Generalized Contagion

Last updated: 2018/03/23, 12:08:15

Complex Networks | @networksvox CSYS/MATH 303, Spring, 2018

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"A generalized model of social and biological contagion" Dodds and Watts, J. Theor. Biol., **232**, 587–604, 2005.^[6]

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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 soc contagion?

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 How can we categorize real-world contagion
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 Focus: mean field models.

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Basic questions about contagion

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Basic questions about contagion

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Can we connect models of disease-like and social contagion?

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> S(t) + I(t) + R(t) = 1Presumes random interactions (mass-action principle) Interactions are independent (no memory) Discrete and continuous time versions

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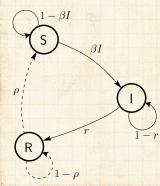
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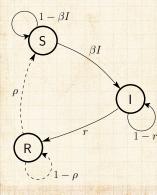
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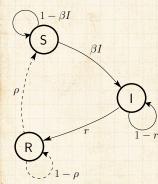
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 β for being infected given contact with infected

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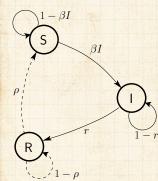
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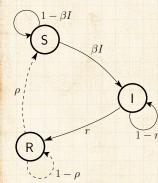
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Differential equations for continuous model

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

 β , r, and ρ are now rates.

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Reproduction Number R_0 :

 R_0 = expected number of infected individuals resulting from a single initial infective Epidemic threshold: If $R_0 > 1$, 'epidemic' occu

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Differential equations for continuous model

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Reproduction Number R_0

Discrete version:

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

At time t = 0, single infective randomly bumps in a Susceptible

Probability of transmission = β At time t = 1, single infective remains infected v probability $1 - \tau$

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

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Discrete version:

- Set up: One Infective in a randomly mixing population of Susceptibles
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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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$$= \beta \frac{1}{1 - (1-r)}$$

Similar story for continuous mode

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Discrete version:

Expected number infected by original Infective:

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🚳 Similar story for continuous model.

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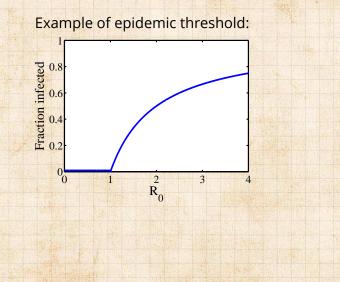
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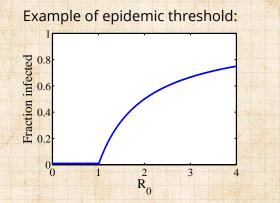
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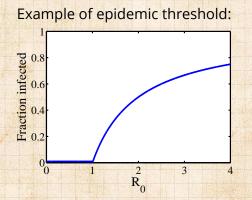
Poccs Principles of Complex Systems @pocsvox What's the Story?



🚳 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) Spread of rumors (Daley & Kendall, 1964, 1965) Diffusion of innovations (Bass, 1969) Spread of fanatical behavior (Castillo-Chávez &

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

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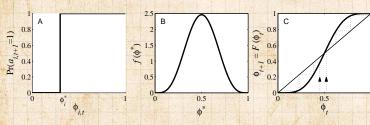
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Granovetter's model (recap of recap)

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.

Threshold models only involve proportions. $3/10 \equiv 30/100$. Threshold models ignore exact sequence of influences Threshold models assume immediate pollin Mean-field models neglect network structur

Metwork effects only part of story: media, advertising, direct marketing.

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Network effects only part of story: media, advertising, direct marketing.

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Basic ingredients:

Incorporate memory of a contagious element^[5, 6]
Population of *N* individuals, each in state S, I, or R
Each individual randomly contacts another at each time step.

 ϕ_t = traction infected at time t = probability of <u>contact</u> with infected individua With probability p_t contact with infective leads to an exposure.

If exposed, individual receives a dose of size ddrawn from distribution *1*. Otherwise d = 0.

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- Incorporate memory of a contagious element^[5, 6]
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Basic ingredients:

- Incorporate memory of a contagious element^[5, 6]
 - \mathbb{B} 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 <u>contact</u> with infected individual

With probability p_i 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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 $S \Rightarrow I$

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 $S \Rightarrow I$

Individuals 'remember' last T contacts: $D_{t,i} = \sum_{t'=t-T+1}^{t} d_i(t')$ Infection occurs if individual 's 'threshold' is

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

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 $S \Rightarrow I$

lndividuals 'remember' last T contacts:

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

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

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

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

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Individuals 'remember' last T contacts:

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

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

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

 $S \Rightarrow I$

 $\underset{i}{\bigotimes}$ 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*.

