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Last updated: 2021/10/07, 17:44:59 EDT

Principles of Complex Systems, Vols. 1 & 2
CSYS/MATH 300 and 303, 2021–2022| @pocsvox

Prof. Peter Sheridan Dodds | @peterdodds

Computational Story Lab | Vermont Complex Systems Center
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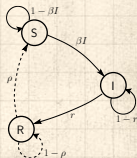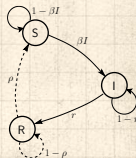Toy metapopulation
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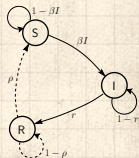Background
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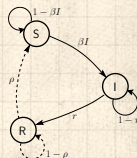Toy metapopulation
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IF FOUND REPEAT KEY
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THE
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THE UNENDING PANDEMICS

An awful recording: Wikipedia's list of epidemics ⧉ from 430 BC on.

Wikipedia
The Free Encyclopedia

Article   Talk

Read   Edit   View history

List of epidemics

From Wikipedia, the free encyclopedia

This article is a **list of epidemics** of infectious disease. Widespread and chronic complaints such as heart disease and allergy are not included if they are not thought to be infectious.

This list is incomplete; you can help by expanding it.

| Death toll (estimate)	Location	Date	Comment	Disease	Reference
ca. 75,000–100,000	Greece	429–426 BC	Known as Plague of Athens, because it was primarily in Athens.	unknown, similar to typhoid	
ca. 30% of population	Europe, Western Asia, Northern Africa	165–180	Known as Antonine Plague, due to the name of the Roman emperor in power at the time.	unknown, symptoms similar to smallpox	
	Europe	250-266 AD	Known as the Plague of Cyprian named after St. Cyprian Bishop of Carthage.	unknown, possibly smallpox	
ca. 40% of population	Europe	541–542	Known as Plague of Justinian, due to the name of the Byzantine emperor in power at the time.	Bubonic plague	[1]
30% to 70% of population	Europe	1346–1350	Known as "Black Death" or Second plague pandemic, first return of the plague to Europe after the Justinianic plague of the 6th century.	plague	[2]
5-15 million (80% of population)	Mexico	1545-1548	Cocoliztli	viral hemorrhagic fever	[3][4][5]
2 - 2.5 million (50% of population)	Mexico	1576	Cocoliztli	viral hemorrhagic fever	[6][7][8]
	Seneca nation	1592–1596		measles	[9]

Plague panel with the triumph of death. 1607–35, Deutsches Historisches Museum Berlin

An artistic portrayal of cholera which was epidemic in the 19th century
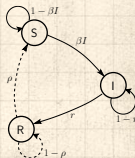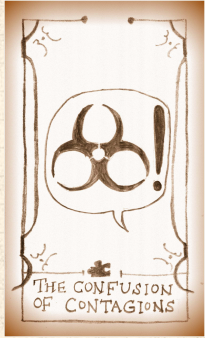
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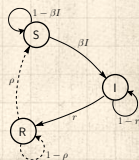More models
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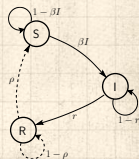More models
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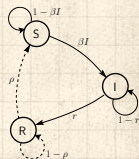Nutshell
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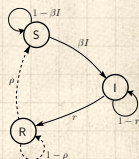
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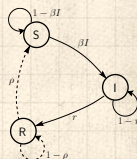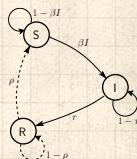models
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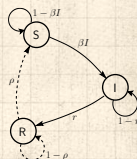More models
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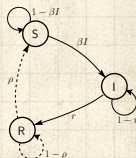More models
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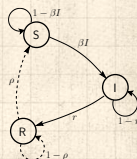
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- 🎲 Stories?

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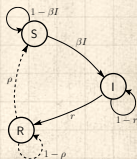Model output
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- 🎲 "The feeling was contagious."

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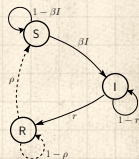Background
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🎲 "The feeling was contagious."

🎲 "The news spread like wildfire."

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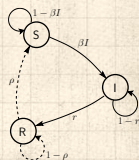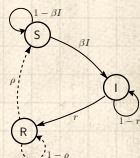Nutshell
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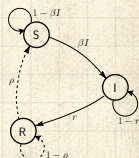Background
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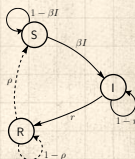Model output
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Optimism according to Ambrose Bierce: ⤢

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

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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.

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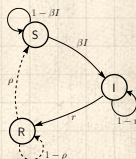spreading models
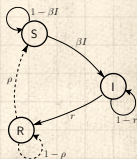Background
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There is a grandeur in the uniformity of the mass.

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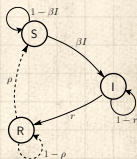Background
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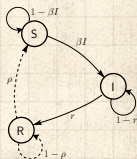Model output
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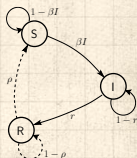Model output
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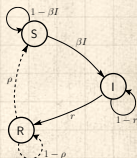Background
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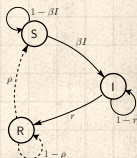Model output
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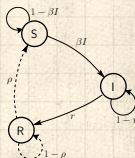Model output
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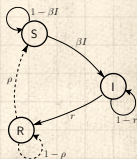Background
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 Hoffer was an interesting fellow…
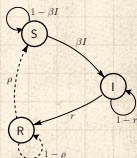
The spread of fanaticism

Hoffer's most famous work: "The True Believer:
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Aphorisms-aplenty:

The spread of fanaticism

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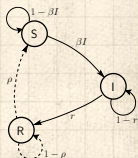Simple disease
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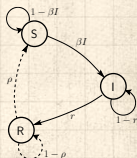Model output
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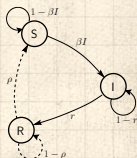models
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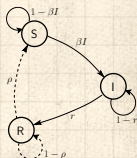Background
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- "Where freedom is real, equality is the passion of
  the masses. Where equality is real, freedom is the
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Imitation

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despair.com

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

—Eric Hoffer
"The Passionate State of Mind" [13]

The collective...

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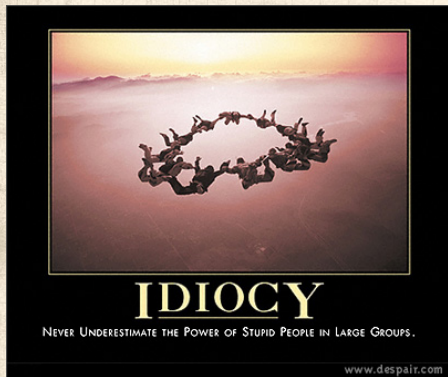
"Never Underestimate the Power of Stupid People in Large Groups."

despair.com

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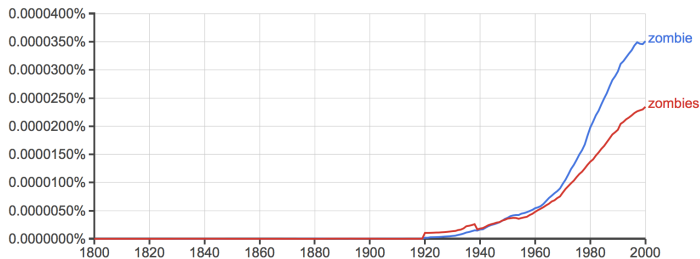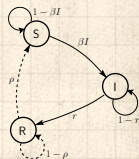Model output
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Examples of non-disease spreading:

Interesting infections:

🎲 Spreading of certain buildings in the US:

http://www.youtube.com/watch?v=EGzHBtoVvpc?rel=0

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Marbleization of the US:

http://www.youtube.com/watch?v=9ihSeSToXOw?rel=0
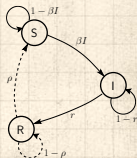
The most terrifying contagious outbreak?

