

Generalized Contagion

Last updated: 2018/03/23, 20:59:06

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CSYS/MATH 303, Spring, 2018

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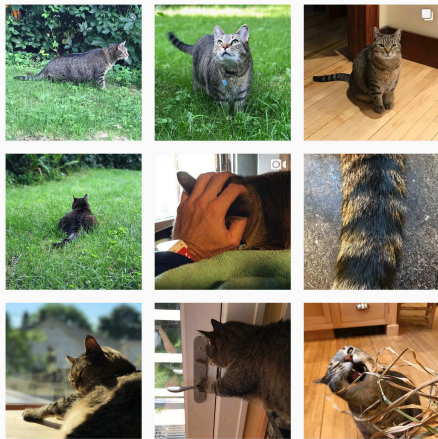
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 On Instagram at [pratchett_the_cat](https://www.instagram.com/pratchett_the_cat) 



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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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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.




Mathematical Epidemiology (recap)


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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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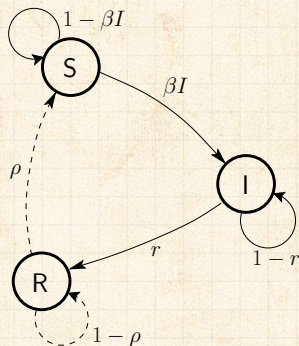
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Discrete time automata example:



Transition Probabilities:

β for being infected given
contact with infected

r for recovery

ρ for loss of immunity

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Original models attributed to

-  1920's: Reed and Frost
-  1920's/1930's: Kermack and McKendrick [8, 10, 9]
-  Coupled differential equations with a mass-action principle



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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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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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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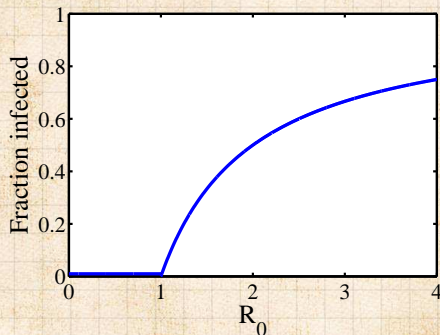
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Example of epidemic threshold:



 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)^[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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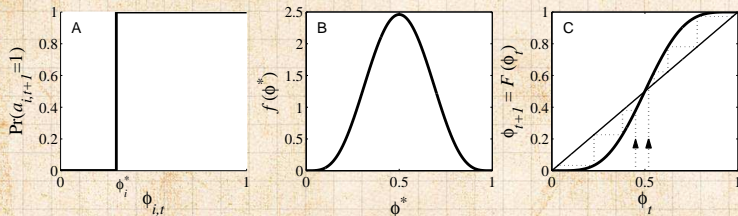
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Granovetter's model (recap of recap)


 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**.

 **Inter**dependent interaction 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.



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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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 \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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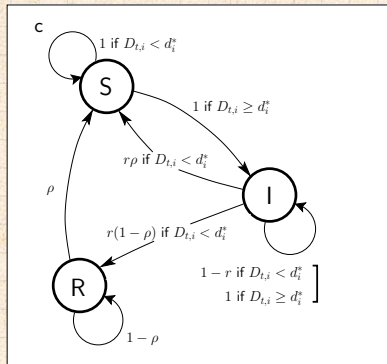
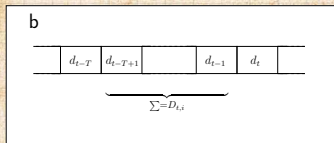
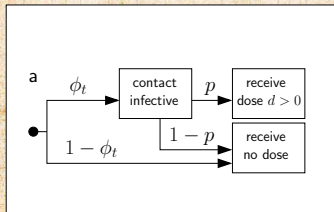
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A visual explanation



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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^* :

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




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:

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

 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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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:

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

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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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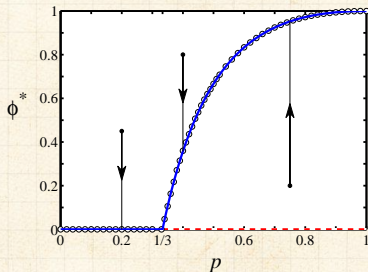
Epidemic threshold:

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.