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

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$I \Rightarrow R$

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

$R \Rightarrow S$

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

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A visual explanation



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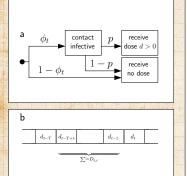
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с

ρ

R

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

 $r\rho \text{ if } D_{t,i} < d_i^*$

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

 $-\rho$

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

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

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

S

Study SIS-type contagion first:

Recovered individuals are immediately susceptible again:

Look for steady-state behavior as a function exposure probability p. Denote fixed points by ϕ^* .

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Study SIS-type contagion first:

Recovered individuals are immediately susceptible again:

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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.

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Study SIS-type contagion first:

Recovered individuals are immediately susceptible again:

 $\rho = 1.$

Look for steady-state behavior as a function of exposure probability *p*.
 Denote fixed points by φ*.

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Study SIS-type contagion first:

Recovered individuals are immediately susceptible again:

 $\rho = 1.$

Look for steady-state behavior as a function of exposure probability *p*.
 Denote fixed points by *φ**.

Homogeneous version: All individuals have threshold dAll dose sizes are equal: d = 1

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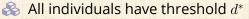
Study SIS-type contagion first:

Recovered individuals are immediately susceptible again:

 $\rho = 1.$

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

Homogeneous version:



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Study SIS-type contagion first:

Recovered individuals are immediately susceptible again:

 $\rho = 1.$

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

Homogeneous version:

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

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Generalized Model Homogeneous version

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

2 < 1 means recovery is probabilistic.
 T = 1 means individuals forget past interactions.
 d = 1 means one positive interaction will infect a individual.

Evolution of infection level:

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Fixed points for r < 1, $d^* = 1$, and T = 1: r < 1 means recovery is probabilistic.

T = 1 means individuals forget past interactions. $d^2 = 1$ means one positive interaction will infect a individual.

Evolution of infection level:

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

r < 1 means recovery is probabilistic.
 T = 1 means individuals forget past interactions.

 I means one positive interaction will infect a individual.

Evolution of infection level:

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

- $rac{1}{2}$ r < 1 means recovery is probabilistic.
- $rac{1}{2}$ T = 1 means individuals forget past interactions.
- $d^* = 1$ means one positive interaction will infect an individual.

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

- $rac{1}{2}$ r < 1 means recovery is probabilistic.
- $rac{1}{2}$ T = 1 means individuals forget past interactions.
- $d^* = 1$ means one positive interaction will infect an individual.
- Evolution of infection level:

$$\phi_{t+1} = p\phi_t + \phi_t (1 - p\phi_t) (1 - r).$$

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

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

- $rac{1}{2}$ r < 1 means recovery is probabilistic.
- $rac{1}{2}$ T = 1 means individuals forget past interactions.
- $d^* = 1$ means one positive interaction will infect an individual.
- Evolution of infection level:

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

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:

- $rac{1}{2}$ means recovery is probabilistic.
- T = 1 means individuals forget past interactions.
- $d^* = 1$ means one positive interaction will infect an individual.
- Evolution of infection level:

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

- 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:

- $rac{1}{2}$ means recovery is probabilistic.
- T = 1 means individuals forget past interactions.
- $d^* = 1$ means one positive interaction will infect an individual.
- Evolution of infection level:

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

- 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:

Set
$$\phi_t = \phi^*$$
:

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

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Fixed points for r < 1, $d^* = 1$, and T = 1: Set $\phi_* = \phi^*$:

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

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

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Fixed points for r < 1, $d^* = 1$, and T = 1: Set $\phi_* = \phi^*$:

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

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

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

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Fixed points for r < 1, $d^* = 1$, and T = 1: Set $\phi_t = \phi^*$:

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

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

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

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

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Fixed points for r < 1, $d^* = 1$, and T = 1: Set $\phi_t = \phi^*$:

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

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

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

Scritical point at $p = p_c = r$. Spreading takes off if p/r > 1Find continuous phase transition as for SIR Goodness. Matches $R_o = p/m > 1$ condition

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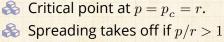


Fixed points for r < 1, $d^* = 1$, and T = 1: Set $\phi_t = \phi^*$:

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

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

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



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: Set $\phi_t = \phi^*$:

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

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

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

Critical point at $p = p_c = r$.
Spreading takes off if p/r > 1Find continuous phase transition as for SIR model.

