

Generalized Contagion

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Complex Networks | @networksvox
CSYS/MATH 303, Spring, 2019

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"Universal Behavior in a Generalized Model of Contagion" [↗](#)
Dodds and Watts,
Phys. Rev. Lett., **92**, 218701, 2004. ^[5]



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

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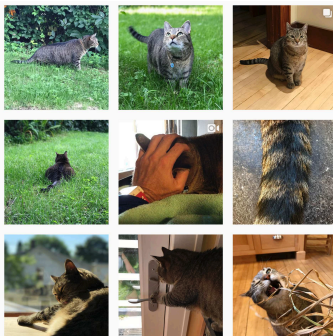
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Generalized contagion model

Basic questions about contagion

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

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Mathematical Epidemiology (recap)

The standard SIR model^[11]

☞ = basic model of disease contagion

☞ Three states:

1. S = Susceptible
2. I = Infective/Infectious
3. R = Recovered or Removed or Refractory

☞ $S(t) + I(t) + R(t) = 1$

☞ Presumes random interactions (mass-action principle)

☞ Interactions are independent (no memory)

☞ Discrete and continuous time versions

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Independent Interaction models

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 R_0 :

☞ R_0 = expected number of infected individuals resulting from a single initial infective

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

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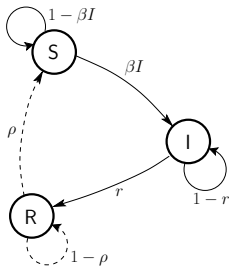
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Independent Interaction Models

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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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 into a Susceptible

☞ 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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Independent Interaction Models

Original models attributed to

☞ 1920's: Reed and Frost

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

☞ Coupled differential equations with a mass-action principle

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Reproduction Number R_0

Discrete version:

☞ Expected number infected by original Infective:

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

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

$$= \beta \frac{1}{1 - (1 - r)} = \beta/r$$

☞ Similar story for continuous model.

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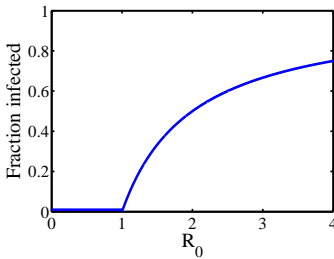
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Independent Interaction models

Example of epidemic threshold:



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

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Some (of many) issues

- Disease models assume independence of infectious events.
- Threshold models only involve proportions: $3/10 \equiv 30/100$.
- Threshold models ignore exact sequence of influences
- Threshold models assume immediate polling.
- Mean-field models neglect network structure
- Network effects only part of story: media, advertising, direct marketing.

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Simple disease spreading models

Valiant attempts to use SIR and co. elsewhere:

- Adoption of ideas/beliefs (Goffman & Newell, 1964) [7]
- Spread of rumors (Daley & Kendall, 1964, 1965) [3, 4]
- Diffusion of innovations (Bass, 1969) [1]
- Spread of fanatical behavior (Castillo-Chávez & Song, 2003) [2]

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Generalized model

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 = fraction infected at time t = probability of contact with infected individual
- With probability p , contact with infective leads to an exposure.
- If exposed, individual receives a dose of size d drawn from distribution f . Otherwise $d = 0$.

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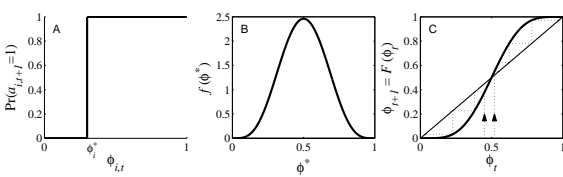
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Granovetter's model (recap of recap)

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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Generalized model—ingredients

S \Rightarrow I

Individuals 'remember' last T contacts:

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

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

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

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

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Generalized model—ingredients

I ⇒ R

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

R ⇒ S

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

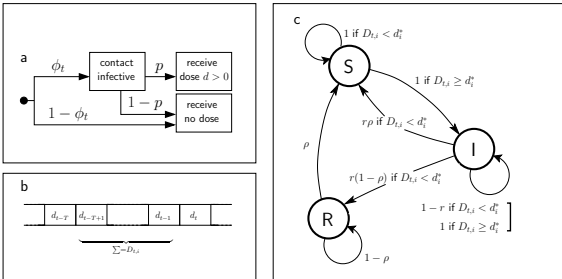
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A visual explanation



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Generalized mean-field model

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 d^*

All dose sizes are equal: $d = 1$

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Homogeneous, one hit models:

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

$r < 1$ 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:

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

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

b: Probability of being infected and not being reinfected.

c: Probability of not recovering.