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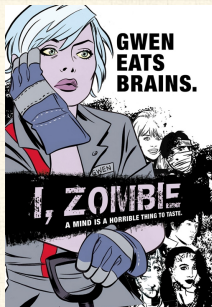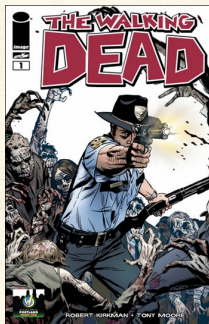spreading models

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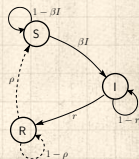Prediction
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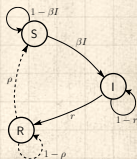Model output
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Definitions

🧊 (1) The spreading of a quality or quantity between individuals in a population.

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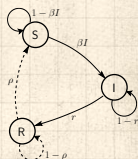More models
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Definitions

- (1) The spreading of a quality or quantity between individuals in a population.

- (2) A disease itself:
  the plague, a blight, the dreaded lurgi, ...

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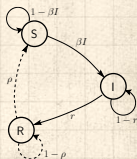Prediction
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Definitions

- (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* = 'with' + *tangere* 'to touch.'

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🎲 (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* = 'with' + *tangere* 'to touch.'

🎲 Contagion has unpleasant overtones...

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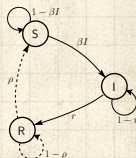models
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- 🧱 (1) The spreading of a quality or quantity between individuals in a population.
- 🧱 (2) A disease itself:
  the plague, a blight, the dreaded lurgi, ...
- 🧱 from Latin: *con* = 'with' + *tangere* 'to touch.'
- 🧱 Contagion has unpleasant overtones...
- 🧱 Just Spreading might be a more neutral word

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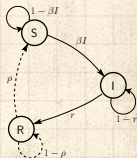Next

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- (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* = '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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Two main classes of contagion

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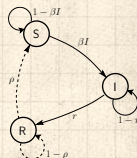More models
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Two main classes of contagion

1. Infectious diseases

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Two main classes of contagion

1. Infectious diseases

2. Social contagion

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Two main classes of contagion

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

2. Social contagion

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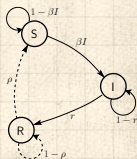Prediction
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Two main classes of contagion

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

2. Social contagion:
   fashion, word usage, rumors, uprisings, religion,
   stories about zombies, ...

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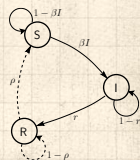More models
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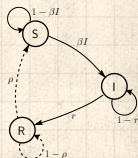models
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Archival footage from the Black Plague

http://www.youtube.com/watch?v=GU0d8kpybVg?rel=0 ↗

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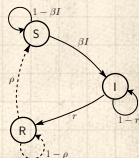More models
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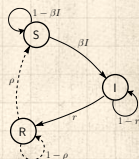Model output
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The standard SIR model [18]

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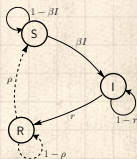Next

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The standard SIR model [18]

🎲 = basic model of disease contagion

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The standard SIR model [18]

📦 = basic model of disease contagion

📦 Three states:

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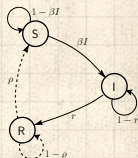Background
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The standard SIR model [18]

- = basic model of disease contagion
- Three states:
  1. S = Susceptible

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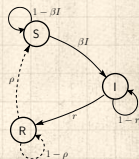Toy metapopulation
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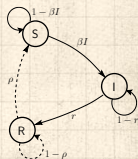Other kinds of prediction
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The standard SIR model [18]

🎲 = basic model of disease contagion

🎲 Three states:
1. S = Susceptible
2. I = Infective/Infectious

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The standard SIR model [18]

🎲 = basic model of disease contagion

🎲 Three states:
  1. S = Susceptible
  2. I = Infective/Infectious
  3. R = Recovered

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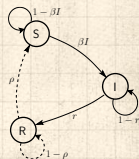Model output
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The standard SIR model [18]

🎲 = basic model of disease contagion

🎲 Three states:
1. S = Susceptible
2. I = Infective/Infectious
3. R = Recovered or Removed or Refractory

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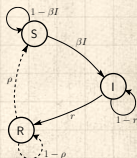Other kinds of prediction
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The standard SIR model [18]

🦠 = basic model of disease contagion

🦠 Three states:
1. S = Susceptible
2. I = Infective/Infectious
3. R = Recovered or Removed or Refractory

🦠 $S(t) + I(t) + R(t) = 1$

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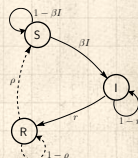Other kinds of prediction
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The standard SIR model [18]

🎲 = 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)

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- 🧩 = 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)
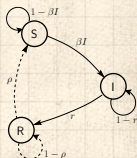- 🧩 Interactions are independent (no memory)

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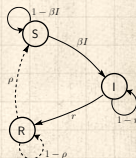
The standard SIR model [18]

🧊 = 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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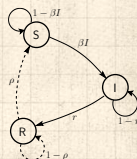Model output
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Discrete time automata example:

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Discrete time automata example:

Transition Probabilities:

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Discrete time automata example:

Transition Probabilities:

β for being infected given contact with infected

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Discrete time automata example:

Transition Probabilities:

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r for recovery

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Discrete time automata example:

Transition Probabilities:

β for being infected given
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r for recovery
ρ for loss of immunity

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Original models attributed to

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Original models attributed to

🎲 1920's: Reed and Frost

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Original models attributed to

- 1920's: Reed and Frost
- 1920's/1930's: Kermack and McKendrick [14, 16, 15]

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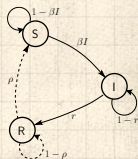
Original models attributed to

- 🧊 1920's: Reed and Frost
- 🧊 1920's/1930's: Kermack and McKendrick [14, 16, 15]
- 🧊 Coupled differential equations with a mass-action principle

Independent Interaction models

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Differential equations for continuous model

$$\frac{\mathrm{d}}{\mathrm{d}t} S = -\beta I S + \rho R$$

$$\frac{\mathrm{d}}{\mathrm{d}t} I = \beta I S - r I$$

$$\frac{\mathrm{d}}{\mathrm{d}t} R = r I - \rho R$$
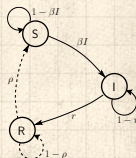
β, r, and ρ are now rates.

Reproduction Number R_0

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Reproduction Number R_0 ⌁

🎲 R_0 = expected number of infected individuals
resulting from a single initial infective

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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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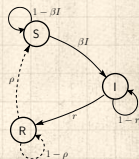More models
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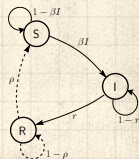Other kinds of prediction
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Reproduction Number R_0 ⤢

- 🎲 R_0 = expected number of infected individuals resulting from a single initial infective
- 🎲 Epidemic threshold: If $R_0 > 1$, 'epidemic' occurs.
- 🎲 Exponential take off: R_0^n where n is the number of generations.

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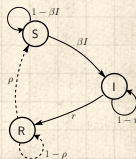models
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Reproduction Number R_0 ⤢

- ♻ R_0 = expected number of infected individuals resulting from a single initial infective

- ♻ Epidemic threshold: If $R_0 > 1$, 'epidemic' occurs.

- ♻ Exponential take off: R_0^n where n is the number of generations.

- ♻ Fantastically awful notation convention: R_0 and the R in SIR.