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Fixed points for r < 1, $d^* = 1$, and T = 1: Set $\phi_t = \phi^*$:

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

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

$$\Rightarrow \phi^* = rac{1-r/p}{1-r}$$
 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 = β/γ > 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 pas
 T interactions will infect individual.
 Effect of individual interactions is independent from effect of others.
 Call o the steady state level of infection.

Pr(infected) = 1 - Pr(uninfected):

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

- $rac{1}{2}$ = 1 means recovery is immediate.
 - T > 1 means individuals remember at least 2 interactions.
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 Effect of individual interactions is independent
 from effect of others.
 Call o the steady state level of infection.

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

Solution r = 1 means recovery is immediate.
T > 1 means individuals remember at least 2 interactions.

d = 1 means only one positive interaction in particular interactions will infect individual.
 Effect of individual interactions is independent from effect of others.
 Call of the steady state level of infection.

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

- $rac{1}{2}$ = 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 independen from effect of others. Call the steady state level of infection. Pr(infected) = 1 - Pr(uninfected):



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

- $rac{1}{3}$ 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 of the steady state level of infection Pr(infected) = 1 - Pr(uninfected):

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

- $rac{1}{3}$ 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.
- \mathfrak{S} Call ϕ^* the steady state level of infection.

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

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- Pr(infected) = 1 Pr(uninfected):

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

- $rac{1}{2}$ = 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.
- \mathfrak{B} Call ϕ^* the steady state level of infection.
- Pr(infected) = 1 Pr(uninfected):

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



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

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

 $p = (\phi^*)^{-1} [1 - (1 - \phi^*)^{1/2}]$

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

 \bigotimes Look for critical infection probability p_c .

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



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

♣ Look for critical infection probability p_c . ♣ As $\phi^* \rightarrow 0$, we see

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

Again find continuous phase transition . Note: we can solve for p but not ϕ^* : $p = (\phi^*)^{-1}[1 - (1 - \phi^*)^{1/T}].$

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

♣ Look for critical infection probability p_c . ♣ As $\phi^* \rightarrow 0$, we see

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

Again find continuous phase transition. Note: we can solve for p but not ϕ^* : $p \models (\phi^*)^{-1}[1 - (1 - \phi^*)^{1/T}].$

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Homogeneous, one hit models: Fixed points for r = 1, $d^* = 1$, and T > 1S Closed form expression for ϕ^* :

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

♣ Look for critical infection probability p_c . ♣ As $\phi^* \rightarrow 0$, we see

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

🙈 Again find continuous phase transition ...



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Homogeneous, one hit models: Fixed points for r = 1, $d^* = 1$, and T > 1S Closed form expression for ϕ^* :

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

♣ Look for critical infection probability p_c . ♣ As $\phi^* \to 0$, we see

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

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

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

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



Start with r = 1, $d^* = 1$, and $T \ge 1$ case we have just examined:

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

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



Start with r = 1, $d^* = 1$, and $T \ge 1$ case we have just examined:

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

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

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



Start with r = 1, $d^* = 1$, and $T \ge 1$ case we have just examined:

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

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

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



Start with r = 1, $d^* = 1$, and $T \ge 1$ case we have just examined:

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

Sor 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.

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



Start with r = 1, $d^* = 1$, and $T \ge 1$ case we have just examined:

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

Sor 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: AA.

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



Start with r = 1, $d^* = 1$, and $T \ge 1$ case we have just examined:

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

Sor 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 $r \leq 1$, $d^* = 1$, and $T \geq 1$



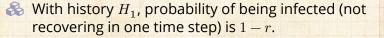
Start with r = 1, $d^* = 1$, and $T \ge 1$ case we have just examined:

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

Sor 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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Homogeneous, one hit models: Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$ 3 In general, relevant dose histories are:

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

Overall probabilities for dose histories occurring

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Homogeneous, one hit models: Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$ 3 In general, relevant dose histories are:

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

Overall probabilities for dose histories occurring:

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

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

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Homogeneous, one hit models: Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$ 3 In general, relevant dose histories are:

