2}+(1-r)^{3}+\ldots\right)$$

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Similar story for continuous model.

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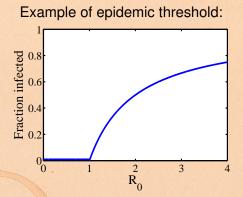
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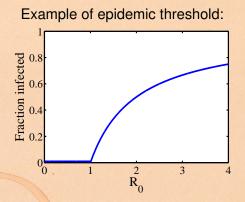
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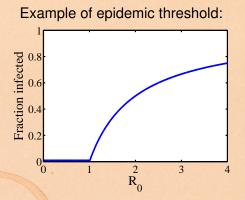
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Continuous phase transition.



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



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Valiant attempts to use SIR and co. elsewhere:

- Adoption of ideas/beliefs (Goffman & Newell, 1964) [6]
- Spread of rumors (Daley & Kendall, 1964, 1965) ^{[2, 3}
 Diffusion of innovations (Bass, 1969) ^[1]
 - Spread of fanetical behavior (Castillo-Chavez 8

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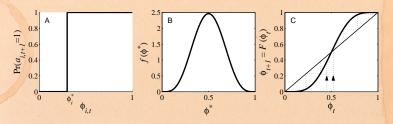
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Granovetter's model (recap of recap)

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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Disease models assume independence of infectious events.

- 3/10 = 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

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Threshold models only involve proportions: $3/10 \equiv 30/100$.

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Basic ingredients:

Incorporate memory of a contagious element [4, 5]

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Basic ingredients:

- Incorporate memory of a contagious element [4, 5]
- Population of N individuals, each in state S, I, or R.

Ip = fraction infected at time t
 probability of contact with infected individua
 With probability p, contact with infective fleads to an exposure

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

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- \$\phi_t\$ = fraction infected at time t
 = probability of <u>contact</u> with infected individual

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] Inviduals tremember last 7 contacts

Infection occurs if individual i's "threshold" i

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

Threshold of drawn from arbitrary distribution g a

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$S \Rightarrow I$

Individuals 'remember' last T contacts:

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

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

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

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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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$\mathsf{I} \Rightarrow \mathsf{R}$

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

$\textbf{R}\Rightarrow\textbf{S}$

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

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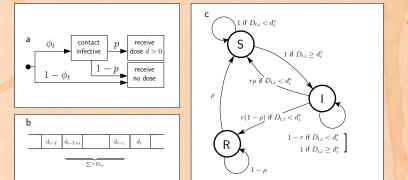
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A visual explanation



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Generalized mean-field model

Study SIS-type contagion first:

Final Hecovered individuals are immediately suscept again: $r = \rho = 1.$

 Look for steady-state behavior as a function o exposure probability p.
 Denote fixed points by ∞.

Homogeneous version:

All individuals have threshold d

All dose sizes are equal: d = 1

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Generalized mean-field model

Study SIS-type contagion first:

Recovered individuals are immediately susceptible again:

$$r = \rho = 1.$$

 Look for steady-state behavior as a function of exposure probability ρ.
 Denote fixed points by φ^{*}.

Homogeneous version:

All individuals have threshold d'

All dose sizes are equal: d = 1

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Generalized mean-field model

Study SIS-type contagion first:

 Recovered individuals are immediately susceptible again:

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 Look for steady-state behavior as a function of exposure probability p.

Homogeneous version:

- All individuals have threshold d^{*}
- All dose sizes are equal: d = 1

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Study SIS-type contagion first:

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Homogeneous version:

- All individuals have threshold d^{*}
- All dose sizes are equal: d = 1

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Study SIS-type contagion first:

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- Denote fixed points by ϕ^* .

Homogeneous version:

All individuals have threshold a
 All dose sizes are equal: d = 1

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Study SIS-type contagion first:

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Homogeneous version:

All individuals have threshold d*

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Study SIS-type contagion first:

 Recovered individuals are immediately susceptible again:

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Homogeneous version:

- All individuals have threshold d*
- All dose sizes are equal: d = 1

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Homogeneous, one hit models: Fixed points for r < 1, $d^* = 1$, and T = 1: • T = 1 means one positive interaction will in individual.

 $\underbrace{\frac{\rho\phi_t}{a} + \underbrace{\phi_t(1 - \rho\phi_t)}_{b}}_{b} \underbrace{(1 - r)}_{c}$

a: Fraction infected between t and t + 1, independent of past state or recovery.
b: Probability of being infected and not being reinfected.

c: Probability of not recovering

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

r < 1 means recovery is probabilistic.</p>

 d' = 1 means one positive interaction will infect a individual.
 Evolution of infection level.

a: Fraction infected between *t* and *t* + 1, independent of past state or recovery.b: Probability of being infected and not being reinfected.

c: Probability of not recovering

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

- r < 1 means recovery is probabilistic.</p>
- \blacktriangleright T = 1 means individuals forget past interactions.
- d* = 1 means one positive interaction will infect individual.
 Evolution of infection level:

 $\frac{p\phi_t}{a} + \underbrace{\phi_t(1-p\phi_t)}_{b} \underbrace{(1-r)}_{c}$

a: Fraction infected between t and t + 1, independent of past state or recovery.
b: Probability of being infected and not being reinfected.

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

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

- r < 1 means recovery is probabilistic.</p>
- \blacktriangleright T = 1 means individuals forget past interactions.
- d* = 1 means one positive interaction will infect an individual.
- Evolution of infection level:

 $\phi_{t+1} =$

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

- r < 1 means recovery is probabilistic.</p>
- \blacktriangleright T = 1 means individuals forget past interactions.
- d* = 1 means one positive interaction will infect an individual.
- Evolution of infection level:

$$\phi_{t+1} = \underbrace{p\phi_t}_{}$$

a: Fraction infected between t and t + 1, independent of past state or recovery.

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

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$$\phi_{t+1} = \underbrace{p\phi_t}_{\mathbf{a}} + \underbrace{\phi_t(1 - p\phi_t)}_{\mathbf{b}}$$

- a: Fraction infected between t and t + 1, independent of past state or recovery.
- b: Probability of being infected and not being reinfected.