Reproduction Number R_0

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Discrete version:

🎲 Set up: One Infective in a randomly mixing
population of Susceptibles

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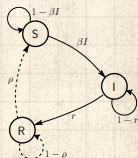
Reproduction Number R_0

Discrete version:

- Set up: One Infective in a randomly mixing population of Susceptibles

- At time $t = 0$, single infective random bumps into a Susceptible

Reproduction Number R_0

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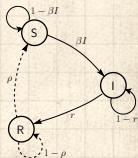More models
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References

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 = β

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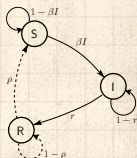Other kinds of prediction
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References

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 = β

♻ At time $t = 1$, single Infective remains infected with probability $1 - r$

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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 = 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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Discrete version:

🎲 Expected number infected by original infective:

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

Reproduction Number R_0

Discrete version:

Expected number infected by original infective:

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

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

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Discrete version:

🎲 Expected number infected by original infective:

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

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

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

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Discrete version:

Expected number infected by original infective:

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

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

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

Reproduction Number R_0

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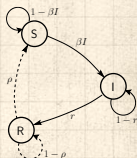Toy metapopulation
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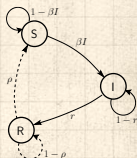
Discrete version:

Expected number infected by original infective:

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

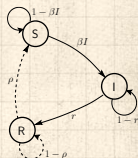$$= \beta\left(1 + (1-r) + (1-r)^2 + (1-r)^3 + \dots\right)$$

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

For $S(0) \simeq 1$ initial susceptibles
($1 - S(0) = R(0)$ = fraction initially immune):

$$R_0 = S(0)\beta/r$$

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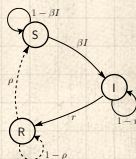
References

Example of epidemic threshold:
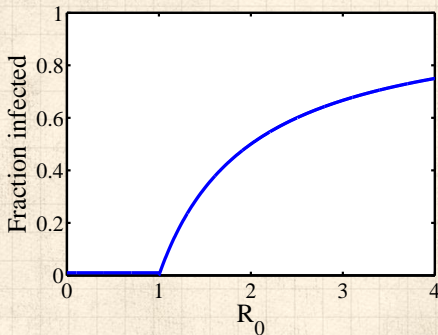
- Continuous phase transition.
- Fine idea from a simple model.

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For the continuous version

❧ Second equation:

$$\frac{\mathsf{d}}{\mathsf{d}t}I = \beta SI - rI$$

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For the continuous version

🎲 Second equation:

$$\frac{\mathrm{d}}{\mathrm{d}t}I = \beta SI - rI$$

$$\frac{\mathrm{d}}{\mathrm{d}t}I = (\beta S - r)I$$

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For the continuous version

🎲 Second equation:

$$\frac{\mathsf{d}}{\mathsf{d}t}I = \beta SI - rI$$

$$\frac{\mathsf{d}}{\mathsf{d}t}I = (\beta S - r)I$$

🎲 Number of infectives grows initially if

$$\beta S(0) - r > 0$$

where $S(0) \simeq 1$.

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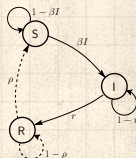
For the continuous version

♟ Second equation:

$$\frac{\mathsf{d}}{\mathsf{d}t}I = \beta S I - r I$$

$$\frac{\mathsf{d}}{\mathsf{d}t}I = (\beta S - r) I$$

♟ Number of infectives grows initially if

$$\beta S(0) - r > 0 \Rightarrow \beta S(0) > r$$

where $S(0) \simeq 1$.

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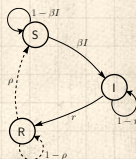
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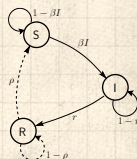# Independent Interaction models

For the continuous version

Second equation:

$$\frac{\mathrm{d}}{\mathrm{d}t}I = \beta SI - rI$$

$$\frac{\mathrm{d}}{\mathrm{d}t}I = (\beta S - r)I$$

Number of infectives grows initially if

$$\beta S(0) - r > 0 \Rightarrow \beta S(0) > r \Rightarrow \beta S(0)/r > 1$$

where $S(0) \simeq 1$.

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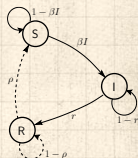Nutshell
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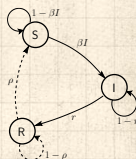
For the continuous version

♻ Second equation:

$$\frac{\mathrm{d}}{\mathrm{d}t}I = \beta SI - rI$$

$$\frac{\mathrm{d}}{\mathrm{d}t}I = (\beta S - r)I$$

♻ Number of infectives grows initially if

$$\beta S(0) - r > 0 \Rightarrow \beta S(0) > r \Rightarrow \beta S(0)/r > 1$$

where $S(0) \simeq 1$.

♻ Same story as for discrete model.

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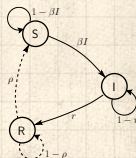
Many variants of the SIR model:

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Many variants of the SIR model:

🎲 SIS: susceptible-infective-susceptible

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Many variants of the SIR model:

🎲 SIS: susceptible-infective-susceptible

🎲 SIRS: susceptible-infective-recovered-susceptible

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Many variants of the SIR model:
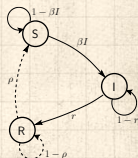
- SIS: susceptible-infective-susceptible
- SIRS: susceptible-infective-recovered-susceptible
- compartment models (age or gender partitions)

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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)

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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)
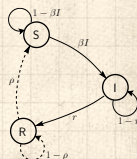
Watch someone else pretend to save the world:

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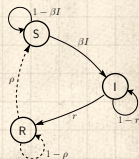Next

References

Save the world yourself: ↗

And you can be the virus. ↗

Also contagious?: Cooperative games ...

Neural reboot—Save another pretend world with Vax: ⧉

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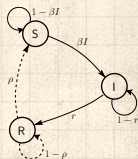More models
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Lesson 4: Quarantine
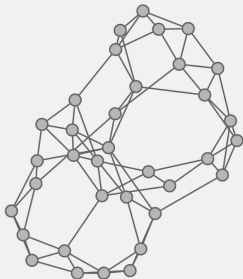
Vaccines take time to 'kick in' so they're ineffective
if an infection has already begun to spread.

Start >

VAX!

Networks   Epidemics   Vaccines   Quarantine
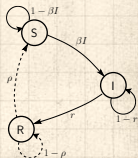
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Pandemic severity index (PSI) ⧉

Classification during/post pandemic:

Case Fatality Ratio		Projected Number of U.S. Deaths (Pop. 2006)
> 2.0%	5	>1,800,000
1.0% - <2.0%	4	900,000 - <1,800,000
0.5% - <1.0%	3	450,000 - <900,000
0.1% - <0.5%	2	90,000 - <450,000
<0.1%	1	<90,000

Assumes 30% illness rate and unmitigated pandemic without interventions

CDC   U.S. Gov.

Category based.

1–5 scale.

Modeled on the
Saffir-Simpson hurricane
scale ⧉.

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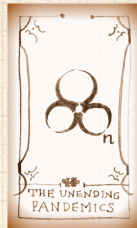
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For novel diseases:

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For novel diseases:

1. Can we predict the size of an epidemic?

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For novel diseases:

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

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For novel diseases:

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

R_0 approximately same for all of the following:

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For novel diseases:

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

R_0 approximately same for all of the following:

- 1918-19 "Spanish Flu" $\sim$ 75,000,000 world-wide, 500,000 deaths in US.