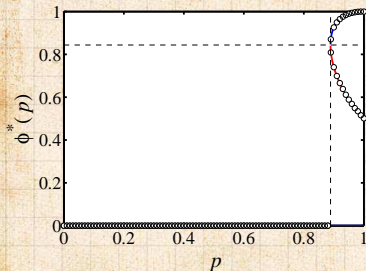
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Homogeneous, multi-hit models:

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** ^[12] appears as p increases.

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

 Behavior akin to output of Granovetter's threshold model.

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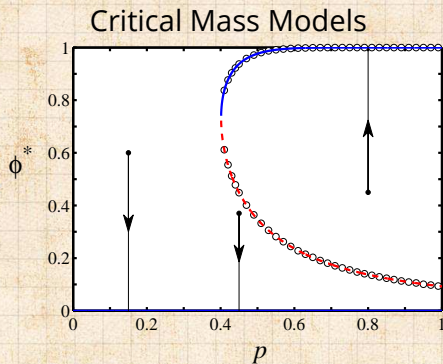
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Homogeneous, multi-hit models:



Another example:



$r = 1, d^* = 3, T = 12$

Saddle-node bifurcation.

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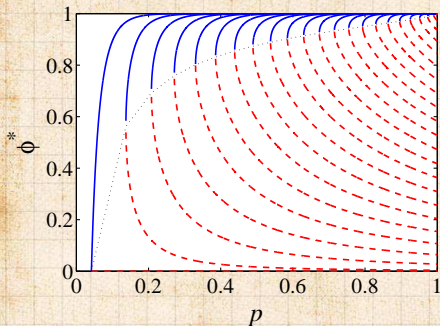
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Fixed points for $r = 1$, $d^* > 1$, and $T \geq 1$

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



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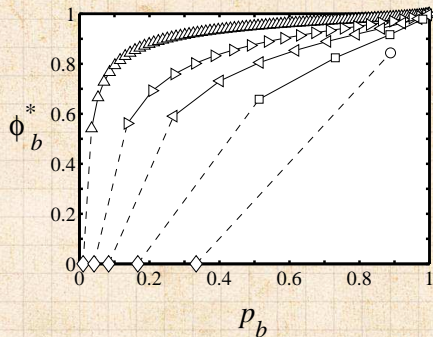
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Fixed points for $r = 1$, $d^* > 1$, and $T \geq 1$


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




 $T = 96$ (.),

 $T = 24$ (\triangleright),

 $T = 12$ (\triangleleft),

 $T = 6$ (\square),

 $T = 3$ (\circ),



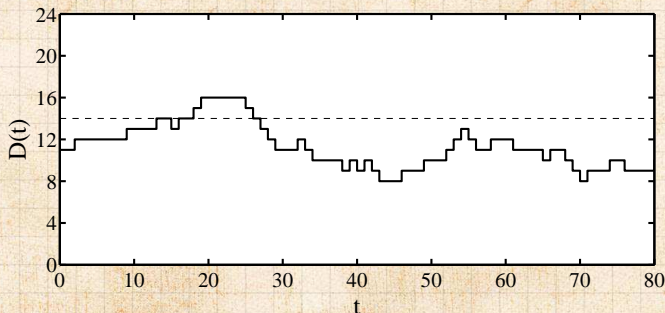
Fixed points for $r < 1$, $d^* > 1$, and $T \geq 1$

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:


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



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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 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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 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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 Nearly there ...must account for details of sequence endings.