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Overall probabilities for dose histories occurring:

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

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

Pr(infection T + m + 1 time steps ago) Pr(no doses received in T + m time steps sinc Pr(no recovery in m chances)

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Homogeneous, one hit models: Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$ \bigotimes In general, relevant dose histories are:

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

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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Homogeneous, one hit models: Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$ \bigotimes In general, relevant dose histories are:

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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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Homogeneous, one hit models: Fixed points for $r \le 1$, $d^* = 1$, and $T \ge 1$ \bigotimes In general, relevant dose histories are:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Solution Using the probability of not recovering, we end up

with a fixed point equation:

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

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

Fixed point equation (again):

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

Find critical exposure probability by examinin, above as $\phi^* \rightarrow 0$.

where $\tau =$ mean recovery time for simple relaxation process. Decreasing r keeps individuals infected for kand decreases p_e .

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

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

Fixed point equation (again):

2

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

Find critical exposure probability by examining above as $\phi^* \rightarrow 0$.

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

where τ = mean recovery time for simple relaxation process.

Decreasing *r* keeps individuals infected for long and decreases *p*_e.

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

Fixed point equation (again):

3

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

Sind critical exposure probability by examining above as $\phi^* \rightarrow 0$.

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

where τ = mean recovery time for simple relaxation process.

Solution Decreasing r keeps individuals infected for longer and decreases p_c .

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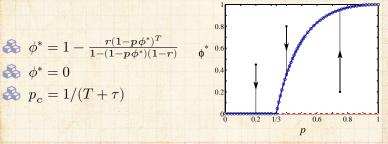
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Epidemic threshold:

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



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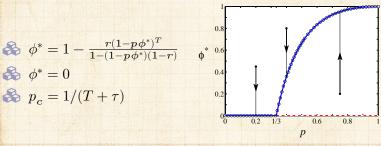
Solution Example details: $T = 2 \& r = 1/2 \Rightarrow p_c = 1/3$. Solution Blue = stable, red = unstable, fixed points. Solution $\tau = 1/r - 1$ = characteristic recovery time = 1. Solution $T + \tau \simeq$ average memory in system = 3.





Epidemic threshold:

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



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& Example details: T = 2 & r = 1/2 ⇒ p_c = 1/3.
& Blue = stable, red = unstable, fixed points.
& τ = 1/r - 1 = characteristic recovery time = 1.
T + τ ≃ average memory in system = 3.
& Phase transition can be seen as a transcritical bifurcation. ^[12]





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

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3

All right: $d^* = 1$ models correspond to simple disease spreading models. 3 What if we allow $d^* \geq 2?$

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

 \Im What if we allow $d^* \ge 2?$

3

Again first consider SIS with immediate recovery (r = 1)

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

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

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

 \mathbf{s} As always, $\phi^* = 0$ works too.

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

e.g., for $d^* = 2, T = 3$:

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

 \bigotimes 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: COcoNuTS

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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: $\phi^* =$

$$\psi = \frac{1}{3p^2 \phi^{*2} (1 - p \phi^*) + p^3 \phi^{*3}}$$

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

Fixed point equation:
 \$\phi^* = \$\$\$ 3p^2 \phi^{*2} (1 - p \phi^*) + p^3 \phi^{*3}\$
 See new structure: a saddle node bifurcation [12] appears as p increases.

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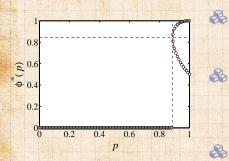
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Fixed points for r = 1, $d^* > 1$, and $T \ge 1$ Solvable for small T. Solvable for small T.



Sized point equation: $\phi^* =$ $3p^2 {\phi^*}^2 (1 - p \phi^*) + p^3 {\phi^*}^3$ See new structure: a saddle node bifurcation^[12] appears as *p* increases. $(p_h, \phi^*) = (8/9, 27/32).$ COcoNuTS

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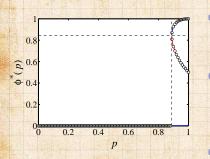
References



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Fixed points for r = 1, $d^* > 1$, and $T \ge 1$ Solvable for small T. Solvable equal to $d^* = 2$, T = 3:



Fixed point equation:
 \$\phi^* = \$\$\$ 3p^2 \phi^{*2}(1 - p \phi^*) + p^3 \phi^{*3}\$
 See new structure: a saddle node bifurcation [12] appears as p increases.