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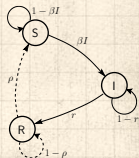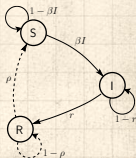Background
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References

For novel diseases:

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R_0 approximately same for all of the following:

- 1918-19 "Spanish Flu" $\sim$ 75,000,000 world-wide, 500,000 deaths in US.
- 1957-58 "Asian Flu" $\sim$ 2,000,000 world-wide, 70,000 deaths in US.

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For novel diseases:

1. Can we predict the size of an epidemic?
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R_0 approximately same for all of the following:

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- 1957-58 "Asian Flu" $\sim$ 2,000,000 world-wide, 70,000 deaths in US.
- 1968-69 "Hong Kong Flu" $\sim$ 1,000,000 world-wide, 34,000 deaths in US.

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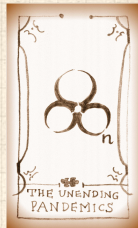Background
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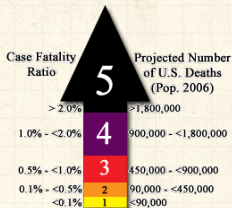Model output
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For novel diseases:

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

R_0 approximately same for all of the following:

- 1918-19 "Spanish Flu" $\sim$ 75,000,000 world-wide, 500,000 deaths in US.
- 1957-58 "Asian Flu" $\sim$ 2,000,000 world-wide, 70,000 deaths in US.
- 1968-69 "Hong Kong Flu" $\sim$ 1,000,000 world-wide, 34,000 deaths in US.
- 2003 "SARS Epidemic" $\sim$ 800 deaths world-wide.

Size distributions

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As we know, heavy-tailed size distributions are
somewhat prevalent in complex systems:

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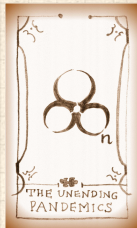Background
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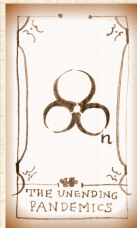Model output
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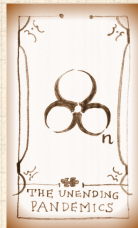Other kinds of prediction
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As we know, heavy-tailed size distributions are somewhat prevalent in complex systems:

🎲 earthquakes (Gutenberg-Richter law)

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As we know, heavy-tailed size distributions are somewhat prevalent in complex systems:

🎲 earthquakes (Gutenberg-Richter law)

🎲 city sizes, forest fires, war fatalities

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As we know, heavy-tailed size distributions are somewhat prevalent in complex systems:

- earthquakes (Gutenberg-Richter law)
- city sizes, forest fires, war fatalities
- wealth distributions

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References

As we know, heavy-tailed size distributions are somewhat prevalent in complex systems:

- earthquakes (Gutenberg-Richter law)
- city sizes, forest fires, war fatalities
- wealth distributions
- 'popularity' (books, music, websites, ideas)

Size distributions

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As we know, heavy-tailed size distributions are somewhat prevalent in complex systems:

- 🎲 earthquakes (Gutenberg-Richter law)
- 🎲 city sizes, forest fires, war fatalities
- 🎲 wealth distributions
- 🎲 'popularity' (books, music, websites, ideas)
- 🎲 Epidemics?

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As we know, heavy-tailed size distributions are somewhat prevalent in complex systems:

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Power law distributions are common but not obligatory…

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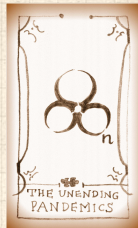models
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References

As we know, heavy-tailed size distributions are somewhat prevalent in complex systems:

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Power law distributions are common but not obligatory...

Really, what about epidemics?

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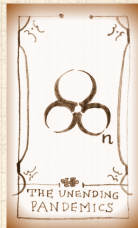Nutshell
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As we know, heavy-tailed size distributions are somewhat prevalent in complex systems:
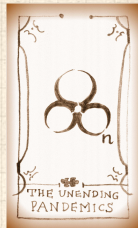
- earthquakes (Gutenberg-Richter law)
- city sizes, forest fires, war fatalities
- wealth distributions
- 'popularity' (books, music, websites, ideas)
- Epidemics?

Power law distributions are common but not obligatory...

Really, what about epidemics?

- Simply hasn't attracted much attention.

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As we know, heavy-tailed size distributions are somewhat prevalent in complex systems:

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- 🎲 wealth distributions
- 🎲 'popularity' (books, music, websites, ideas)
- 🎲 Epidemics?

Power law distributions are common but not obligatory...

Really, what about epidemics?

- 🎲 Simply hasn't attracted much attention.
- 🎲 Data not as clean as for other phenomena.

Feeling Ill in Iceland 🔗

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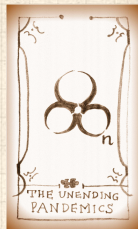
Caseload recorded monthly for range of diseases in
Iceland, 1888-1990

Iceland: measles
normalized count
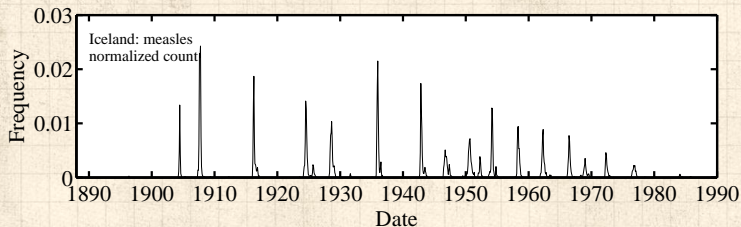
Treat outbreaks separated in time as 'novel'
diseases.
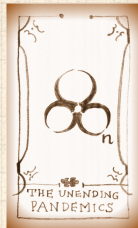
Really not so good at all in Iceland

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

Spike near $S = 0$, relatively flat otherwise.

Measles & Pertussis

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Measles & Pertussis

Insert plots:

Complementary cumulative frequency distributions:

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

Limited scaling with a possible break.

Power law distributions

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Measured values of γ:
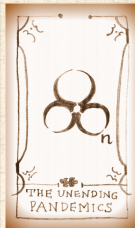
Power law distributions

Measured values of γ:

🎲 measles: 1.40 (low Ψ) and 1.13 (high Ψ)

Power law distributions

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Measured values of γ:

- measles: 1.40 (low Ψ) and 1.13 (high Ψ)
- pertussis: 1.39 (low Ψ) and 1.16 (high Ψ)

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Measured values of γ:

🎲 measles: 1.40 (low Ψ) and 1.13 (high Ψ)

🎲 pertussis: 1.39 (low Ψ) and 1.16 (high Ψ)

🎲 Expect $2 \leq \gamma < 3$ (finite mean, infinite variance)

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Measured values of γ:

- measles: 1.40 (low Ψ) and 1.13 (high Ψ)
- pertussis: 1.39 (low Ψ) and 1.16 (high Ψ)

- Expect $2 \le \gamma < 3$ (finite mean, infinite variance)
- When $\gamma < 1$, can't normalize

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Measured values of γ:

- measles: 1.40 (low Ψ) and 1.13 (high Ψ)
- pertussis: 1.39 (low Ψ) and 1.16 (high Ψ)

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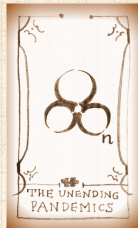
Resurgence—example of SARS
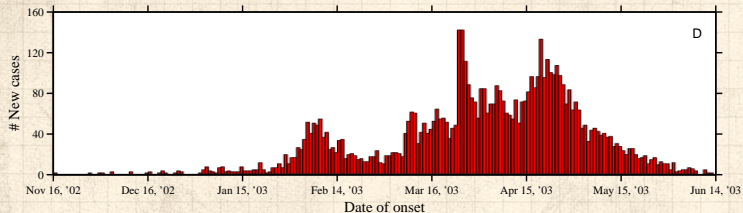
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Resurgence—example of SARS

