Generalized Contagion
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Outline

Introduction

Independent Interaction models

Interdependent interaction models

Generalized Model
  Homogeneous version
  Heterogeneous version

Appendix

References
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.
Mathematical Epidemiology (recap)

The standard SIR model \(^{[10]}\)

- = 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
Independent Interaction Models

Discrete time automata example:

Transition Probabilities:

- $\beta$ for being infected given contact with infected
- $r$ for recovery
- $\rho$ for loss of immunity
Independent Interaction Models

Original models attributed to

- 1920’s: Reed and Frost
- 1920’s/1930’s: Kermack and McKendrick [7, 9, 8]
- Coupled differential equations with a mass-action principle
Independent Interaction models

Differential equations for continuous model

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

\(\beta, r, \) and \(\rho\) 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.
Reproduction Number $R_0$

Discrete version:

- Set up: One Infective in a randomly mixing population of Susceptibles
- At time $t = 0$, single infective random bumps into a Susceptible
- Probability of transmission $= \beta$
- At time $t = 1$, single Infective remains infected with probability $1 - r$
- At time $t = k$, single Infective remains infected with probability $(1 - r)^k$
Reproduction Number $R_0$

Discrete version:

- Expected number infected by original Infective:

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

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

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

- Similar story for continuous model.
Independent Interaction models

Example of epidemic threshold:

- Continuous phase transition.
- Fine idea from a simple model.
Simple disease spreading models

Valiant attempts to use SIR and co. elsewhere:

- Adoption of ideas/beliefs (Goffman & Newell, 1964) [6]
- Spread of rumors (Daley & Kendall, 1964, 1965) [2, 3]
- Diffusion of innovations (Bass, 1969) [1]
- Spread of fanatical behavior (Castillo-Chávez & Song, 2003)
Granovetter’s model (recap of recap)

- Action based on perceived behavior of others.

- Two states: S and I.
- Recovery now possible (SIS).
- $\phi = \text{fraction of contacts ‘on’ (e.g., rioting)}$.
- Discrete time, synchronous update.
- This is a Critical mass model.
- Interdependent interaction model.
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.
Generalized model

Basic ingredients:

- Incorporate memory of a contagious element [4, 5]
- 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 $t$
  $= \text{probability of contact}$ 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 $d = 0$. 
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 \( t = 0 \).
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 $\rho$. 
A visual explanation

Generalized Contagion

Introduction
Independent Interaction models
Interdependent interaction models
Generalized Model
Homogeneous version
Heterogeneous version
Appendix
References

Frame 17/63
Generalized mean-field model

Study SIS-type contagion first:

- Recovered individuals are immediately susceptible again:
  \[ r = \rho = 1. \]

- Look for steady-state behavior as a function of exposure probability \( \rho \).

- Denote fixed points by \( \phi^* \).

Homogeneous version:

- All individuals have threshold \( d^* \)
- All dose sizes are equal: \( d = 1 \)
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:

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

- **a**: Fraction infected between $t$ and $t + 1$, independent of past state or recovery.
- **b**: Probability of being infected and not being reinfected.
- **c**: Probability of not recovering.
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.
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 $\phi^*$ the steady state level of infection.
- $\Pr(\text{infected}) = 1 - \Pr(\text{uninfected})$:

$$\phi^* = 1 - (1 - p\phi^*)^T.$$
Homogeneous, one hit models:

Fixed points for \( r = 1, \, d^\ast = 1, \) and \( T > 1 \)

- Closed form expression for \( \phi^\ast \):
  \[
  \phi^\ast = 1 - (1 - p\phi^\ast)^T.
  \]
- Look for critical infection probability \( p_c \).
- As \( \phi^\ast \to 0 \), we see
  \[
  \phi^\ast \approx pT\phi^\ast \implies p_c = 1/T.
  \]
- Again find continuous phase transition...
- Note: we can solve for \( p \) but not \( \phi^\ast \):
  \[
  p = (\phi^\ast)^{-1}[1 - (1 - \phi^\ast)^{1/T}].
  \]
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:

  \[
  H_1 = \{\ldots, d_{t-T-2}, d_{t-T-1}, 1, 0, 0, \ldots, 0, 0\}, \quad T \text{ 0's}
  \]

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

Homogeneous, one hit models:

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

- In general, relevant dose histories are:

$$H_{m+1} = \{ \ldots, d_{t-T-m-1}, 1, 0, 0, \ldots, 0, 0, 0, \ldots, 0, 0 \}.$$  
  \hspace{2cm} \text{m 0's} \hspace{2cm} \text{T 0's}

- Overall probabilities for dose histories occurring:

$$P(H_1) = p_{\phi^*}(1 - p_{\phi^*})^T(1 - r),$$

$$P(H_{m+1}) = p_{\phi^*} \left(1 - p_{\phi^*}\right)^{T+m} (1 - r)^{m+1}.$$  

\hspace{1cm} a \hspace{1cm} b \hspace{1cm} 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)
Homogeneous, one hit models:

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

- \( \Pr(\text{recovery}) = \Pr(\text{seeing no doses for at least } T \text{ time steps and recovering}) \)

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

- 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 \( \phi^* \to 0. \)

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

where \( \tau = \text{mean recovery time} \) for simple relaxation process.

- Decreasing \( r \) keeps individuals infected for longer and decreases \( p_c. \)
Epidemic threshold:

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

- $\phi^* = 1 - \frac{r(1-p\phi^*)^T}{1-(1-p\phi^*)(1-r)}$
- $\phi^* = 0$
- $p_c = 1/(T + \tau)$

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

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

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

\[
\phi^* = 3p^2\phi^* (1 - p\phi^*) + p^3 \phi^*^3
\]

- See new structure: see a saddle node bifurcation\textsuperscript{[11]} appear as $p$ increases.