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

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- Evolution of infection level:

$$\phi_{t+1} = \underbrace{p\phi_t}_{\mathbf{a}} + \underbrace{\phi_t(1-p\phi_t)}_{\mathbf{b}} \underbrace{(1-r)}_{\mathbf{c}}.$$

- a: Fraction infected between t and t + 1, independent of past state or recovery.
- b: Probability of being infected and not being reinfected.
- c: Probability of not recovering.

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• Set
$$\phi_t = \phi^*$$
:

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

• Set
$$\phi_t = \phi^*$$
:

$$\phi^* = \rho \phi^* + (1 - \rho \phi^*) \phi^* (1 - r)$$

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

• Set
$$\phi_t = \phi^*$$
:

$$\phi^* = p\phi^* + (1 - p\phi^*)\phi^*(1 - r)$$

 $\Rightarrow 1 = p + (1 - p\phi^*)(1 - r), \quad \phi^* \neq 0,$

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

• Set
$$\phi_t = \phi^*$$
:

$$\phi^* = p\phi^* + (1 - p\phi^*)\phi^*(1 - r)$$

 $\Rightarrow 1 = p + (1 - p\phi^*)(1 - r), \quad \phi^* \neq 0,$

$$\Rightarrow \phi^* = \frac{1 - r/p}{1 - r}$$
 and $\phi^* = 0$.

Spreading takes of it *p*/*r* > 1
 End continuous phase transition as for SIR r
 Goodness: Matches *B_i* = *d*/*y_i* > 1 condition

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

• Set
$$\phi_t = \phi^*$$
:

$$\phi^* = \rho \phi^* + (1 - \rho \phi^*) \phi^* (1 - r)$$

 $\Rightarrow 1 = p + (1 - p\phi^*)(1 - r), \quad \phi^* \neq 0,$

$$\Rightarrow \phi^* = \frac{1 - r/p}{1 - r}$$
 and $\phi^* = 0$.

• Critical point at $p = p_c = r$.

Find continuous phase transition as for SIR mo
 Goodness: Matches *B₀* = *d/n* > 1 condition

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

• Set $\phi_t = \phi^*$:

$$\phi^* = p\phi^* + (1 - p\phi^*)\phi^*(1 - r)$$

 $\Rightarrow 1 = p + (1 - p\phi^*)(1 - r), \quad \phi^* \neq 0,$

 $\Rightarrow \phi^* = \frac{1 - r/p}{1 - r}$ and $\phi^* = 0$.

Critical point at p = p_c = r.
 Spreading takes off if p/r > 1

Goodness: I

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

• Set
$$\phi_t = \phi^*$$
:

$$\phi^* = p\phi^* + (1 - p\phi^*)\phi^*(1 - r)$$

 $\Rightarrow 1 = p + (1 - p\phi^*)(1 - r), \quad \phi^* \neq 0,$

$$\Rightarrow \phi^* = \frac{1 - r/p}{1 - r}$$
 and $\phi^* = 0$.

• Critical point at $p = p_c = r$.

Spreading takes off if p/r > 1

Find continuous phase transition as for SIR model.

Goodness:

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

• Set
$$\phi_t = \phi^*$$
:

$$\phi^* = p\phi^* + (1 - p\phi^*)\phi^*(1 - r)$$

$$\Rightarrow \mathbf{1} = \mathbf{p} + (\mathbf{1} - \mathbf{p}\phi^*)(\mathbf{1} - \mathbf{r}), \quad \phi^* \neq \mathbf{0},$$

$$\Rightarrow \phi^* = \frac{1 - r/p}{1 - r}$$
 and $\phi^* = 0$.

- Critical point at $p = p_c = r$.
- Spreading takes off if p/r > 1
- Find continuous phase transition as for SIR model.
- Goodness: Matches $R_o = \beta/\gamma > 1$ condition.

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- Fixed points for r = 1, $d^* = 1$, and T > 1
 - r = 1 means recovery is immediate.
 T > 1 means individuals remember at least 2 interactions.
 - d* = 1 means only one positive interaction in pa interactions will infect individual.
 - Effect of individual interactions is independent from effect of others.
 - > Call of the steady state level of infection.
 - Pr(infected) = 1 Pr(uninfected)

 $\phi^* = \mathbf{1} - (\mathbf{1} - \boldsymbol{\rho} \phi^*)^T$

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Simple homogeneous examples Fixed points for r = 1, $d^* = 1$, and T > 1r = 1 means recovery is immediate.

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

- r = 1 means recovery is immediate.
- T > 1 means individuals remember at least 2 interactions.
- $d^* = 1$ means only one positive interaction in painteractions will infect individual.
- Effect of individual interactions is independent from the effect of others.
- Gall of the steady state level of infection.
- Pr(infected) = 1 Pr(uninfected)

 $\phi^* = \mathbf{1} - (\mathbf{1} - \boldsymbol{\rho} \phi^*)^T$

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

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

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- Effect of individual interactions is independent from effect of others.

 $\phi^* = \mathbf{1} - (\mathbf{1} - \boldsymbol{p}\phi^*)^T$

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

- r = 1 means recovery is immediate.
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- Call ϕ^* the steady state level of infection.

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

- r = 1 means recovery is immediate.
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- Effect of individual interactions is independent from effect of others.
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- Pr(infected) = 1 Pr(uninfected):

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

- r = 1 means recovery is immediate.
- T > 1 means individuals remember at least 2 interactions.
- d* = 1 means only one positive interaction in past T interactions will infect individual.
- Effect of individual interactions is independent from effect of others.
- Call ϕ^* the steady state level of infection.
- Pr(infected) = 1 Pr(uninfected):

$$\phi^* = 1 - (1 - p\phi^*)^T$$

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Closed form expression for \u03c6*:

$$\phi^* = 1 - (1 - p\phi^*)^T.$$

 $\Rightarrow p_c = 1/T$

Again find continuous phase transition
 Note: we can solve for *p* but not *a*^{*}

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Closed form expression for \u03c6*:

$$\phi^* = 1 - (1 - p\phi^*)^T.$$

Look for critical infection probability p_c.