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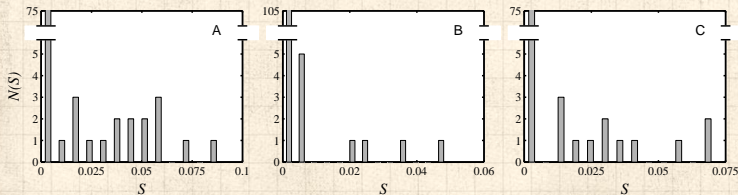More models
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Epidemic slows…

Resurgence—example of SARS

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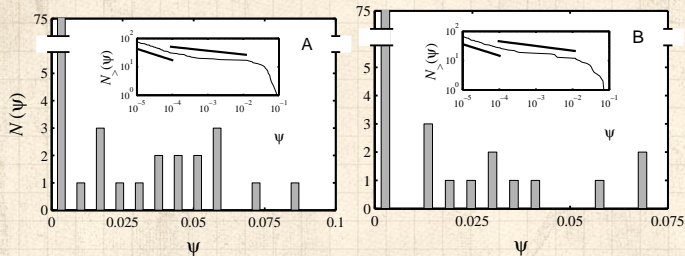Other kinds of prediction
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Epidemic slows...
then an infective moves to a new context.

Resurgence—example of SARS

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- Epidemic slows...
  then an infective moves to a new context.
- Epidemic discovers new 'pools' of susceptibles:
  Resurgence.

Resurgence—example of SARS

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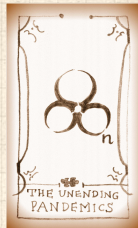Background
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- Epidemic slows...
  then an infective moves to a new context.
- Epidemic discovers new 'pools' of susceptibles:
  Resurgence.
- Importance of rare, stochastic events.

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Community—S2E6: Epidemiology

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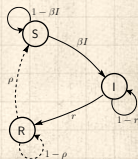
The challenge

So... can a simple model produce

1. broad epidemic distributions
   and
2. resurgence ?

Size distributions

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Simple models
typically produce
bimodal or unimodal
size distributions.

Size distributions
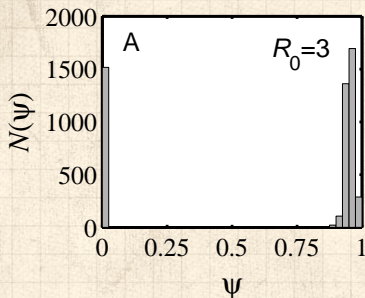
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Simple models
typically produce
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This includes network models:
random, small-world, scale-free, ...

Size distributions
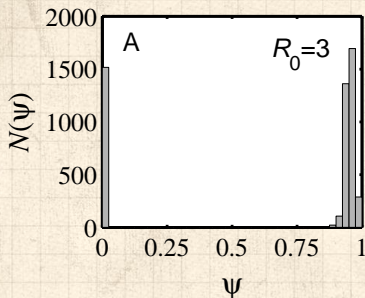
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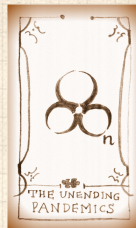Model output
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Simple models
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bimodal or unimodal
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🧩 This includes network models:
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🧩 Exceptions:

Size distributions
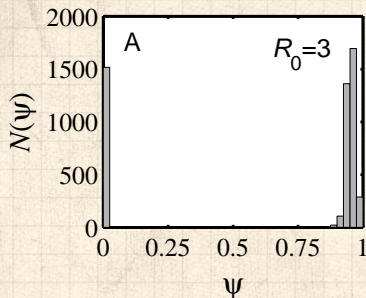
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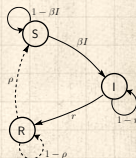
Simple models
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🧩 This includes network models:
random, small-world, scale-free, ...
🧩 Exceptions:
1. Forest fire models

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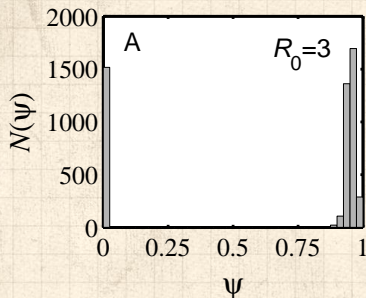
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Simple models
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♣ This includes network models:
random, small-world, scale-free, ...
♣ Exceptions:
1. Forest fire models
2. Sophisticated metapopulation models
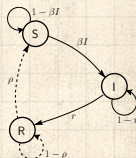
Burning through the population

Forest fire models: [19]

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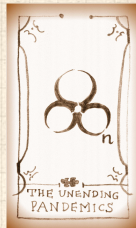Background
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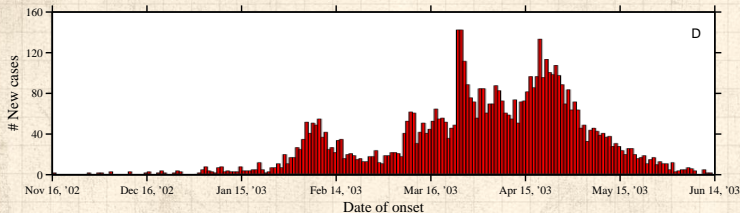models
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Forest fire models: [19]

🎲 Rhodes & Anderson, 1996

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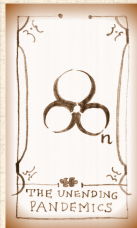Background
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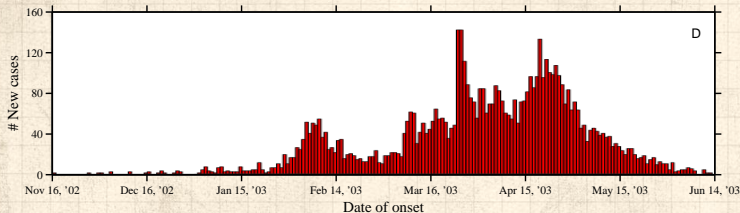models
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Forest fire models: [19]

- Rhodes & Anderson, 1996
- The physicist's approach:
  "if it works for magnets, it'll work for people..."

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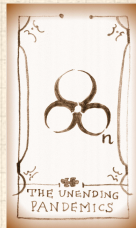Background
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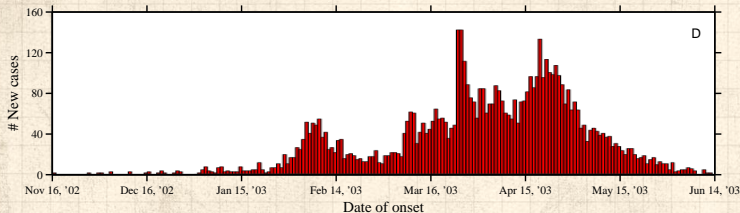Nutshell
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A bit of a stretch:

Burning through the population

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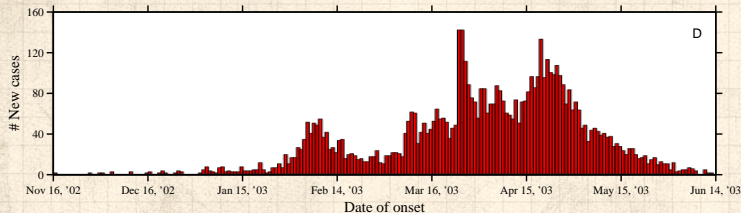models
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Forest fire models: [19]

⬡ Rhodes & Anderson, 1996

⬡ The physicist's approach:
"if it works for magnets, it'll work for people..."

A bit of a stretch:

1. Epidemics ≡ forest fires
   spreading on 3-d and 5-d lattices.

Burning through the population

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Forest fire models: [19]

♣ Rhodes & Anderson, 1996
♣ The physicist's approach:
   "if it works for magnets, it'll work for people..."