 $\textcircled{b} (p_b,\phi^*) = (8/9,27/32).$

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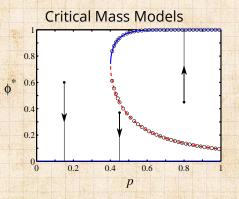


Behavior akin to output of Granovetter's threshold model.

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Another example:



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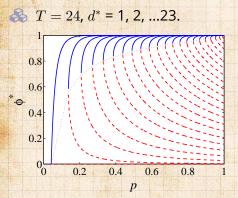
References



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



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 $d^* = 1 \rightarrow d^* > 1;$ jump between continuous phase transition and pure critical mass model. Unstable curve for $d^* = 2$ does not hit $\phi^* = 0$.

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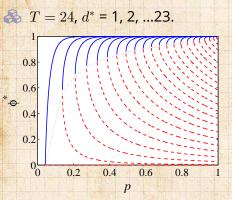
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 $d^* = 1 \rightarrow d^* > 1;$ jump between continuous phase transition and pure critical mass model. Unstable curve for $d^* = 2$ does not hit $\phi^* = 0$. Introduction

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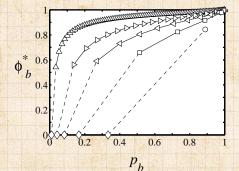
References





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

Sifurcation points for example fixed T, varying d^* :



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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:

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

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

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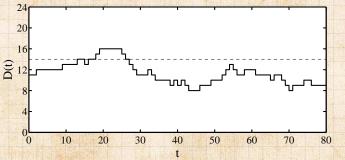


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For r < 1, need to determine probability of recovering as a function of time since dose load last dropped below threshold.
 Partially summed random walks:

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

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



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

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

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

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

Fraction of individuals below threshold but not recovered:

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

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Fixed point equation:

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

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

fwo subsequences do this:

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:

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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 $d^* = 2$:

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

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

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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 $\{d_{n-2}, d_{n-1}, d_n, d_{n+1}, d_{n+2}\} = \{1, 0, 1, 0, 0\}.$

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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 $d^* = 2$.

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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 $d^* = 2$. lacktriangleright Start 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 $d^* = 2$.

where [] means floor. Corresponding possible values fo

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

- N_a = number of $a = \{0\}$ subsequences.
- $\Im N_b$ = number of $b = \{1, 0, 0\}$ subsequences.

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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.

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

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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.

 $\Im N_b$ = number of $b = \{1, 0, 0\}$ subsequences.

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

Possible values for N_b :

$$0, 1, 2, \ldots, \left\lfloor \frac{m}{3}
ight
floor$$
 .

where [.] means floor.

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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.

 $\Im N_b$ = number of $b = \{1, 0, 0\}$ subsequences.

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

Possible values for N_b :

$$0, 1, 2, \dots, \left\lfloor \frac{m}{3}
ight
floor$$
.

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

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

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\circledast 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:

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

 $\Im N_a + N_b$ 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 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 $P(b) = p\phi^*(1 - p\phi^*)^2$ Total probability of allowable sequences of length m:

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

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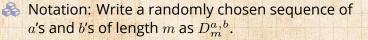


Total number of allowable sequences of length m:

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



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Sequence endings.
 Six possible sequences:

 $D_1 = \{1, 1, 0, 0, D_{m-1}^{a, b}\}$ $D_2 = \{1, 1, 0, 0, D_m^{a,b}, 1\}$ $D_3 = \{1, 1, 0, 0, D_{m-3}^{a,b}, 1, 0\}$ $D_4 = \{1, 0, 1, 0, 0, D_{m-2}^{a, b}\}$ $D_5 = \{1, 0, 1, 0, 0, D_{m-3}^{a,b}, 1\}$ $D_6 = \{1, 0, 1, 0, 0, D_m^{a, b}, 1, 0\}$ COcoNuTS

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Sequence endings.
 Six possible sequences:

 $D_1 = \{1, 1, 0, 0, D_{m-1}^{a, b}\}$ $D_2 = \{1, 1, 0, 0, D_m^{a,b}, 1\}$ $D_3 = \{1, 1, 0, 0, D_{m-3}^{a,b}, 1, 0\}$ $D_4 = \{1, 0, 1, 0, 0, D_{m-2}^{a, b}\}$ $D_5 = \{1, 0, 1, 0, 0, D_{m-3}^{a,b}, 1\}$ $D_6 = \{1, 0, 1, 0, 0, D_m^{a, b}, 1, 0\}$ COcoNuTS