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Homogeneous, one hit models:

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

Set $\phi_t = \phi^*$:

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

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

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

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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Simple homogeneous examples

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.

$\text{Pr}(\text{infected}) = 1 - \text{Pr}(\text{uninfected})$:

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

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Homogeneous, one hit models:

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

🔗 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 ...

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

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

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Homogeneous, one hit models:

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

🔗 Start with $r = 1$, $d^* = 1$, and $T \geq 1$ 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:

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

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

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Homogeneous, one hit models:

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

🔗 In general, relevant dose histories are:

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

🔗 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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Homogeneous, one hit models:

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)

$$\begin{aligned} &= r \sum_{m=0}^{\infty} P(H_{T+m}) = r \sum_{m=0}^{\infty} p\phi^*(1 - p\phi^*)^{T+m}(1 - r)^m \\ &= r \frac{p\phi^*(1 - p\phi^*)^T}{1 - (1 - p\phi^*)(1 - r)}. \end{aligned}$$

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

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

Homogeneous, one hit models:

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 examining above as $\phi^* \rightarrow 0$.

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

where τ = mean recovery time for simple relaxation process.

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

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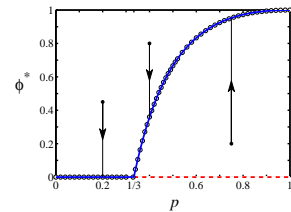
Epidemic threshold:

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

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

$$\phi^* = 0$$

$$p_c = 1/(T + \tau)$$



🔗 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**.^[12]

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Homogeneous, multi-hit models:

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

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

- As always, $\phi^* = 0$ works too.

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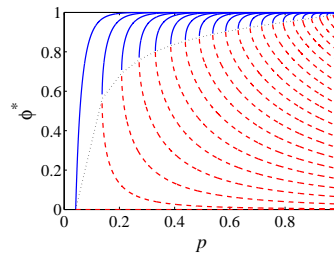
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Fixed points for $r = 1, d^* > 1$, and $T \geq 1$

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



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

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

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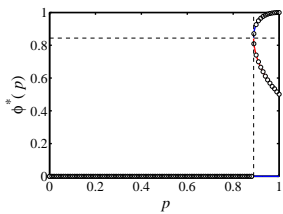


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Homogeneous, multi-hit models:

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

- 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: a saddle node bifurcation appears as p increases.
- $(p_b, \phi^*) = (8/9, 27/32)$.

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

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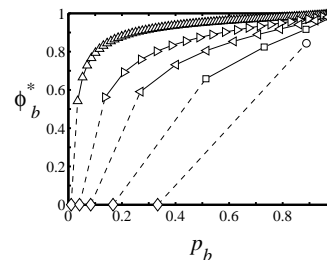
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Fixed points for $r = 1, d^* > 1$, and $T \geq 1$

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



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

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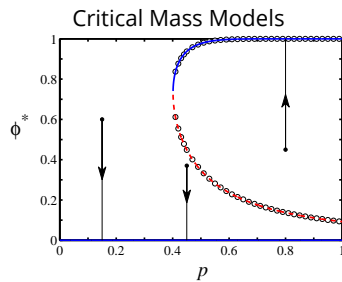
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Homogeneous, multi-hit models:

- Another example:



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

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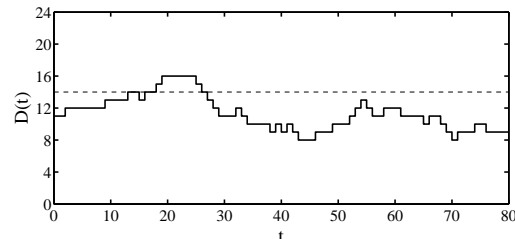
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Fixed points for $r < 1, d^* > 1$, and $T \geq 1$

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

- 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:

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

- Fixed point equation:

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

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

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

- 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:

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

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

- 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:

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

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

- 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.

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

Possible values for N_b :

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

where $\lfloor \cdot \rfloor$ means floor.