A bit of a stretch:

1. Epidemics ≡ forest fires
   spreading on 3-d and 5-d lattices.
2. Claim Iceland and Faroe Islands exhibit power law
   distributions for outbreaks.

Burning through the population

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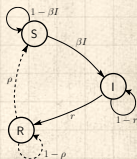models
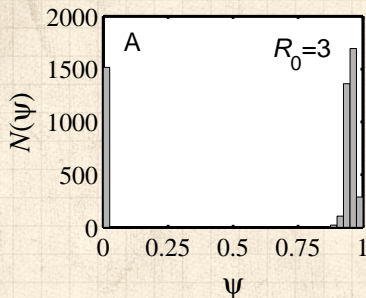Model output
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Forest fire models: [19]

- 🎲 Rhodes & Anderson, 1996
- 🎲 The physicist's approach:
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A bit of a stretch:

1. Epidemics ≡ 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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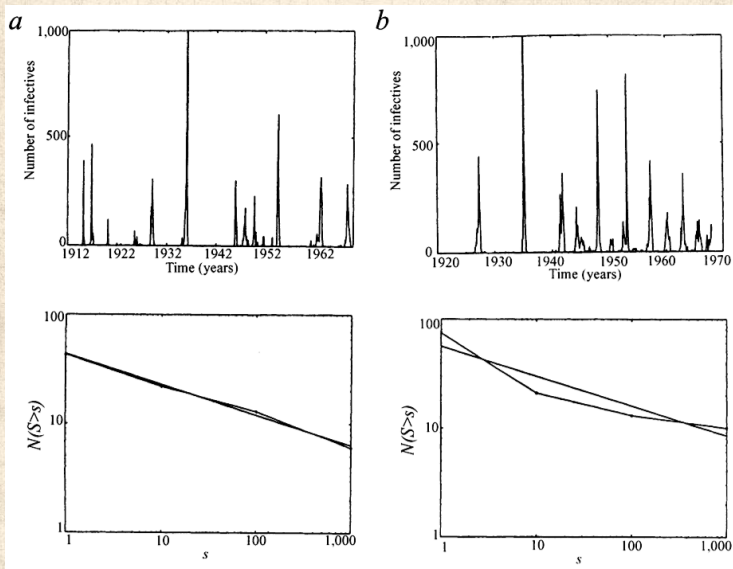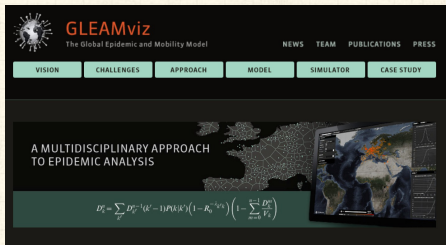
From Rhodes and Anderson, 1996.

Sophisticated metapopulation models:

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- Multiscale models suggested earlier by others but not formalized (Bailey [1], Cliff and Haggett [6], Ferguson et al.)

- Community based mixing (two scales)—Longini. [17]

- Eubank et al.'s EpiSims/TRANSIMS—city simulations. [9]

- Spreading through countries—Airlines: Germann et al., Colizza et al. [7]
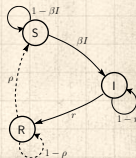
- GLEAM: Global pandemic simulations by Vespignani et al.

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"The hidden geometry of complex,
network-driven contagion phenomena" ☐
Brockmann and Helbing,
Science, **342**, 1337–1342, 2013. [5]

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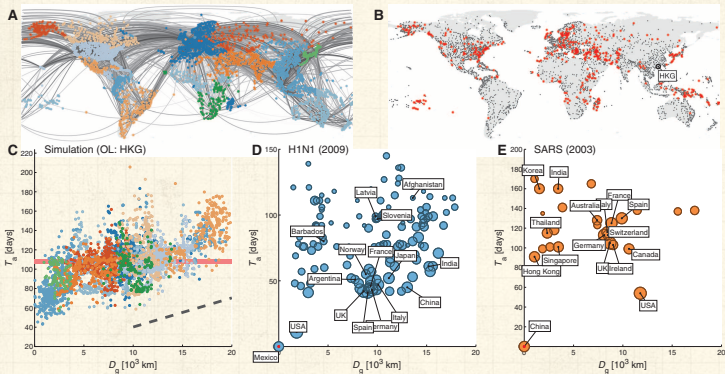
Fig. 1. Complexity in global, network-driven contagion phenomena. (A) The global mobility network (GMN). Gray lines represent passenger flows along direct connections between 4069 airports worldwide. Geographic regions are distinguished by color [classified according to network modularity maximization (39)]. **(B)** Temporal snapshot of a simulated global pandemic with initial outbreak location (OL) in Hong Kong (HKG). The simulation is based on the metapopulation model defined by Eq. 3 with parameters $R_0 = 1.5$, $\beta = 0.285$ day^{-1}, $\gamma = 2.8 \times 10^{-3}$ day^{-1}, $\varepsilon = 10^{-4}$. Red symbols depict locations with epidemic arrival times in the time window 105 days $\leq T_a \leq 110$ days. Because of the multiscale structure of the underlying network, the spatial distribution of disease prevalence (i.e., the fraction of infected individuals) lacks geometric coherence. No clear wavefront is visible, and based on this dynamic state, the OL cannot be easily deduced. **(C)** For the same simulation as in (B), the panel depicts arrival times T_a as a function of geographic distance D_g from the OL [nodes are colored according to geographic region as in (A)] for each of the 4069 nodes in the network. On a global scale, T_a weakly correlates with geographic distance D_g ($R^2 = 0.34$). A linear fit yields an average global spreading speed of $v_g = 331$ km/day (see also fig. S7). Using D_g and v_g to estimate arrival times for specific locations, however, does not work well owing to the strong variability of the arrival times for a given geographic distance. The red horizontal bar corresponds to the arrival time window shown in (B). **(D)** Arrival times versus geographic distance from the source (Mexico) for the 2009 H1N1 pandemic. Symbols represent 140 affected countries, and symbol size quantifies total traffic per country. Arrival times are defined as the date of the first confirmed case in a given country after the initial outbreak on 17 March 2009. As in the simulated scenario, arrival time and geographic distance are only weakly correlated ($R^2 = 0.0394$). **(E)** In analogy to (D), the panel depicts the arrival times versus geographic distance from the source (China) of the 2003 SARS pandemic for 29 affected countries worldwide. Arrival times are taken from WHO published data (2). As in (C) and (D), arrival time correlates weakly with geographic distance.