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Nearly there ...must account for details of sequence endings.
 Three endings ⇒ Six possible sequences:

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

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

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

$$\begin{split} & [\chi_{m-1} + \chi_{m-2} + 2p\phi(1-p\phi)\chi_{m-3} + p\phi(1-p\phi)^2\chi_{m-4}] \\ & \text{and} \end{split}$$

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

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

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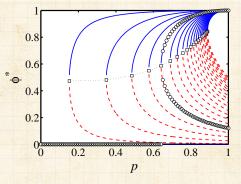
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 $T = 3, d^* = 2$



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

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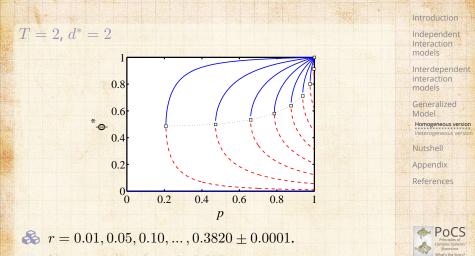
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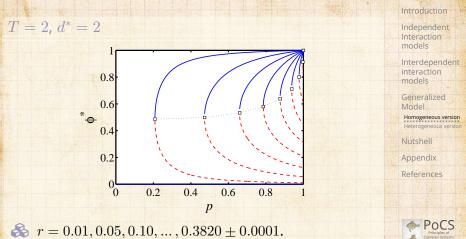
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to spreading for $r \gtrsim 0.382$.

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 \Im No spreading for $r \gtrsim 0.382$.

What's the Story?

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🚳 Two kinds of contagion processes:

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

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

2. Saddle-node bifurcation: threshold model-like.

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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.

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Two kinds of contagion processes:

 Continuous phase transition: SIR-like.
 Saddle-node bifurcation: threshold model-like.

 d* = 1: spreading from small seeds possible.
 d* > 1: critical mass model.

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Structure
 Two kinds of contagion processes:

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

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

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Now allow for general dose distributions (*f*) and threshold distributions (*g*).
 Key quantities:

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

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Now allow for general dose distributions (*f*) and threshold distributions (*g*).
 Key quantities:

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

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

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Now allow for general dose distributions (*f*) and threshold distributions (*g*).
 Key quantities:

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

 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. COcoNuTS

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🚳 Fixed point equation:

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

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Pinciples of Complex Systems @poccvvx What's the Story?



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 P₁T is the expected number of vulnerables the initial infected individual meets before recoverin
 p₁P₁T is - the expected number of successful infections (equivalent to B₀).

🙈 Fixed point equation:

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

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

$$\boxed{pP_1T\geq 1}$$

 P₁T is the expected number of vulnerables the initial infected individual meets before recovering 2. pP₁T is - the expected number of successful infections (equivalent to R₀).

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

$$pP_1T \ge 1$$
 or $\Rightarrow p_c$

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

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 P₁ T is the expected number of vulnerables the initial infected individual meets before recovering 2. pP₁T is - the expected number of successful infections (equivalent to R₀).

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

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

$$\left| pP_{1}T \ge 1 \right|$$
 or =

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

🚳 Very good:

 P₁T is the expected number of vulnerables the initial infected individual meets before recovering.



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

$$pP_1T \ge 1$$
 or

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

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🚳 Very good:

- 1. P_1T is the expected number of vulnerables the initial infected individual meets before recovering.
- 2. pP_1T is \therefore the expected number of successful infections (equivalent to R_0).





Fixed point equation:

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

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

$$pP_1T \ge 1$$
 or

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

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Very good:

- 1. P_1T is the expected number of vulnerables the initial infected individual meets before recovering.
- 2. pP_1T is : the expected number of successful infections (equivalent to R_0).



Solution Observe: p, 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.

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Next: Determine slope of fixed point curve at critical point p_c.
 Expand fixed point equation around (p, φ*) = (p_c, 0).

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Next: Determine slope of fixed point curve at critical point p_c.
 Expand fixed point equation around (p, φ*) = (p_c, 0).
 Find slope depends on (P₁ - P₂/2)^[6] (see Appendix).