- Corresponding possible values for N_a :

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

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

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

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

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

- 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 :

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

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

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

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

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

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

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

$$D_4 = \{1, 0, 1, 0, 0, D_{m-2}^{a,b}\}$$

$$D_5 = \{1, 0, 1, 0, 0, D_{m-3}^{a,b}, 1\}$$

$$D_6 = \{1, 0, 1, 0, 0, D_{m-4}^{a,b}, 1, 0\}$$

$$P_1 = (p\phi)^2(1-p\phi)^2\chi_{m-1}(p, \phi)$$

$$P_2 = (p\phi)^3(1-p\phi)^2\chi_{m-2}(p, \phi)$$

$$P_3 = (p\phi)^3(1-p\phi)^3\chi_{m-3}(p, \phi)$$

$$P_4 = (p\phi)^2(1-p\phi)^3\chi_{m-2}(p, \phi)$$

$$P_5 = (p\phi)^3(1-p\phi)^3\chi_{m-3}(p, \phi)$$

$$P_6 = (p\phi)^3(1-p\phi)^4\chi_{m-4}(p, \phi)$$

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

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

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

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

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

and

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

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

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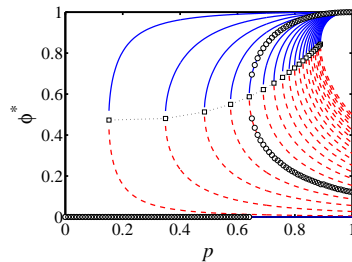
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Fixed points for $r < 1$, $d^* > 1$, and $T \geq 1$

$T = 3, d^* = 2$



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

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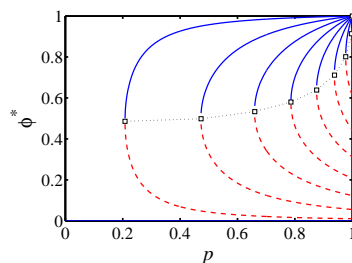
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Fixed points for $r < 1$, $d^* > 1$, and $T \geq 1$

$T = 2, d^* = 2$



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

No spreading for $r \gtrsim 0.382.$

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What we have now:

- 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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Generalized model

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

Key quantities:

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

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

e.g.,

P_1 = Probability that one dose will exceed the threshold of a random individual = Fraction of most vulnerable individuals.

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Generalized model—heterogeneity, $r = 1$

Fixed point equation:

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

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

$$pP_1T \geq 1 \quad \text{or} \quad \Rightarrow p_c = 1/(TP_1)$$

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).

Observe: p_c may exceed 1 meaning no spreading from a small seed.

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Heterogeneous case

- 🔗 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 **three** basic universal classes of contagion models ...

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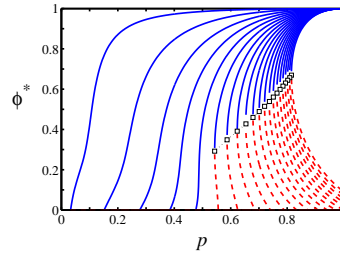
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Heterogeneous case

Now allow $r < 1$:



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

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Heterogeneous case

Example configuration:

- 🔗 Dose sizes are lognormally distributed with mean 1 and variance 0.433.
- 🔗 Memory span: $T = 10$.
- 🔗 Thresholds are uniformly set at
 1. $d_* = 0.5$
 2. $d_* = 1.6$
 3. $d_* = 3$
- 🔗 Spread of dose sizes matters, details are not important.

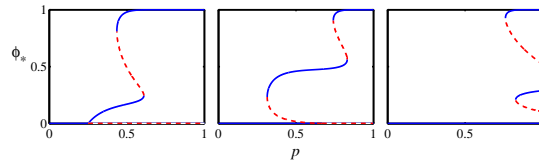
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More complicated models



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

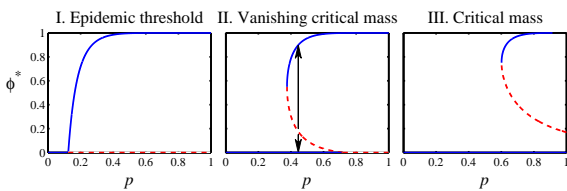
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Three universal classes



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

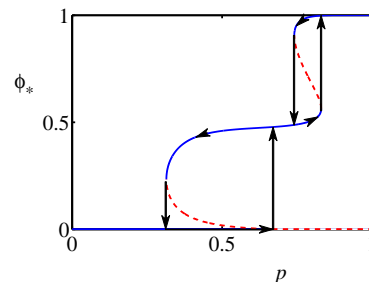
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Hysteresis in vanishing critical mass models



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Nutshell (one half)

- ☞ 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 (ϕ_0).

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Appendix: Details for Class I-II transition:

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

since

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

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Nutshell (other half)

- ☞ Single seed infects others if $pP_1(T + \tau) \geq 1$.
- ☞ 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).
- ☞ 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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Appendix: Details for Class I-II transition:

- ☞ Linearization gives

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

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

- ☞ Using $p_c = 1/(TP_1)$:

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

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

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Appendix: Details for Class I-II transition:

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

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