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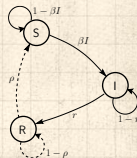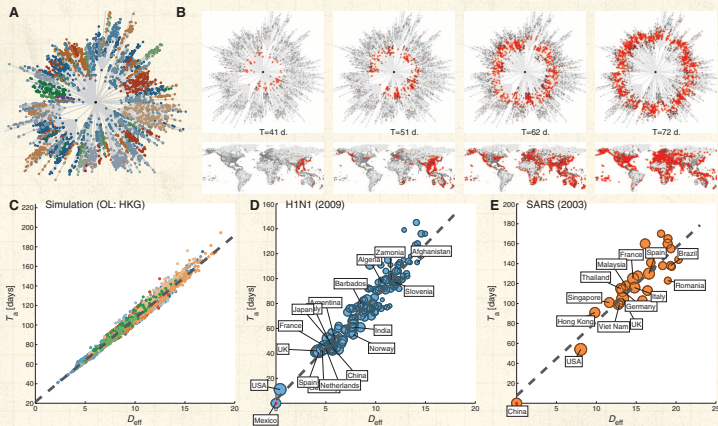
Fig. 2. Understanding global contagion phenomena using effective distance. (A) The structure of the shortest path tree (in gray) from Hong Kong (central node). Radial distance represents effective distance D_{eff} as defined by Eqs. 4 and 5. Nodes are colored according to the same scheme as in Fig. 1A. **(B)** The sequence (from left to right) of panels depicts the time course of a simulated model disease with initial outbreak in Hong Kong (HKG), for the same parameter set as used in Fig. 1B. Prevalence is reflected by the redness of the symbols. Each panel compares the state of the system in the conventional geographic representation (bottom) with the effective distance representation (top). The complex spatial pattern in the conventional view is equivalent to the homogeneous wave that propagates outwards at constant effective speed in the effective distance representation. **(C)** Epidemic arrival time T_a versus effective distance D_{eff} for the same simulated epidemic as in (B). In contrast to geographic distance (Fig. 1C), effective distance correlates strongly with arrival time ($R^2 = 0.973$), i.e., effective distance is an excellent predictor of arrival times. **(D and E)** Linear relationship between effective distance and arrival time for the 2009 H1N1 pandemic (D) and the 2003 SARS epidemic (E). The arrival time data are the same as in Fig. 1, D and E. The effective distance was computed from the projected global mobility network between countries. As in the model system, we observe a strong correlation between arrival time and effective distance.

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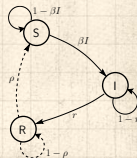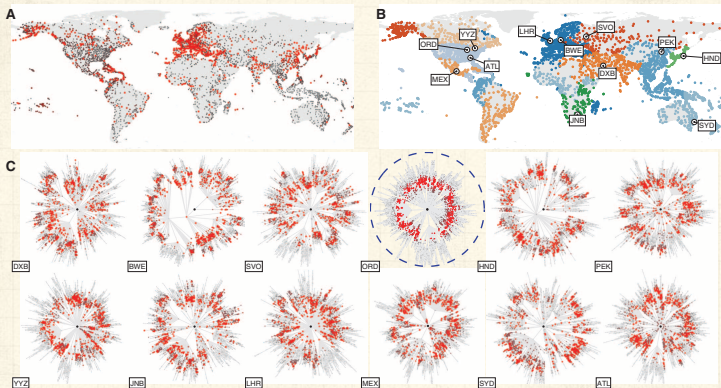
Fig. 3. Qualitative outbreak reconstruction based on effective distance. (**A**) Spatial distribution of prevalence $j_n(t)$ at time $T = 81$ days for OL Chicago (parameters $\beta = 0.28$ day^{-1}, $R_0 = 1.9$, $\gamma = 2.8 \times 10^{-3}$ day^{-1}, and $\varepsilon = 10^{-6}$). After this time, it is difficult, if not impossible, to determine the correct OL from snapshots of the dynamics. (**B**) Candidate OLs chosen from different geographic regions. (**C**) Panels depict the state of the system shown in (A) from the perspective of each candidate OL, using each OL's shortest path tree representation. Only the actual OL (ORD, circled in blue) produces a circular wavefront. Even for comparable North American airports [Atlanta (ATL), Toronto (YYZ), and Mexico City (MEX)], the wavefronts are not nearly as concentric. Effective distances thus permit the extraction of the correct OL, based on information on the mobility network and a single snapshot of the dynamics.
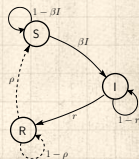
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🎲 Vital work but perhaps hard to generalize from...

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📦 Vital work but perhaps hard to generalize from...

📦 $\Rightarrow$ Create a simple model involving multiscale
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- ⬢ Vital work but perhaps hard to generalize from...
- ⬢ ⇒ Create a simple model involving multiscale travel
- ⬢ Very big question: What is N?

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- Vital work but perhaps hard to generalize from...
- $\Rightarrow$ Create a simple model involving multiscale travel
- Very big question: What is N?
- Should we model SARS in Hong Kong as spreading in a neighborhood, in Hong Kong, Asia, or the world?

Size distributions

- ⚅ Vital work but perhaps hard to generalize from...
- ⚅ ⇒ Create a simple model involving multiscale travel
- ⚅ Very big question: What is N?
- ⚅ Should we model SARS in Hong Kong as spreading in a neighborhood, in Hong Kong, Asia, or the world?
- ⚅ For simple models, we need to know the final size beforehand...
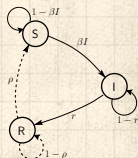
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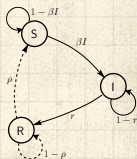Prediction
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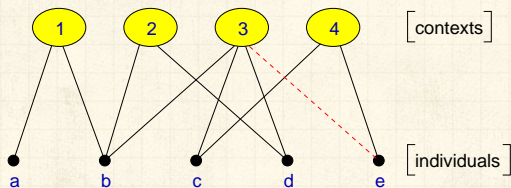
🎲 boards of directors

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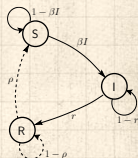Nutshell
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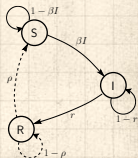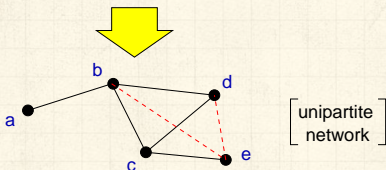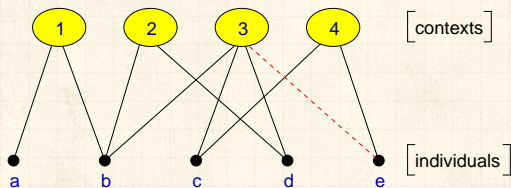
boards of directors

movies

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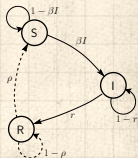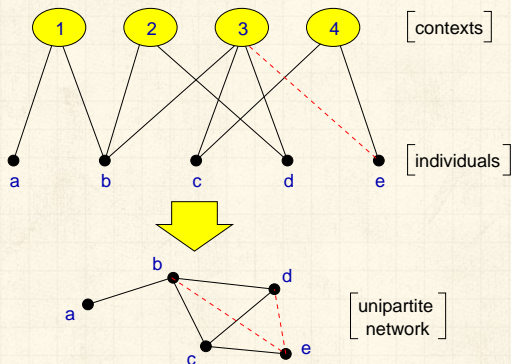
🎲 boards of directors

🎲 movies

🎲 transportation modes (subway)
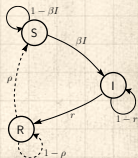
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Idea for social networks: incorporate identity

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Identity is formed from attributes such as:

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Identity is formed from attributes such as:

🔶 Geographic location

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Idea for social networks: incorporate identity

Identity is formed from attributes such as:

🔩 Geographic location

🔩 Type of employment

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Identity is formed from attributes such as:

- 🎲 Geographic location
- 🎲 Type of employment
- 🎲 Age

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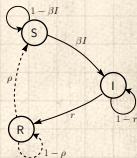spreading models
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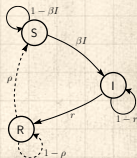models
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Idea for social networks: incorporate identity

Identity is formed from attributes such as:

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

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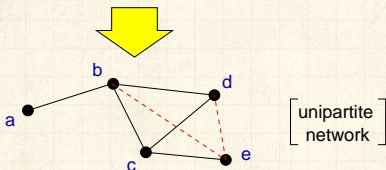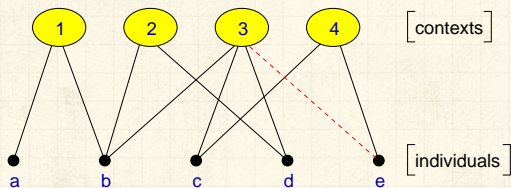models
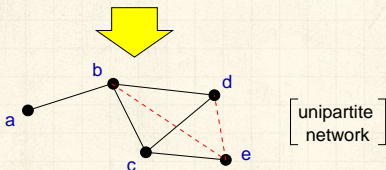Model output
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Identity is formed from attributes such as:

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

Groups are crucial...