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

- See behavior akin to output of Granovetter’s threshold model.
Homogeneous, multi-hit models:

- Another example:

![Critical Mass Models Diagram]

- $r = 1, \ d^* = 3, \ T = 12$  Saddle-node bifurcation.
Fixed points for $r = 1$, $d^* > 1$, and $T \geq 1$

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

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

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

- $T = 96$ ($\triangle$).
- $T = 24$ ($\triangleright$),
- $T = 12$ ($\triangleleft$),
- $T = 6$ ($\Box$),
- $T = 3$ ($\bigcirc$),

![Graph showing fixed points for $r = 1$, $d^* > 1$, and $T \geq 1$]
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 $T = 24$, $d^* = 14$: 

![Graph showing the function $D(t)$ over time.]
Fixed points for $r < 1$, $d^* > 1$, and $T \geq 1$

- Define $\gamma_m$ 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:

\[
\phi^* = \Gamma(p, \phi^*; r) + \sum_{i=d^*}^{T} \binom{T}{i} (p\phi^*)^i (1 - p\phi^*)^{T-i}.
\]
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:
  \[
  \{d_{n-2}, d_{n-1}, d_n, d_{n+1}\} = \{1, 1, 0, 0\}
  \]
  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 $d^* = 2$.
- $N_a = \text{number of } a = \{0\} \text{ subsequences}$.
- $N_b = \text{number of } b = \{1, 0, 0\} \text{ subsequences}$.

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

Possible values for $N_b$:

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

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

- Corresponding possible values for $N_a$:

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

\[ \{Z_1, Z_2, \ldots, Z_{N_a+N_b}\} \]

- $N_a + N_b$ slots for subsequences.
- Choose positions of either a’s or b’s:

\[
\binom{N_a + N_b}{N_a} = \binom{N_a + N_b}{N_b}.
\]
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 $D_{m,a,b}^a$. 

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:

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

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

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

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

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

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

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

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

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

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

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

\[
P_6 = (p\phi)^3(1 - p\phi)^4 \chi_{m-4}(p, \phi)
\]
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 \( \Gamma(p, \phi^*; r) = \)

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

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

and

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

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 $T \geq 1$

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

$r = 0.01, 0.05, 0.10, 0.15, 0.20, \ldots, 1.00$. 
Fixed points for $r < 1, d^* > 1$, and $T \geq 1$

$T = 2, d^* = 2$

- $r = 0.01, 0.05, 0.10, \ldots, 0.3820 \pm 0.0001$.  
- No spreading for $r \gtrsim 0.382$. 
What we have now:

- Two kinds of contagion processes:
- $d^* = 1$: spreading from small seeds possible.
- $d^* > 1$: critical mass model.
- Are other behaviors possible?
Generalized model

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

- Key quantities:

\[
P_k = \int_0^\infty d \, d^* \, g(d^*) \, P \left( \sum_{j=1}^{k} d_j \geq d^* \right)
\]

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.
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:**
  \[
  pP_1 T \geq 1 \quad \text{or} \quad \Rightarrow p_c = 1/(TP_1)
  \]

- **Very good:**
  1. $P_1 T$ is the expected number of vulnerables the initial infected individual meets before recovering.
  2. $pP_1 T$ is the expected number of successful infections (equivalent to $R_0$).

- **Observe:** $p_c$ may exceed 1 meaning no spreading from a small seed.
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 $(P_1 - P_2/2)^5$ (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...
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. $d^*_1 = 0.5$
  2. $d^*_2 = 1.6$
  3. $d^*_3 = 3$
- Spread of dose sizes matters, details are not important.
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 $\tau = 1/r - 1 = \text{expected recovery time}$
- I-II transition less pleasant analytically.
More complicated models

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

- 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 ($T, r, \rho, P_1$, and/or $P_2$).
- To change behavior given model: ‘adjust’ probability of exposure ($\rho$) and/or initial number infected ($\phi_0$).
Discussion

- Single seed infects others if \( pP_1(T + \tau) \geq 1 \).
- Key quantity: \( p_c = \frac{1}{P_1(T + \tau)} \)
- 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.
Details for Class I-II transition:

\( \phi^* = \sum_{k=1}^{T} \left( \begin{array}{c} T \\ k \end{array} \right) P_k (p\phi^*)^k (1 - p\phi^*)^{T-k} \),

\( = \sum_{k=1}^{T} \left( \begin{array}{c} T \\ k \end{array} \right) P_k (p\phi^*)^k \sum_{j=0}^{T-k} \left( \begin{array}{c} T - k \\ j \end{array} \right) (-p\phi^*)^j \),

\( = \sum_{k=1}^{T} \sum_{j=0}^{T-k} \left( \begin{array}{c} T \\ k \end{array} \right) \left( \begin{array}{c} T - k \\ j \end{array} \right) P_k (-1)^j (p\phi^*)^{k+j} \),

\( = \sum_{m=1}^{T} \sum_{k=1}^{m} \left( \begin{array}{c} T \\ k \end{array} \right) \left( \begin{array}{c} T - k \\ m - k \end{array} \right) P_k (-1)^{m-k} (p\phi^*)^m \),

\( = \sum_{m=1}^{T} C_m (p\phi^*)^m \)
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

\[
\binom{T}{k} \binom{T-k}{m-k} = \frac{T!}{k!(T-k)!} \frac{(T-k)!}{(m-k)!(T-m)!} \frac{T!}{m!} \frac{m!}{k!(m-k)!} = \frac{T!}{m!(T-m)!} \frac{k!(m-k)!}{k!}\binom{m}{k} = \binom{T}{m} \binom{m}{k}.
\]
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** \( P_1 - P_2/2 \).
References


References II


References III


References IV