 Three endings \Rightarrow Six possible sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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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

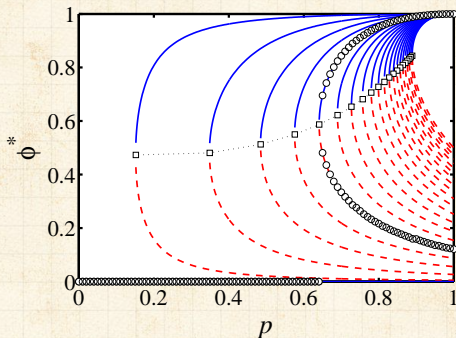
$$\chi_m(p, \phi^*) = \sum_{k=0}^{\lfloor m/3 \rfloor} \binom{m-2k}{k} (1-p\phi^*)^{m-k} (p\phi^*)^k.$$

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



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

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

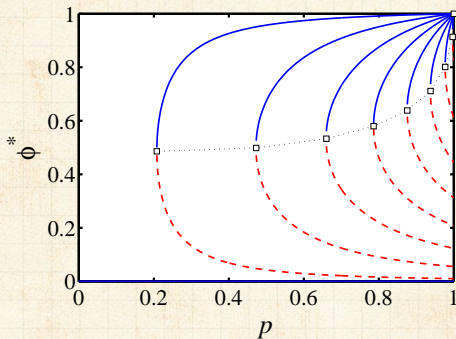



$r = 0.01, 0.05, 0.10, 0.15, 0.20, \dots, 1.00.$




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:

COCoNuTS

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Two kinds of contagion processes:

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



$d^* = 1$: spreading from small seeds possible.




$d^* > 1$: critical mass model.




Are other behaviors possible?





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:

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

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

$$pP_1T \geq 1$$

or

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

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 ...

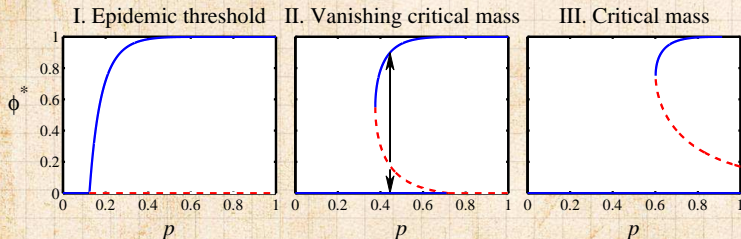
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Example configuration:


-  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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Three universal classes



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

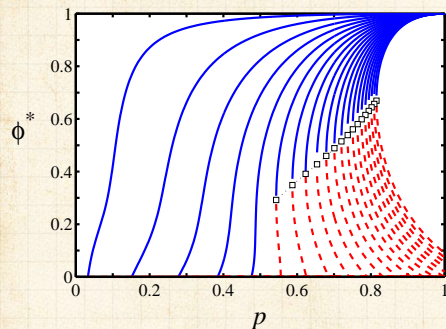
 Vanishing critical mass: $P_1 < P_2/2, p_c = 1/(TP_1) < 1$

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



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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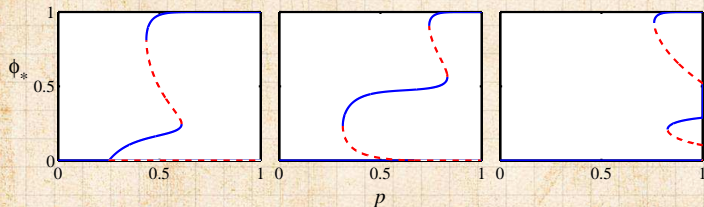
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More complicated models



- 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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Hysteresis in vanishing critical mass models

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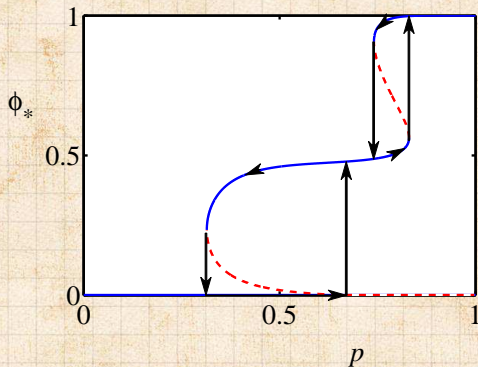
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Memory is a natural ingredient.



Three universal classes of contagion processes:

1. I. Epidemic Threshold
2. II. Vanishing Critical Mass
3. III. Critical Mass



Dramatic changes in behavior possible.



To change kind of model: 'adjust' memory, recovery, fraction of vulnerable individuals (T , r , ρ , P_1 , and/or P_2).



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

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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:
 - System Memory ($T + \tau$).
 - 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:

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



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

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



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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