 $\Rightarrow p_c = 1/T$

• Again find continuous phase transition • • Note: we can solve for p but not ϕ^* :

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Closed form expression for \u03c6*:

$$\phi^* = 1 - (1 - p\phi^*)^T.$$

Look for critical infection probability p_c.
 As φ^{*} → 0, we see

$$\phi^* \simeq pT\phi^*$$

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Closed form expression for \u03c6*:

$$\phi^* = 1 - (1 - p\phi^*)^T.$$

Look for critical infection probability p_c.
 As φ^{*} → 0, we see

$$\phi^* \simeq \rho T \phi^* \Rightarrow \rho_c = 1/T.$$

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Closed form expression for \u03c6*:

$$\phi^* = 1 - (1 - p\phi^*)^T.$$

Look for critical infection probability p_c.
 As φ^{*} → 0, we see

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Again find continuous phase transition...

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Closed form expression for \u03c6*:

$$\phi^* = 1 - (1 - p\phi^*)^T.$$

Look for critical infection probability p_c.
 As φ^{*} → 0, we see

$$\phi^* \simeq pT\phi^* \Rightarrow p_c = 1/T$$

Again find continuous phase transition...
 Note: we can solve for p but not \$\phi^*\$:

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

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

Start with r = 1, d^{*} = 1, and T ≥ 1 case we have just examined:

$$\phi^* = 1 - (1 - p\phi^*)^T.$$

Did not receive any infections in last T time steps
 And did not recover from a previous infection.

 $H_1 = \{\dots, d_{t-T-2}, d_{t-T-1}, 1, \underbrace{0, 0, \dots, 0, 0}_{T \text{ 0's}}\}$

 With history F_n, probability of being infected (n recovering mone time step) is 1 - r

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

Start with r = 1, d^{*} = 1, and T ≥ 1 case we have just examined:

$$\phi^* = 1 - (1 - p\phi^*)^T.$$

For r < 1, add to right hand side fraction who:</p>

 $H_1 = \{\dots, d_{t-T-2}, d_{t-T-1}, 1, \underbrace{0, 0, \dots, 0, 0}_{T \ 0's}\}$

With history H₁, probability of being infected (necessary) is 1 - x.

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

Start with r = 1, d^{*} = 1, and T ≥ 1 case we have just examined:

$$\phi^* = 1 - (1 - p\phi^*)^T$$
.

For r < 1, add to right hand side fraction who:
 1. Did not receive any infections in last T time steps,

 $H_1 = \{\dots, d_{t-T-2}, d_{t-T-1}, 1, \underbrace{0, 0, \dots, 0, 0}_{T \text{ 0's}}\}$

 With history H, probability of being infected (n removering n one time step) is 1 – n.

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

Start with r = 1, d^{*} = 1, and T ≥ 1 case we have just examined:

$$\phi^* = 1 - (1 - p\phi^*)^T$$
.

For r < 1, add to right hand side fraction who:

- 1. Did not receive any infections in last T time steps,
- 2. And did not recover from a previous infection.

$$H_1 = \{\dots, d_{t-T-2}, d_{t-T-1}, 1, \underbrace{0, 0, \dots, 0, 0}_{T \text{ 0's}}\}$$

 With history F_h, probability of being infected (n recovering in one time step) is 1 - it

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

Start with r = 1, d[∗] = 1, and T ≥ 1 case we have just examined:

$$\phi^* = 1 - (1 - p\phi^*)^T$$
.

For r < 1, add to right hand side fraction who:

- 1. Did not receive any infections in last T time steps,
- 2. And did not recover from a previous infection.

Define corresponding dose histories. Example:

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

Start with r = 1, d^{*} = 1, and T ≥ 1 case we have just examined:

$$\phi^* = 1 - (1 - p\phi^*)^T$$
.

For r < 1, add to right hand side fraction who:
 1. Did not receive any infections in last T time steps,
 2. And did not recover from a previous infection.

Define corresponding dose histories. Example:

$$H_1 = \{\dots, d_{t-T-2}, d_{t-T-1}, 1, \underbrace{0, 0, \dots, 0, 0}_{T \text{ 0's}}\},$$

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

Start with r = 1, d^{*} = 1, and T ≥ 1 case we have just examined:

$$\phi^* = 1 - (1 - p\phi^*)^T$$
.

For r < 1, add to right hand side fraction who:

- 1. Did not receive any infections in last T time steps,
- 2. And did not recover from a previous infection.

Define corresponding dose histories. Example:

$$H_1 = \{\dots, d_{t-T-2}, d_{t-T-1}, 1, \underbrace{0, 0, \dots, 0, 0}_{T \text{ 0's}}\},$$

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

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

In general, relevant dose histories are:

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

Overall probabilities for dose histories occurring:

 $P(H_1) = p\phi^*(1 - p\phi^*)^T(1 - r),$

$$P(H_{m+1}) = \underbrace{p\phi^*}_{a} \underbrace{(1 - p\phi^*)^{T+m}}_{b} \underbrace{(1 - r)^{m+1}}_{c}$$

a: Pr(infection T + m + 1 time steps ago) b: Pr(no doses received in T + m time steps since c: Pr(no recovery in *m* chances)

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

In general, relevant dose histories are:

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

Overall probabilities for dose histories occurring:

$$P(H_1) = p\phi^*(1 - p\phi^*)^T(1 - r),$$

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

In general, relevant dose histories are:

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

Overall probabilities for dose histories occurring:

$$P(H_1) = p\phi^*(1 - p\phi^*)^T(1 - r),$$

 $P(H_{m+1}) =$



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

In general, relevant dose histories are:

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

Overall probabilities for dose histories occurring:

$$P(H_1) = p\phi^*(1 - p\phi^*)^T(1 - r)$$

$$P(H_{m+1}) = \underbrace{p\phi^*}_{a}$$

a: Pr(infection T + m + 1 time steps ago)

