Biological Contagion
Principles of Complex Systems
Course 300, Fall, 2008

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Outline

Introduction

Simple disease spreading models
  Background
  Prediction

References
Contagion

A confusion of contagions:

► Is Harry Potter some kind of virus?
► What about the Da Vinci Code?
► Does Sudoku spread like a disease?
► Religion?
► Democracy...?
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Naturomorphisms

- “The feeling was contagious.”
- “The news spread like wildfire.”
- “Freedom is the most contagious virus known to man.”
  —Hubert H. Humphrey, Johnson’s vice president
- “Nothing is so contagious as enthusiasm.”
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Social contagion

Optimism according to Ambrose Bierce: (⧫)

The doctrine that everything is beautiful, including what is ugly, everything good, especially the bad, and everything right that is wrong. ...
Social contagion

Optimism according to Ambrose Bierce: (⊞)
The doctrine that everything is beautiful, including what is ugly, everything good, especially the bad, and everything right that is wrong. ... It is hereditary, but fortunately not contagious.
Social contagion

Eric Hoffer, 1902–1983

There is a grandeur in the uniformity of the mass. When a fashion, a dance, a song, a slogan or a joke sweeps like wildfire from one end of the continent to the other, and a hundred million people roar with laughter, sway their bodies in unison, hum one song or break forth in anger and denunciation, there is the overpowering feeling that in this country we have come nearer the brotherhood of man than ever before.

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The spread of fanaticism


Quotes-aplenty:

- “We can be absolutely certain only about things we do not understand.”
- “Mass movements can rise and spread without belief in a God, but never without belief in a devil.”
- “Where freedom is real, equality is the passion of the masses. Where equality is real, freedom is the passion of a small minority.”
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Hoffer’s acclaimed work:

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Hoffer’s acclaimed work:
“The True Believer:
Thoughts On The Nature Of Mass Movements” (1951) [3]

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Imitation

“When people are free to do as they please, they usually imitate each other.”

—Eric Hoffer


despair.com
The collective...

“Never Underestimate the Power of Stupid People in Large Groups.”

despair.com
Contagion

Definitions

- (1) The spreading of a quality or quantity between individuals in a population.
- (2) A disease itself:
  - the plague, a blight, the dreaded lurgi, ...
- from Latin: *con* = ‘together with’ + *tangere* ‘to touch.’
- Contagion has unpleasant overtones...
- Just *Spreading* might be a more neutral word
- But contagion is kind of exciting...
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Interesting infections:

- Spreading of buildings in the US. (圄)
- Spreading of spreading (圄).
- Viral get-out-the-vote video. (圄)
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Two main classes of contagion

1. Infectious diseases

2. Social contagion
Contagions

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1. **Infectious diseases**: tuberculosis, HIV, ebola, SARS, influenza, ...

2. **Social contagion**
Two main classes of contagion

1. **Infectious diseases:**
   tuberculosis, HIV, ebola, SARS, influenza, ...

2. **Social contagion:**
   fashion, word usage, rumors, riots, religion, ...
Mathematical Epidemiology

The standard SIR model [8]

- The basic model of disease contagion
- Three states:
  1. S = Susceptible
  2. I = Infective/Infectious
  3. R = Recovered
- $S(t) + I(t) + R(t) = 1$
- Presumes random interactions (mass-action principle)
- Interactions are independent (no memory)
- Discrete and continuous time versions
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Discrete time automata example:

- Transition Probabilities:
  - $\beta I$ for being infected given contact with infected
  - $r$ for recovery
  - $\rho$ for loss of immunity

- States:
  - $S$: Susceptible
  - $I$: Infectious
  - $R$: Recovered

- Transition rates:
  - $1 - \beta I$: from $S$ to $I$
  - $\beta I$: from $S$ to $I$
  - $\rho$: from $I$ to $R$
  - $1 - \rho$: from $R$ to $S$
  - $r$: from $I$ to $R$
  - $1 - r$: from $I$ to $R$
Mathematical Epidemiology

Discrete time automata example:

\[
\begin{align*}
S &\rightarrow 1 - \beta I \\
\beta I &\rightarrow I \\
\rho &\rightarrow R \\
1 - r &\rightarrow I \\
r &\rightarrow I \\
1 - \rho &\rightarrow S
\end{align*}
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Original models attributed to