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- Next: Determine slope of fixed point curve at critical point p_c.
 Expand fixed point equation around (p, φ*) = (p_c, 0).
 - Find slope depends on $(P_1 P_2/2)^{[6]}$ (see Appendix).
- Behavior near fixed point depends on whether this slope is

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- Solution 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 $(P_1 P_2/2)^{[6]}$ (see Appendix).
- Behavior near fixed point depends on whether this slope is
 - 1. positive: $P_1 > P_2/2$ (continuous phase transition)

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- Solution 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 $(P_1 P_2/2)^{[6]}$ (see Appendix).
- Behavior near fixed point depends on whether this slope is
 - 1. positive: $P_1 > P_2/2$ (continuous phase transition)
 - 2. negative: $P_1 < P_2/2$ (discontinuous phase transition)

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- Solution 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 $(P_1 P_2/2)^{[6]}$ (see Appendix).
- Behavior near fixed point depends on whether this slope is
 - 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.

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Example configuration:



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

3 Memory span: T = 10.

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Example configuration:

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

Solution 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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Example configuration:

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

3 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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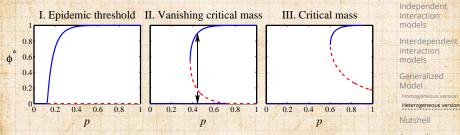




Three universal classes







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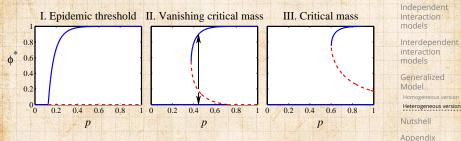


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Three universal classes







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



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Three universal classes





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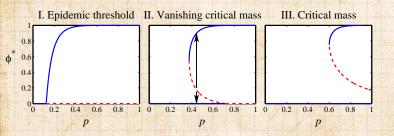
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Three universal classes





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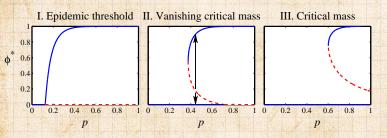
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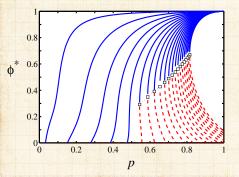




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Heterogeneous case

Now allow r < 1:



II-III transition generalizes: p_c = 1/[P₁(T + τ)] where τ = 1/r - 1 = expected recovery time
 I-II transition less pleasant analytically.

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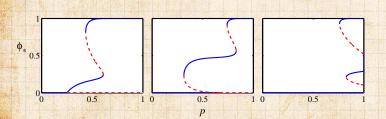
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More complicated models



Due to heterogeneity in individual thresholds. 1 Three classes based on behavior for small seeds. Same model classification holds: I, II, and III.



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Hysteresis in vanishing critical mass models

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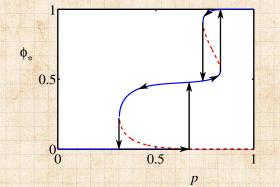
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Memory is a natural ingredient.

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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:

> 1. I. Epidemic Threshold 2. 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, 4 recovery, fraction of vulnerable individuals (T, r, ρ , P_1 , and/or P_2). 🚳 To change behavior given model: 'adjust' probability of exposure (p) and/or initial number infected (ϕ_0).

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

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Single seed infects others if $pP_1(T + \tau) \ge 1$. Key quantity: $p_c = 1/[P_1(T + \tau)]$

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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.

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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. Depends only on:

- 1. System Memory $(T + \tau)$.
- 2. Fraction of highly vulnerable individuals (P_1) .

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Single seed infects others if pP₁(T + τ) ≥ 1.
Key quantity: p_c = 1/[P₁(T + τ)]
If p_c < 1 ⇒ contagion can spread from single seed.
Depends only on:

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

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

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Single seed infects others if $pP_1(T + \tau) > 1$. Key quantity: $p_c = 1/[P_1(T+\tau)]$ rightarrow If $p_c < 1 \Rightarrow$ contagion can spread from single seed. Depends only on: 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 vulnerable/gullible population may be more important than a small group of super-spreaders or influentials.

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

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

since

$$\binom{T}{k}\binom{T-k}{m-k}$$

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

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

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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 $C_2 = {T \choose 2}(-2P_1 + P_2).$

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\delta Linearization gives

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

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

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



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\delta Linearization gives

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

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

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