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

In general, relevant dose histories are:

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

Overall probabilities for dose histories occurring:

$$P(H_1) = p\phi^*(1 - p\phi^*)^T(1 - r),$$

$$P(H_{m+1}) = \underbrace{p\phi^*}_{a} \underbrace{(1 - p\phi^*)^{T+m}}_{b}$$

a: Pr(infection T + m + 1 time steps ago)
b: Pr(no doses received in T + m time steps since)

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

In general, relevant dose histories are:

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

Overall probabilities for dose histories occurring:

$$P(H_1) = p\phi^*(1 - p\phi^*)^T(1 - r),$$

$$P(H_{m+1}) = \underbrace{p\phi^{*}}_{a} \underbrace{(1 - p\phi^{*})^{T+m}}_{b} \underbrace{(1 - r)^{m+1}}_{c}$$

a: Pr(infection T + m + 1 time steps ago)
b: Pr(no doses received in T + m time steps since)
c: Pr(no recovery in m chances)

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

Pr(recovery) = Pr(seeing no doses for at least T time steps and recovering)

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

 Pr(recovery) = Pr(seeing no doses for at least T time steps and recovering)

$$= r \sum_{m=0}^{\infty} P(H_{T+m})$$

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

 Pr(recovery) = Pr(seeing no doses for at least T time steps and recovering)

$$= r \sum_{m=0}^{\infty} P(H_{T+m}) = r \sum_{m=0}^{\infty} p \phi^* (1 - p \phi^*)^{T+m} (1 - r)^n$$

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

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$$= r \frac{p\phi^*(1-p\phi^*)^T}{1-(1-p\phi^*)(1-r)}$$

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

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$$= r \frac{p\phi^*(1 - p\phi^*)^T}{1 - (1 - p\phi^*)(1 - r)}$$

Fixed point equation:

$$\phi^* = 1 - \frac{r(1 - p\phi^*)^T}{1 - (1 - p\phi^*)(1 - r)}.$$

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

Fixed point equation (again):

$$\phi^* = 1 - \frac{r(1 - p\phi^*)^T}{1 - (1 - p\phi^*)(1 - r)}.$$

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Decreasing r keeps individuals infected for long



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

Fixed point equation (again):

$$\phi^* = 1 - \frac{r(1 - p\phi^*)^T}{1 - (1 - p\phi^*)(1 - r)}.$$

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Find critical exposure probability by examining above as φ^{*} → 0.

mean recovery time for simple relaxat





Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

Fixed point equation (again):

$$\phi^* = 1 - \frac{r(1 - p\phi^*)^T}{1 - (1 - p\phi^*)(1 - r)}.$$

Find critical exposure probability by examining above as φ^{*} → 0.

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

where τ = mean recovery time for simple relaxation process.

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Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$

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$$\phi^* = 1 - \frac{r(1 - p\phi^*)^T}{1 - (1 - p\phi^*)(1 - r)}.$$

Find critical exposure probability by examining above as φ^{*} → 0.

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

where τ = mean recovery time for simple relaxation process.

 Decreasing r keeps individuals infected for longer and decreases p_c.

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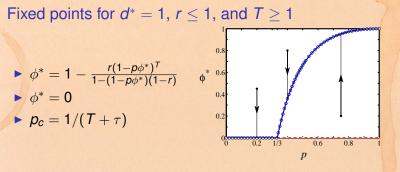
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Epidemic threshold:



- Example details: $T = 2 \& r = 1/2 \Rightarrow p_c = 1/3$.
- Blue = stable, red = unstable, fixed points.
- $\tau = 1/r 1$ = characteristic recovery time = 1.
- $T + \tau \simeq$ average memory in system = 3.

oifurcation.

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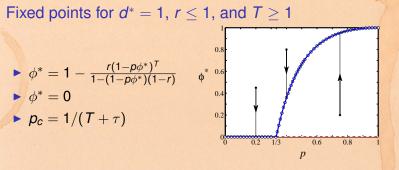
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Epidemic threshold:



- Example details: $T = 2 \& r = 1/2 \Rightarrow p_c = 1/3$.
- Blue = stable, red = unstable, fixed points.
- $\tau = 1/r 1$ = characteristic recovery time = 1.
- $T + \tau \simeq$ average memory in system = 3.
- Phase transition can be seen as a transcritical bifurcation.^[11]

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All right: d* = 1 models correspond to simple disease spreading models.

Again first consider SIS with immediate recovery (*t* = 1)
 Also continue to assume unit dose sizes (*f*(*d*) = δ(*d* - 1)).
 To be infected, must have at least *d*⁺ exposures it least *T* time steps

Fixed point equation:

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- All right: d* = 1 models correspond to simple disease spreading models.
- What if we allow $d^* \ge 2$?

- Also continue to assume unit dose sizes $(l(d) = \delta(d 1))$.
- To be infected, must have at least d^{*} exposures i last T time steps.
 - Fixed point equation:

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- All right: d* = 1 models correspond to simple disease spreading models.
- What if we allow $d^* \ge 2$?
- Again first consider SIS with immediate recovery (r = 1)

 To be intected, must have at least d^{*} exposures i last T time steps.

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- All right: d* = 1 models correspond to simple disease spreading models.
- What if we allow $d^* \ge 2$?
- Again first consider SIS with immediate recovery (r = 1)
- Also continue to assume unit dose sizes $(f(d) = \delta(d-1)).$

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- All right: d* = 1 models correspond to simple disease spreading models.
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- Also continue to assume unit dose sizes $(f(d) = \delta(d-1)).$
- To be infected, must have at least d* exposures in last T time steps.