- 1920’s: Reed and Frost
- 1920’s/1930’s: Kermack and McKendrick \[^{5, 7, 6}\]
- Coupled differential equations with a mass-action principle
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Independent Interaction models

Differential equations for continuous model

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

\(\beta, r,\) 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.
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\frac{dI}{dt} &= \beta IS - rI \\
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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 $(1 - r)^k$
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Discrete version:

- Expected number infected by original Infective:

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

Discrete version:

- Expected number infected by original Infective:

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$$= \beta \left( 1 + (1 - r) + (1 - r)^2 + (1 - r)^3 + \ldots \right)$$
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\[ = \beta \frac{1}{1 - (1 - r)} \]
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$$= \beta \frac{1}{1 - (1 - r)} = \beta / r$$
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\]

For $S_0$ initial infectives ($1 - S_0 = R_0$ immune):

\[
R_0 = S_0\beta/r
\]
Independent Interaction models

For the continuous version

- Second equation:

\[
\frac{d}{dt} I = \beta SI - rI
\]

- Number of infectives grows initially if

\[
\beta S(0) - r > 0
\]

- Same story as for discrete model.
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Example of epidemic threshold:

- Continuous phase transition.
- Fine idea from a simple model.
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Fraction infected vs. $R_0$.
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Example of epidemic threshold:

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- Fine idea from a simple model.
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Many variants of the SIR model:

- **SIS**: susceptible-infective-susceptible
- **SIRS**: susceptible-infective-recovered-susceptible
- compartment models (age or gender partitions)
- more categories such as ‘exposed’ (**SEIRS**)
- recruitment (migration, birth)
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- Recruitment (migration, birth)
Independent Interaction models

Many variants of the SIR model:

- **SIS**: susceptible-infective-susceptible
- **SIRS**: susceptible-infective-recovered-susceptible
- compartment models (age or gender partitions)
- more categories such as ‘exposed’ (**SEIRS**)
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Outline

Introduction

Simple disease spreading models
  Background
  Prediction

References
Disease spreading models

For novel diseases:

1. Can we predict the size of an epidemic?
2. How important is the reproduction number $R_0$?
Disease spreading models

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$R_0$ approximately same for all of the following:

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- 1957-58 “Asian Flu” $\sim 70,000$ deaths in US
- 1968-69 “Hong Kong Flu” $\sim 34,000$ deaths in US
- 2003 “SARS Epidemic” $\sim 800$ deaths world-wide
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- earthquakes (Gutenberg-Richter law)
- city sizes, forest fires, war fatalities
- wealth distributions
- ‘popularity’ (books, music, websites, ideas)
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Power laws distributions are common but not obligatory...
Really, what about epidemics?

- Simply hasn’t attracted much attention.
- Data not as clean as for other phenomena.
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Feeling Ill in Iceland

Caseload recorded monthly for range of diseases in Iceland, 1888-1890

Treat outbreaks separated in time as ‘novel’ diseases.
Really not so good at all in Iceland

Epidemic size distributions $N(S)$ for Measles, Rubella, and Whooping Cough.

Spike near $S = 0$, relatively flat otherwise.
Measles & Pertussis

Insert plots:
Complementary cumulative frequency distributions:

$$N(\Psi^{'}) \propto \Psi^{-\gamma + 1}$$

Limited scaling with a possible break.
Measles & Pertussis

Insert plots:
Complementary cumulative frequency distributions:

\[ N(\psi' > \psi) \propto \psi^{-\gamma + 1} \]

Limited scaling with a possible break.
Power law distributions

Measured values of $\gamma$:

- measles: $1.40$ (low $\psi$) and $1.13$ (high $\psi$)
- pertussis: $1.39$ (low $\psi$) and $1.16$ (high $\psi$)

- Expect $2 \leq \gamma < 3$ (finite mean, infinite variance)
- When $\gamma < 1$, can’t normalize
- Distribution is quite flat.
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Resurgence—example of SARS

- Epidemic slows...
- Epidemic discovers new ‘pools’ of susceptibles: Resurgence.
- Importance of rare, stochastic events.
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The challenge

So... can a simple model produce

1. broad epidemic distributions
   and
2. resurgence?
Size distributions

Simple models typically produce bimodal or unimodal size distributions.

