Outline

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Simple disease spreading models
  Background
  Prediction
  More models
  Toy metapopulation models
  Model output
  Conclusions

Predicting social catastrophe

References
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: (تفاعل)
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.

▶ Hoffer (سعد) was an interesting fellow...
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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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"When people are free to do as they please, they usually imitate each other."

—Eric Hoffer

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

despair.com
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...
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Examples of non-disease spreading:

- Spreading of buildings in the US.
- Viral get-out-the-vote video.
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Interesting infections:

- Spreading of buildings in the US. (𹾅)
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Contagions

Two main classes of contagion

1. Infectious diseases
2. Social contagion
Contagions

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1. Infectious diseases
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Two main classes of contagion

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

2. **Social contagion**
Contagions

Two main classes of contagion

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

2. **Social contagion:**
   fashion, word usage, rumors, riots, religion, ...
Simple disease spreading models

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Mathematical Epidemiology

The standard SIR model \[^5\]

- = 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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Discrete time automata example:

\[
\begin{align*}
S &\rightarrow 1 - \beta I \\
S &\rightarrow \beta I \\
S &\rightarrow \rho \\
I &\rightarrow r \\
I &\rightarrow 1 - r \\
R &\rightarrow 1 - \rho \\
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\end{align*}
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Mathematical Epidemiology

Discrete time automata example:

Transition Probabilities:
Mathematical Epidemiology

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\( \beta \) for being infected given contact with infected
Discrete time automata example:

Transition Probabilities:

- $\beta$ for being infected given contact with infected
- $r$ for recovery
Mathematical Epidemiology

Discrete time automata example:

Transition Probabilities:

- $\beta$ for being infected given contact with infected
- $r$ for recovery
- $\rho$ for loss of immunity
Mathematical Epidemiology

Original models attributed to

- 1920’s: Reed and Frost
- 1920’s/1930’s: Kermack and McKendrick [?, ?, ?]
- 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.
Independent Interaction models

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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 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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Reproduction Number $R_0$

Discrete version:

- Expected number infected by original Infective:

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

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- Expected number infected by original Infective:

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

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

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

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.
Independent Interaction models

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- Second equation:
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  \]
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Independent Interaction models

Example of epidemic threshold:

\[ R_0 \]

- Fraction infected
Independent Interaction models

Example of epidemic threshold:

- Continuous phase transition.
Independent Interaction models

- Continuous phase transition.
- Fine idea from a simple model.
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)
- recruitment (migration, birth)
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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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$R_0$ and variation in epidemic sizes

$R_0$ approximately same for all of the following:

- 1918-19 “Spanish Flu” $\sim$ 500,000 deaths in US
- 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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Size distributions

Size distributions are important elsewhere:

- 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, 1888-1990

- 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

![Graph A](chart.png)

![Graph B](chart.png)
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.
Resurgence—example of SARS

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  then an infective moves to a new context.
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The challenge

So... can a simple model produce

1. broad epidemic distributions
and
2. resurgence?
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: [6]
  - 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.
2. Claim Iceland and Faroe Islands exhibit power law distributions for outbreaks.
3. Original forest fire model not completely understood.
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From Rhodes and Anderson, 1996.
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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Very big question: What is $N$?

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- 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. [8]
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Infer interactions/network from identities

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

(Blau & Schwartz [1], Simmel [7], 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:
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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.
Define $P_0 = \text{Expected number of infected individuals leaving initially infected context.}$
Need $P_0 > 1$ for disease to spread (independent of $R_0$).
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Model output

Varying $\xi$:

- Transition in expected final size based on typical movement distance
Model output

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 $P_0$. 

Frame 50/66
Varying $P_0$:

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

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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
Example model output: size distributions

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Model output—resurgence

Standard model:

\[ R_0 = 3 \]
Model output—resurgence

Standard model with transport:

---

**E**

\[ R_0 = 3 \]

---

**G**

\[ R_0 = 3 \]
The upshot

Simple multiscale population structure
The upshot

Simple multiscale population structure
+
stochasticity
The upshot

Simple multiscale population structure
+
Stochasticity

leads to

Resurgence
+
Broad epidemic size distributions
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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 terribly 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, the price of bananas, everything.
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- Problem: $R_0$ summarises one epidemic after the fact and enfolds movement, the price of bananas, everything.
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 terribly useful.
- $R_0$, however measured, is not informative about:
  1. how likely the observed epidemic size was,
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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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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:

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  Prediction
  More models
  Toy metapopulation models
  Model output
  Conclusions

Predicting social catastrophe

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Jon Stewart:
“You just bummed the @*!# out of me.”

► From the Daily Show ( september 18, 2007)
► The full interview is here.
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From the New York Times, 11/02/2008 (￼)
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