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- All right: d* = 1 models correspond to simple disease spreading models.
- What if we allow $d^* \ge 2$?
- Again first consider SIS with immediate recovery (r = 1)
- Also continue to assume unit dose sizes $(f(d) = \delta(d-1)).$
- To be infected, must have at least d* exposures in last T time steps.
- Fixed point equation:

$$\phi^* = \sum_{i=d^*}^T \binom{T}{i} (p\phi^*)^i (1-p\phi^*)^{T-i}.$$

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- All right: d* = 1 models correspond to simple disease spreading models.
- What if we allow $d^* \ge 2$?
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- Also continue to assume unit dose sizes $(f(d) = \delta(d-1)).$
- To be infected, must have at least d* exposures in last T time steps.
- Fixed point equation:

$$\phi^* = \sum_{i=d^*}^T \binom{T}{i} (p\phi^*)^i (1-p\phi^*)^{T-i}.$$

• As always, $\phi^* = 0$ works too.

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

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ture: see appear s. 8.27/32).



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

Exactly solvable for small T.

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

Exactly solvable for small *T*.
 e.g., for *d** = 2, *T* = 3:

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

Exactly solvable for small T.

• e.g., for $d^* = 2$, T = 3:

Fixed point equation: $\phi^* =$ $3p^2 \phi^{*2}(1 - p\phi^*) + p^3 \phi^{*3}$ Generalized Contagion

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

Exactly solvable for small T.

• e.g., for $d^* = 2$, T = 3:

- Fixed point equation: $\phi^* =$ $3p^2\phi^{*2}(1-p\phi^*)+p^3\phi^{*3}$
- See new structure: see a saddle node bifurcation^[11] appear as p increases.

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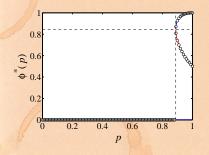
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Fixed points for r = 1, $d^* > 1$, and $T \ge 1$

Exactly solvable for small T.



- Fixed point equation: φ^{*} = 3p²φ^{*2}(1 - pφ^{*}) + p³φ^{*3}

 See new structure: see a saddle node bifurcation ^[11] appear as *p* increases.
- $(p_b, \phi^*) = (8/9, 27/32).$

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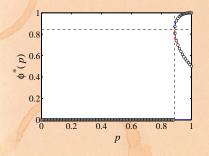
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Homogeneous, multi-hit models:

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

Exactly solvable for small T.

• e.g., for
$$d^* = 2$$
, $T = 3$:



 Fixed point equation: φ* = 3p²φ*²(1 - pφ*) + p³φ*³

 See new structure: see a saddle node bifurcation ^[11] appear as *p* increases.

 See behavior akin to output of Granovetter's threshold model.

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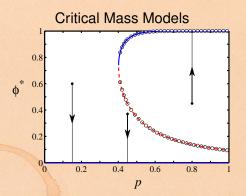
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Homogeneous, multi-hit models:

Another example:



▶ $r = 1, d^* = 3, T = 12$

Saddle-node bifurcation.

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

d^{*} = 1 → d^{*} > 1: jump between continuous phase transition and pure critical mass model.

Unstable curve for d* = 2 does not hit of a = 0.

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

 d^{*} = 1 → d^{*} > 1: jump between continuous phase transition and pure critical mass model.

Unstable curve for d* = 2 does not hit of a = 0. Generalized Contagion

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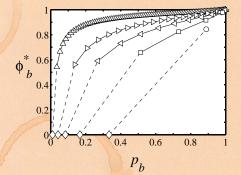
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See either simple phase transition or saddle-node bifurcation, nothing in between.



Bifurcation points for example fixed T, varying d*:



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▶ T = 96 (△).▶ T = 24 (▷),▶ T = 12 (⊲),▶ T = 6 (□),▶ $T = 3 (\bigcirc),$



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Fun with amazon's recommender system (⊞). [amaznode.fladdict.net]



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For r < 1, need to determine probability of recovering as a function of time since dose load last dropped below threshold.



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For r < 1, need to determine probability of recovering as a function of time since dose load last dropped below threshold.

Partially summed random walks:

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

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For r < 1, need to determine probability of recovering as a function of time since dose load last dropped below threshold.

Partially summed random walks:

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

• Example for T = 24, $d^* = 14$:

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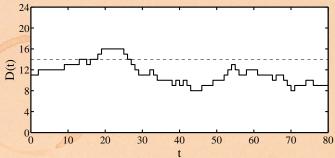


For r < 1, need to determine probability of recovering as a function of time since dose load last dropped below threshold.

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• Example for
$$T = 24$$
, $d^* = 14$:



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• Define γ_m as fraction of individuals for whom D(t) last equaled, and his since been below, their threshold *m* time steps ago,

Fixed point equation

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- Define γ_m as fraction of individuals for whom D(t) last equaled, and his since been below, their threshold *m* time steps ago,
- Fraction of individuals below threshold but not recovered:

$$\Gamma(\boldsymbol{\rho},\phi^*;\boldsymbol{r})=\sum_{m=1}^{\infty}(1-\boldsymbol{r})^m\gamma_m(\boldsymbol{\rho},\phi^*).$$

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- Define γ_m as fraction of individuals for whom D(t) last equaled, and his since been below, their threshold m time steps ago,
- Fraction of individuals below threshold but not recovered:

$$\Gamma(\boldsymbol{p},\phi^*;\boldsymbol{r})=\sum_{m=1}^{\infty}(1-\boldsymbol{r})^m\gamma_m(\boldsymbol{p},\phi^*).$$

Fixed point equation:

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

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Two subsequences do this: $\{d_{n-2}, d_{n-1}, d_n, d_{n+1}\} = \{1, 1, 0, 0\}$ and $\{d_{n-2}, d_{n-1}, d_n, d_{n+1}\} = \{1, 1, 0, 0\}$

 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 an combination of two subsequences:

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Want to examine how dose load can drop below threshold of d* = 2:

$$D_n = 2 \Rightarrow D_{n+1} = 1$$

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Want to examine how dose load can drop below threshold of d* = 2:

$$D_n = 2 \Rightarrow D_{n+1} = 1$$

Two subsequences do this:

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Want to examine how dose load can drop below threshold of d* = 2:

$$D_n = 2 \Rightarrow D_{n+1} = 1$$

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Want to examine how dose load can drop below threshold of d* = 2:

$$D_n = 2 \Rightarrow D_{n+1} = 1$$

 ► Two subsequences do this: {*d_{n-2}*, *d_{n-1}*, *d_n*, *d_{n+1}*} = {1, 1, 0, 0} and {*d_{n-2}*, *d_{n-1}*, *d_n*, *d_{n+1}*, *d_{n+2}*} = {1, 0, 1, 0, 0}.
 ► 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:

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

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Determine number of sequences of length *m* that keep dose load below d* = 2.