- This includes network models: random, small-world, scale-free, ...
- Exceptions:
  1. Forest fire models
  2. Sophisticated metapopulation models
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Burning through the population

Forest fire models: [9]

- Rhodes & Anderson, 1996
- The physicist’s approach:
  “if it works for magnets, it’ll work for people…”

A bit of a stretch:

1. Epidemics $\equiv$ forest fires spreading on 3-d and 5-d lattices.
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Sophisticated metapopulation models

- Community based mixing: Longini (two scales).
  - Eubank et al.’s EpiSims/TRANSIMS—city simulations.
  - Spreading through countries—Airlines: Germann et al., Corlizza et al.
  - Vital work but perhaps hard to generalize from...
  - ➞ Create a simple model involving multiscale travel
  - Multiscale models suggested by others but not formalized (Bailey, Cliff and Haggett, Ferguson et al.)
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Should we model SARS in Hong Kong as spreading?

For simple models, we need to know the final size beforehand...
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Improving simple models

Contexts and Identities—Bipartite networks

- boards of directors
- movies
- transportation modes (subway)
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Idea for social networks: incorporate identity.

Identity is formed from attributes such as:

- Geographic location
- Type of employment
- Age
- Recreational activities

Groups are crucial...

- formed by people with at least one similar attribute
- Attributes ↔ Contexts ↔ Interactions ↔ Networks. [11]
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Infer interactions/network from identities

Distance makes sense in identity/context space.
Generalized context space

(Blau & Schwartz [1], Simmel [10], Breiger [2])
A toy agent-based model

Geography—allow people to move between contexts:

- Locally: standard SIR model with random mixing
- discrete time simulation
- $\beta =$ infection probability
- $\gamma =$ recovery probability
- $P =$ probability of travel
- Movement distance: $\Pr(d) \propto \exp(-d/\xi)$
- $\xi =$ typical travel distance
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Schematic:

\[ b = 2 \]

\[ x_{ij} = 2 \]

\[ l = 3 \]

\[ n = 8 \]
Model output

- Define $P_0 =$ Expected number of infected individuals leaving initially infected context.
- Need $P_0 > 1$ for disease to spread (independent of $R_0$).
- Limit epidemic size by restricting frequency of travel and/or range.
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Varying $\xi$:

- Transition in expected final size based on typical movement distance
Varying $\xi$: Transition in expected final size based on typical movement distance (sensible)
Model output

Varying $P_0$:

- Transition in expected final size based on typical number of infectives leaving first group
- Travel advisories: $\xi$ has larger effect than $P_0$. 
Model output

Varying $P_0$:

- Transition in expected final size based on typical number of infectives leaving first group (also sensible)
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- Travel advisories: $\xi$ has larger effect than $P_0$. 
Example model output: size distributions

- Flat distributions are possible for certain $\xi$ and $P$.
- Different $R_0$’s may produce similar distributions.
- Same epidemic sizes may arise from different $R_0$’s.
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Model output—resurgence

Standard model:

\[ R_0 = 3 \]
Model output—resurgence

Standard model with transport:

\[ \text{# New cases} \]

\[ R_0 = 3 \]

\[ E \]

\[ G \]
The upshot

Multiscale population structure
The upshot

Multiscale population structure
+
stochasticity
The upshot

Multiscale population structure + stochasticity

leads to

resurgence + broad epidemic size distributions
Conclusions

- For this model, epidemic size is highly unpredictable
- Model is more complicated than SIR but still simple
- We haven’t even included normal social responses such as travel bans and self-quarantine.
- The reproduction number $R_0$ is not very useful.
- $R_0$, however measured, is not informative about
  1. how likely the observed epidemic size was,
  2. and how likely future epidemics will be.
- Problem: $R_0$ summarises one epidemic after the fact and enfolds movement, everything.
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- Disease spread highly sensitive to population structure
- Rare events may matter enormously
- More support for controlling population movement
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- More support for controlling population movement (e.g., travel advisories, quarantine)
Conclusions

What to do:

► Need to separate movement from disease
  ► $R_0$ needs a friend or two.
  ► Need $R_0 > 1$ and $P_0 > 1$ and $\xi$ sufficiently large for disease to have a chance of spreading

More wondering:

► Exactly how important are rare events in disease spreading?
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Attempts to use beyond disease:

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- Spread of rumors (Daley & Kendall, 1965)
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