Generalized contagion
Complex Networks, Course 303A, Spring, 2009

Prof. Peter Dodds
Department of Mathematics & Statistics
University of Vermont

Licensed under the Creative Commons Attribution-NonCommercial-ShareAlike 3.0 License.

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

- $S(t) + I(t) + R(t) = 1$
- 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

Differential equations for continuous model

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

$\beta$, $r$, 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.

Original models attributed to

- 1920's: Reed and Frost
- 1920's/1930's: Kermack and McKendrick
- Coupled differential equations with a mass-action principle

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:
  \[ R_0 = \beta + (1-r)\beta + (1-r)^2\beta + (1-r)^3\beta + \ldots \]
  \[ = \beta \left( 1 + (1-r) + (1-r)^2 + (1-r)^3 + \ldots \right) \]
  \[ = \frac{\beta}{1-(1-r)} = \frac{\beta}{r} \]
- Similar story for continuous 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).
- $\phi =$ 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.
- $\phi_t = \text{fraction infected at time } t$ = probability of contact with infected individual.
- With probability $p$, contact with infective leads to 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 $t = 0$.

**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 $\rho$. 

A visual explanation

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 \( p \).
- 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 \( \phi_t = \phi^* \):
  \[ \phi^* = p\phi^* + (1 - p\phi^*)(1 - r) \]
  \[ \Rightarrow 1 = p + (1 - p\phi^*)(1 - r), \quad \phi^* \neq 0, \]
  \[ \Rightarrow \phi^* = \frac{1 - r/p}{1 - r} \]
  \[ \text{and} \quad \phi^* = 0. \]
- 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 \( r = 1, d^* = 1, \text{ and } T > 1 \)

- \( r = 1 \) 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 \( r \le 1, d^* = 1, \text{ and } T \ge 1 \)

- Start with \( r = 1, d^* = 1, \text{ and } T \ge 1 \) 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:
  \[
  H_1 = \{ \ldots, d_t - T - 2, d_t - T - 1, 1, 0, 0, \ldots, 0, 0 \},
  \text{T 0's}
  \]
- With history \( H_1 \), probability of being infected (not recovering in one time step) is \( 1 - r \).

Homogeneous, one hit models:

Fixed points for \( r \le 1, d^* = 1, \text{ and } T \ge 1 \)

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

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

- \( \Pr(\text{recovery}) = \Pr(\text{seeing no doses for at least } T \text{ time steps and recovering}) \)
  \[
  = r \sum_{m=0}^{\infty} P(HT+m) = r \sum_{m=0}^{\infty} p^* (1 - p^*)^{T+m}(1 - r)^m
  \]
  \[
  = r \frac{p^*(1 - p^*)^T}{1 - (1 - p^*)(1 - r)}.
  \]
- Fixed point equation:
  \[
  \phi^* = 1 - \frac{r(1 - p^*)^T}{1 - (1 - p^*)(1 - r)}.
  \]

Epidemic threshold:

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

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

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.
- \( T + \tau \approx \text{average memory in system} = 3. \)
- Phase transition can be seen as a transcritical bifurcation.\(^{[11]}\)

Homogeneous, multi-hit models:

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

- Fixed point equation (again):
  \[
  \phi^* = 1 - \frac{r(1 - p^*)^T}{1 - (1 - p^*)(1 - r)}.
  \]
- 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 \( \tau = \text{mean recovery time for simple relaxation process}. \)
- Decreasing \( r \) keeps individuals infected for longer and decreases \( p_c. \)

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:
  \[
  \phi^* = \sum_{i=d^*}^{T} \binom{T}{i} (p^*)^i (1 - p^*)^{T-i}.
  \]
- 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 $d^* = 2$, $T = 3$:

  - Fixed point equation:
    \[
    \phi^* = \frac{3p^2\phi^* (1-p\phi^*) + p^3\phi^*^3}{1-p\phi^*}
    \]
  - 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:

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.

Homogeneous, multi-hit models:

- Another example:

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

Homogeneous, multi-hit models:

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

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

  - $T = 96 (\triangle)$.
  - $T = 24 (>)$.
  - $T = 12 (<)$.
  - $T = 6 (\square)$.
  - $T = 3 (\bigcirc)$. 
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 $T = 24$, $d^* = 14$:

<table>
<thead>
<tr>
<th>$t$</th>
<th>0</th>
<th>10</th>
<th>20</th>
<th>30</th>
<th>40</th>
<th>50</th>
<th>60</th>
<th>70</th>
<th>80</th>
</tr>
</thead>
<tbody>
<tr>
<td>$D(t)$</td>
<td>24</td>
<td>20</td>
<td>16</td>
<td>12</td>
<td>8</td>
<td>4</td>
<td>0</td>
<td>4</td>
<td>8</td>
</tr>
</tbody>
</table>

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 $d^* = 2$:
  \[ D_n = 2 \implies D_{n+1} = 1 \]
- 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 $T \geq 1$

- Define $\gamma_m$ as fraction of individuals for whom $D(t)$ last equaled, and his since been below, their threshold $m$ time steps ago,
- Fraction of individuals below threshold but not recovered:
  \[ \Gamma(p, \phi^*; r) = \sum_{m=1}^{\infty} (1 - r)^m \gamma_m(p, \phi^*). \]
- Fixed point equation:
  \[ \phi^* = \Gamma(p, \phi^*; r) + \sum_{i=d^*}^{T} \left( \frac{T_i}{i} \right) (p^\phi*)^i (1 - p\phi^*)^T - i. \]

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 $N_b$:
  \[ 0, 1, 2, \ldots, \left\lfloor \frac{m}{3} \right\rfloor \]
  where $\lfloor \cdot \rfloor$ means floor.
- Corresponding possible values for $N_a$:
  \[ m, m-3, m-6, \ldots, m-3 \cdot \left\lfloor \frac{m}{3} \right\rfloor \].