 $m = N_a \cdot 1 + N_b \cdot 3$

Possible values for N_b:

 $0, 1, 2, \ldots, \left\lfloor \frac{m}{3} \right\rfloor$

where $\lfloor \cdot \rfloor$ means floor. Corresponding possible values for N_a :

 $m, m-3, m-6, \ldots, m-3 \left| \frac{m}{3} \right|$

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- Determine number of sequences of length *m* that keep dose load below d* = 2.
- N_a = number of $a = \{0\}$ subsequences.

 $m = N_a \cdot 1 + N_b \cdot 3$

Possible values for N_b:

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- Determine number of sequences of length *m* that keep dose load below d* = 2.
- N_a = number of $a = \{0\}$ subsequences.
- N_b = number of $b = \{1, 0, 0\}$ subsequences.

Corresponding possible values for N_{a} :

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 $m = N_a \cdot 1 + N_b \cdot 3$

Corresponding possible values for N_a :

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- N_a = number of $a = \{0\}$ subsequences.
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$$m = N_a \cdot 1 + N_b \cdot 3$$

Possible values for N_b :

$$0, 1, 2, \ldots, \left\lfloor \frac{m}{3} \right\rfloor$$

where $\lfloor \cdot \rfloor$ means floor. Corresponding possible values for N_a : $m, m - 3, m - 6, \dots, m - 3$

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- Determine number of sequences of length *m* that keep dose load below d* = 2.
- N_a = number of $a = \{0\}$ subsequences.
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$$m = N_a \cdot 1 + N_b \cdot 3$$

Possible values for N_b :

$$0, 1, 2, \ldots, \left\lfloor \frac{m}{3} \right\rfloor$$

where [·] means floor.
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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How many ways to arrange N_a a's and N_b b's?

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How many ways to arrange N_a a's and N_b b's?
 Think of overall sequence in terms of subsequences:

 $\{Z_1, Z_2, \ldots, Z_{N_a+N_b}\}$

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How many ways to arrange N_a a's and N_b b's?
 Think of overall sequence in terms of subsequences:

 $\{Z_1, Z_2, \ldots, Z_{N_a+N_b}\}$

• $N_a + N_b$ slots for subsequences.

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How many ways to arrange N_a a's and N_b b's?
 Think of overall sequence in terms of subsequences:

 $\{Z_1, Z_2, \ldots, Z_{N_a+N_b}\}$

N_a + *N_b* slots for subsequences.
 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:

$$\sum_{N_b=0}^{\lfloor m/3 \rfloor} \binom{N_b+N_a}{N_b} = \sum_{k=0}^{\lfloor m/3 \rfloor} \binom{m-2k}{k}$$

where $k = N_b$ and we have used $m = N_a + 3N_b$.

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Total number of allowable sequences of length m:

$$\sum_{N_b=0}^{\lfloor m/3 \rfloor} \binom{N_b+N_a}{N_b} = \sum_{k=0}^{\lfloor m/3 \rfloor} \binom{m-2k}{k}$$

where $k = N_b$ and we have used $m = N_a + 3N_b$. $P(a) = (1 - p\phi^*)$ and $P(b) = p\phi^*(1 - p\phi^*)^2$

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Total probability of allowable sequences of length m:

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

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

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

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

$$\begin{split} D_{1} &= \{1, 1, 0, 0, D_{m-1}^{a,b}\} \\ D_{2} &= \{1, 1, 0, 0, D_{m-2}^{a,b}, 1\} \\ D_{3} &= \{1, 1, 0, 0, D_{m-3}^{a,b}, 1, 0\} \\ D_{4} &= \{1, 0, 1, 0, 0, D_{m-2}^{a,b}\} \\ D_{5} &= \{1, 0, 1, 0, 0, D_{m-3}^{a,b}, 1\} \\ D_{6} &= \{1, 0, 1, 0, 0, D_{m-4}^{a,b}, 1, 0\} \\ \end{split}$$

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

$= (p\phi)^2 (1 - p\phi)^2 \chi_{m-1}(p, \phi)$ $= (p\phi)^3(1-p\phi)^2\chi_{m-2}(p,\phi)$ $= (\rho\phi)^3(1-\rho\phi)^3\chi_{m-3}(\rho,\phi)$ $= (p\phi)^2(1-p\phi)^3\chi_{m-2}(p,\phi)$ $= (p\phi)^3(1-p\phi)^3\chi_{m-3}(p,\phi)$ $= (p\phi)^3 (1 - p\phi)^4 \chi_{m-4}(p, \phi)$

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

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

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

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

and

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

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

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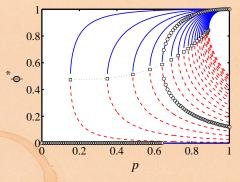
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$$T = 3, d^* = 2$$



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

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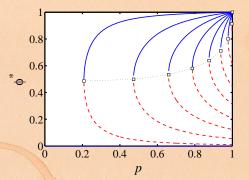
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 $T = 2, d^* = 2$



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

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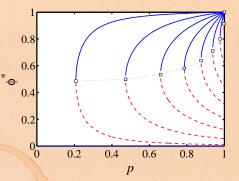
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 $T = 2, d^* = 2$



r = 0.01, 0.05, 0.10, ..., 0.3820 ± 0.0001.
 No spreading for r ≥ 0.382.

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Two kinds of contagion processes:

Continuous phase transition: STR-like
 Saddle node bifurcation: threshold model-like
 d* = 1: spreading from small seeds possible
 d* > 1: critical mass model.
 Are other behaviors possible?

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Two kinds of contagion processes:

 Continuous phase transition: SIR-like.
 and the phase transition threshold model-like
 Are other behaviors possible?

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Two kinds of contagion processes:

- 1. Continuous phase transition: SIR-like.
- 2. Saddle-node bifurcation: threshold model-like.
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 d* > 1: critical mass model.
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Two kinds of contagion processes:

- 1. Continuous phase transition: SIR-like.
- 2. Saddle-node bifurcation: threshold model-like.
- $d^* = 1$: spreading from small seeds possible.

Are other behaviors possible?

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Two kinds of contagion processes:
 1. Continuous phase transition: SIR-like.

- 2. Saddle-node bifurcation: threshold model-like.
- $d^* = 1$: spreading from small seeds possible.
- $d^* > 1$: critical mass model.

Are other behaviors possible?

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Two kinds of contagion processes:

- 1. Continuous phase transition: SIR-like.
- 2. Saddle-node bifurcation: threshold model-like.
- $d^* = 1$: spreading from small seeds possible.
- $d^* > 1$: critical mass model.

Are other behaviors possible?

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Now allow for dose distributions (f) and threshold distributions (g) with width.

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

> > bility that <u>one dose</u> will exceed reshold of a random individual in of most vulnerable individual

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n a (~ 47 of 63

- Now allow for dose distributions (f) and threshold distributions (g) with width.
- Key quantities:

$$oldsymbol{P}_k = \int_0^\infty \mathrm{d} d^* \, g(d^*) oldsymbol{P}\left(\sum_{j=1}^k d_j \geq d^*
ight) \, ext{where 1} \leq k \leq T.$$

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- Key quantities:

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

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

▶ e.g.,

- P₁ = Probability that <u>one dose</u> will exceed the threshold of a random individual
 - = Fraction of most vulnerable individuals.

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Fixed point equation:

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

Expand around at = 0 to find when spread from single seed is possible;

 $|pP_1T \ge 1|$ or $|\Rightarrow p_c = 1/(TP_1)|$

P₁T is the expected number of vulnerables the initial infected individual meets before recovering.
 pP₁T is the expected number of successful infections (equivalent to R₀).

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Very good:

1. P_1T is the expected number of vulnerables the initial infected individual meets before recovering.

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Expand around $\phi^* = 0$ to find when spread from single seed is possible:

$$pP_1T \ge 1$$
 or $\Rightarrow p_c = 1/(TP_1)$

Very good:

- 1. $P_1 T$ is the expected number of vulnerables the initial infected individual meets before recovering.
- pP₁T is ... the expected number of successful infections (equivalent to R₀).
- Observe: p_c may exceed 1 meaning no spreading from a small seed.

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Next: Determine slope of fixed point curve at critical point p_c.

 Expand fixed point equation around (p, o^{*}) = (p_o
 Find slope depends on (P₁ − P₂/2)^[5] (see appendix).

Behavior near fixed point depends on whether the

1. positive: $P_1 > P_2/2$ (continuous phase transition) 2. negative: $P_1 < P_2/2$ (discontinuous phase transition)

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Next: Determine slope of fixed point curve at critical point p_c.

Expand fixed point equation around $(p, \phi^*) = (p_c, 0)$.

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1. positive: $P_1 > P_2/2$ (continuous phase transition) 2. pegative: $P_1 < P_2/2$ (discontinuous phase transition)

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- Next: Determine slope of fixed point curve at critical point p_c.
- Expand fixed point equation around $(p, \phi^*) = (p_c, 0)$.
- Find slope depends on $(P_1 P_2/2)^{[5]}$ (see appendix).

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- Behavior near fixed point depends on whether this slope is

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- Next: Determine slope of fixed point curve at critical point p_c.
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 - 1. positive: $P_1 > P_2/2$ (continuous phase transition)
 - 2. negative: $P_1 < P_2/2$ (discontinuous phase transition)

Now find <u>three</u> basic universal classes of contagion models...

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Example configuration:

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

1. $d_* = 0.5$ 2. $d_* = 1.6$ 3. $d_* = 3$

sizes matters, details are not

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Example configuration:

- Dose sizes are lognormally distributed with mean 1 and variance 0.433.
- Memory span: T = 10.

1. $d_* = 0.5$ 2. $d_* = 1.6$ 3. $d_* = 3$

izes matters, details are not

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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. $d_* = 3$

zes matters, details are no

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Example configuration:

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- 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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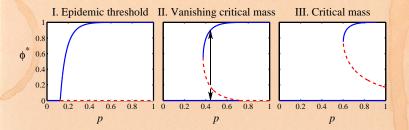
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Three universal classes



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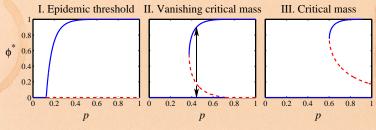
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Three universal classes



Epidemic threshold:

 $P_1 > P_2/2, p_c = 1/(TP_1) < 1$

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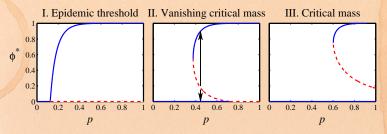
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Three universal classes



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

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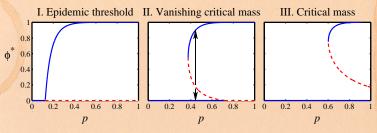
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Three universal classes



- Epidemic threshold:
- Vanishing critical mass:
- Pure critical mass:

 $P_1 > P_2/2, p_c = 1/(TP_1) < 1$ $P_1 < P_2/2, p_c = 1/(TP_1) < 1$ $P_1 < P_2/2, p_c = 1/(TP_1) > 1$

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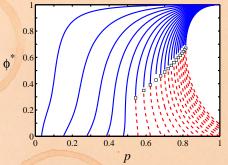
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Heterogeneous case

Now allow r < 1:



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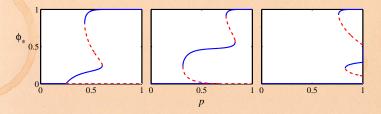
References

► 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





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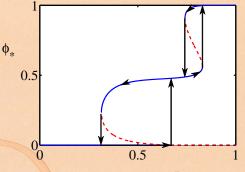
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- Due to heterogeneity in individual thresholds.
- Three classes based on behavior for small seeds.
- Same model classification holds: I, II, and III.