References

Appendix

Generalized Contagion
Fixed points for \( r < 1, \ n^* > 1, \) 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 \( r < 1, \ n^* > 1, \) and \( T \geq 1 \)

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

\[
D_1 = \{1, 1, 0, 0, D_{m-1}\} \\
D_2 = \{1, 1, 0, 0, D_{m-2}, 1\} \\
D_3 = \{1, 1, 0, 0, D_{m-3}, 1, 0\} \\
D_4 = \{1, 0, 1, 0, 0, D_{m-2}\} \\
D_5 = \{1, 0, 1, 0, 0, D_{m-3}, 1\} \\
D_6 = \{1, 0, 1, 0, 0, D_{m-4}, 1, 0\}
\]

- \( P_1 = (p\phi)^2(1-p\phi)^2\chi_{m-1}(p, \phi) \)
- \( P_2 = (p\phi)^3(1-p\phi)^2\chi_{m-2}(p, \phi) \)
- \( P_3 = (p\phi)^3(1-p\phi)^3\chi_{m-3}(p, \phi) \)
- \( P_4 = (p\phi)^2(1-p\phi)^3\chi_{m-2}(p, \phi) \)
- \( P_5 = (p\phi)^3(1-p\phi)^3\chi_{m-3}(p, \phi) \)
- \( P_6 = (p\phi)^3(1-p\phi)^4\chi_{m-4}(p, \phi) \)

Fixed points for \( r < 1, \ n^* > 1, \) and \( T \geq 1 \)

- Total number of allowable sequences of length \( m \):

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

where \( k = N_b \) and we have used \( m = N_a + 3N_b \).

- \( P(a) = (1-p\phi^*)^3 \) 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 \( D_{m}^{a,b} \).

Fixed points for \( r < 1, \ n^* = 2, \) and \( T = 3 \)

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 $T \geq 1$

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

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

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

  - 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:
  \[
  P_k = \int_0^\infty \dd d^* \, g(d^*) P \left( \sum_{j=1}^k d_j \geq d^* \right) \quad \text{where} \quad 1 \leq k \leq T.
  \]
  - $P_k =$ Probability that the threshold of a randomly selected individual will be exceeded by $k$ doses.
  - e.g., $P_1 =$ Probability that \textbf{one dose} will exceed the threshold of a random individual = Fraction of \textbf{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

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 \( \tau = 1/r \) = 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 \((T, r, \rho, P_1, \text{and/or } P_2)\).
- To change behavior given model: ‘adjust’ probability of exposure \((p)\) and/or initial number infected \((\phi_0)\).
Discussion

- 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 \( P_k \).
- Most vulnerable/gullible population may be more important than small group of super-spreaders or influentials.

Details for Class I-II transition:

\[
C_m = (-1)^m \left( \frac{T}{m} \right) \sum_{k=1}^{m} (-1)^k \binom{m}{k} P_k,
\]

since

\[
\binom{T}{k} \binom{T-k}{m-k} = \frac{T!}{k!(T-k)!} \frac{(T-k)!}{(m-k)!(T-k)!} = \frac{T!}{m!(T-m)!} \frac{k!(l-k)!}{k!(l-k)!} = \left( \frac{T}{m} \right) \binom{m}{k}.
\]

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 \( C_2 = \left( \frac{T}{2} \right) (-2P_1 + P_2) \).
- Using \( p_c = 1/(TP_1) \):
  \[ \phi^* \simeq \frac{C_1}{C_2 p_c^2} (p - p_c) = \frac{T^2 p_c^3}{(T - 1)(P_1 - P_2/2)} (p - p_c). \]
- Sign of derivative governed by \( P_1 - P_2/2 \).
References I

F. Bass.
A new product growth model for consumer durables.

D. J. Daley and D. G. Kendall.
Epidemics and rumours.

D. J. Daley and D. G. Kendall.
Stochastic rumours.

P. S. Dodds and D. J. Watts.
Universal behavior in a generalized model of contagion.

References II

P. S. Dodds and D. J. Watts.
A generalized model of social and biological contagion.

W. Goffman and V. A. Newill.
Generalization of epidemic theory: An application to the transmission of ideas.

A contribution to the mathematical theory of epidemics.

References III

A contribution to the mathematical theory of epidemics. III. Further studies of the problem of endemicity.

Contributions to the mathematical theory of epidemics. II. The problem of endemicity.

J. D. Murray.
*Mathematical Biology*.

References IV

S. H. Strogatz.
*Nonlinear Dynamics and Chaos*.
Addison Wesley, Reading, Massachusetts, 1994.