Hysteresis in vanishing critical mass models



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Memory is a natural ingredient.

I. Epidemic Threshold
 II. Vanishing Critical Mass
 III. Critical Mass

Dramatic changes in behavior possible.

To change kind of model: adjust memory, recover fraction of vulnerable individuals (*T*, *r*, *p*, *P*₁, and/o

 To change behavior given model: "adjust" probabili of exposure (p) and/or initial number infected (p₀).

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Memory is a natural ingredient.
 Three universal classes of contagion processes:

 I. Epidemic Threshold
 II. Vanishing Critical Mass
 III. Critical Mass

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Memory is a natural ingredient.
 Three universal classes of contagion processes:

 I. Epidemic Threshold
 II. Vanishing Critical Mass

- 3. III. Critical Mass
- Dramatic changes in behavior possible.

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Memory is a natural ingredient.

- Three universal classes of contagion processes:
 - 1. I. Epidemic Threshold
 - 2. II. Vanishing Critical Mass
 - 3. 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).

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Memory is a natural ingredient.

- Three universal classes of contagion processes:
 - 1. I. Epidemic Threshold
 - 2. II. Vanishing Critical Mass
 - 3. 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 (\u03c6₀).

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Single seed infects others if $pP_1(T + \tau) \ge 1$.

than a small group of super-spreaders or influentials

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Single seed infects others if pP₁(T + τ) ≥ 1.
Key quantity: p_c = 1/[P₁(T + τ)]

Depends only on:

 System Memory (T + τ).
 Fraction of highly vulnerable individuals (P₁).

 Details unimportant: Many threshold and dose distributions give same P_k.

Another example of a model where

vulnerable/guilible population may be more importation than a small group of super-spreaders or influentials

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- Single seed infects others if $pP_1(T + \tau) \ge 1$.
- Key quantity: $p_c = 1/[P_1(T + \tau)]$
- If $p_c < 1 \Rightarrow$ contagion can spread from single seed.
 - 1. System Memory ($T + \tau$
 - 2. Fraction of highly vulnerable individuals (P_1)
- Details unimportant: Many threshold and dose distributions give same P_k.
- Another example of a model where
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$$\phi^* = \sum_{k=1}^T {T \choose k} \mathcal{P}_k (\mathcal{p}\phi^*)^k (1-\mathcal{p}\phi^*)^{T-k},$$

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

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

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$$\begin{split} b^{*} &= \sum_{k=1}^{T} {T \choose k} P_{k} (p\phi^{*})^{k} (1 - p\phi^{*})^{T-k}, \\ &= \sum_{k=1}^{T} {T \choose k} P_{k} (p\phi^{*})^{k} \sum_{j=0}^{T-k} {T-k \choose j} (-p\phi^{*})^{j}, \\ &= \sum_{k=1}^{T} \sum_{j=0}^{T-k} {T \choose k} {T-k \choose j} P_{k} (-1)^{j} (p\phi^{*})^{k+j}, \\ &= \sum_{m=1}^{T} \sum_{k=1}^{m} {T \choose k} {T-k \choose m-k} P_{k} (-1)^{m-k} (p\phi^{*})^{m}, \end{split}$$

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$$\begin{split} \dot{\phi}^{*} &= \sum_{k=1}^{T} {\binom{T}{k}} P_{k} (p\phi^{*})^{k} (1-p\phi^{*})^{T-k}, \\ &= \sum_{k=1}^{T} {\binom{T}{k}} P_{k} (p\phi^{*})^{k} \sum_{j=0}^{T-k} {\binom{T-k}{j}} (-p\phi^{*})^{j}, \\ &= \sum_{k=1}^{T} \sum_{j=0}^{T-k} {\binom{T}{k}} {\binom{T-k}{j}} P_{k} (-1)^{j} (p\phi^{*})^{k+j}, \\ &= \sum_{m=1}^{T} \sum_{k=1}^{m} {\binom{T}{k}} {\binom{T-k}{m-k}} P_{k} (-1)^{m-k} (p\phi^{*})^{m}, \\ &= \sum_{m=1}^{T} C_{m} (p\phi^{*})^{m} \end{split}$$

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

since

$$\binom{T}{k}\binom{T-k}{m-k} = \frac{1}{2}$$

$$= \frac{T!}{k!(T-k)!} \frac{(T-k)!}{(m-k)!(T-m)!} \\= \frac{T!}{m!(T-m)!} \frac{m!}{k!(m-k)!} \\= \binom{T}{m} \binom{m}{k}.$$

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Linearization gives

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

where $C_1 = TP_1(=1/p_c)$ and $C_2 = \binom{T}{2}(-2P_1 + P_2)$.

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Linearization gives

$$\phi^* \simeq C_1 \rho \phi^* + C_2 \rho_c^2 \phi^{*2}.$$

where $C_1 = TP_1(=1/p_c)$ and $C_2 = {T \choose 2}(-2P_1 + P_2)$. Using $p_c = 1/(TP_1)$:

$$\phi^* \simeq rac{C_1}{C_2 p_c^2} (\rho - \rho_c) = rac{T^2 P_1^3}{(T-1)(P_1 - P_2/2)} (\rho - \rho_c).$$

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Linearization gives

$$\phi^* \simeq C_1 \rho \phi^* + C_2 \rho_c^2 {\phi^*}^2.$$

where $C_1 = TP_1(=1/p_c)$ and $C_2 = {T \choose 2}(-2P_1 + P_2)$. • Using $p_c = 1/(TP_1)$:

$$\phi^* \simeq rac{C_1}{C_2 \rho_c^2} (p - p_c) = rac{T^2 P_1^3}{(T - 1)(P_1 - P_2/2)} (p - p_c).$$

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

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