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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

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Identity is formed from attributes such as:

- Geographic location
- Type of employment
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- Recreational activities

Groups are crucial...

- formed by people with at least one similar attribute
- Attributes ⇔ Contexts ⇔ Interactions ⇔ Networks. [23]
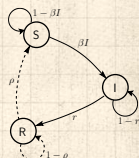
Infer interactions/network from identities

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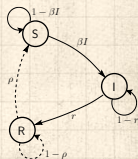Model output
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Distance makes sense in identity/context space.

Generalized context space

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geography   occupation   age

0   100

a   b   c   d   e
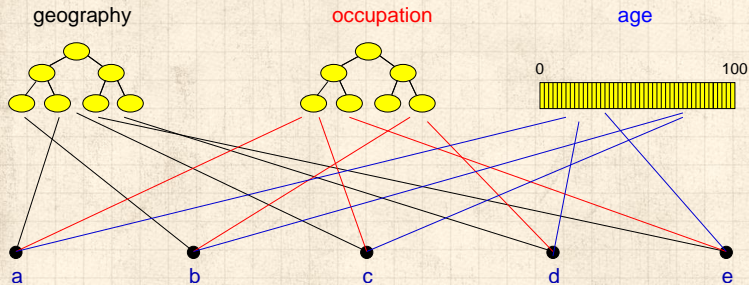
(Blau & Schwartz [3], Simmel [20], Breiger [4])

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Watts et al.,
Proc. Natl. Acad. Sci., **102**, 11157–11162,
2005. [24]

Geography: allow people to move between contexts

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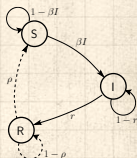models
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🎲 Locally: standard SIR model with random mixing

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Geography: allow people to move between contexts

- 🧱 Locally: standard SIR model with random mixing
- 🧱 discrete time simulation

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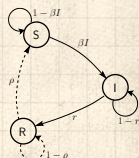spreading models
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Geography: allow people to move between contexts

- Locally: standard SIR model with random mixing
- discrete time simulation
- β = infection probability

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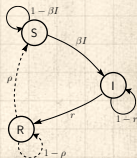spreading models
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Geography: allow people to move between contexts

🧊 Locally: standard SIR model with random mixing

🧊 discrete time simulation

🧊 β = infection probability

🧊 γ = recovery probability

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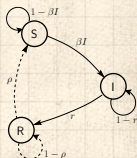
"Multiscale, resurgent epidemics in a
hierarchcial metapopulation model" ☐
Watts et al.,
Proc. Natl. Acad. Sci., **102**, 11157–11162,
2005. [24]

Geography: allow people to move between
contexts

- 🧱 Locally: standard SIR model with random mixing
- 🧱 discrete time simulation
- 🧱 β = infection probability
- 🧱 γ = recovery probability
- 🧱 P = probability of travel

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Geography: allow people to move between contexts

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

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Geography: allow people to move between contexts

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

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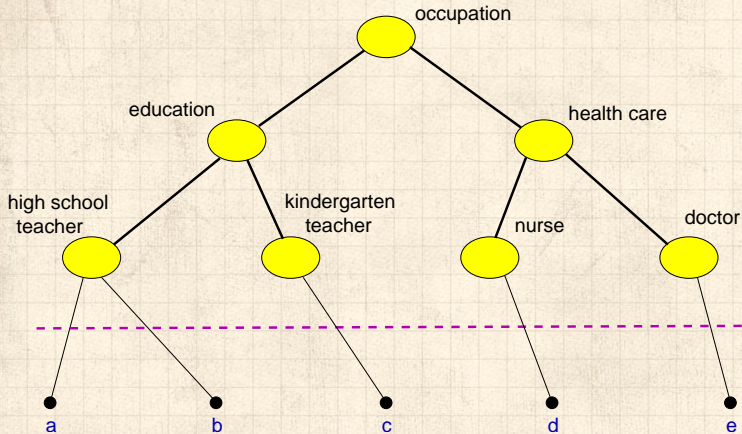More models
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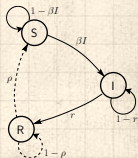Toy metapopulation
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Define P_0 = Expected number of infected individuals leaving initially infected context.

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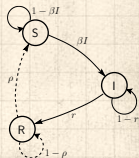Nutshell
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- Define P_0 = Expected number of infected individuals leaving initially infected context.
- Need $P_0 > 1$ for disease to spread (independent of R_0).

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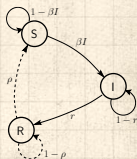Background
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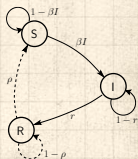
- Define P_0 = Expected number of infected individuals leaving initially infected context.
- Need $P_0 > 1$ for disease to spread (independent of R_0).
- Limit epidemic size by restricting frequency of travel and/or range
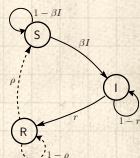
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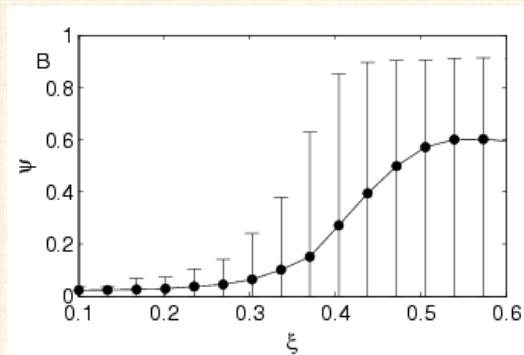
Varying ξ:

🎲 Transition in expected final size based on typical
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Varying ξ:

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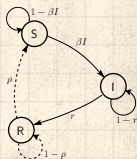Background
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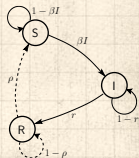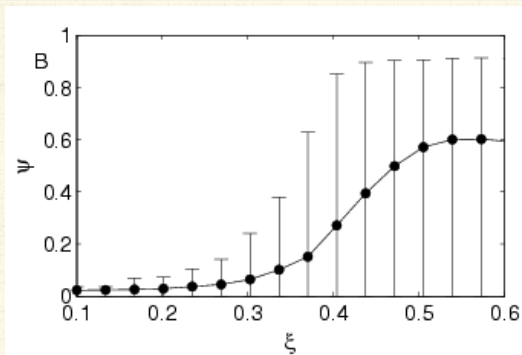
Transition in expected final size based on typical movement distance (sensible)

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🎲 Transition in expected final size based on typical
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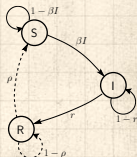Background
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Transition in expected final size based on typical number of infectives leaving first group (also sensible)

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

Example model output: size distributions

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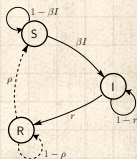Background
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Example model output: size distributions

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Flat distributions are possible for certain ξ and P.

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Two histograms showing $N(\psi)$ versus ψ. Left panel labeled $R_0 = 3$ with y-axis values 0, 100, 200, 300, 400, 1942 and x-axis 0, 0.25, 0.5, 0.75, 1. Right panel labeled $R_0 = 12$ with y-axis values 0, 100, 200, 300, 400, 683 and x-axis 0, 0.25, 0.5, 0.75, 1.

- Flat distributions are possible for certain ξ and P.
- Different R_0's may produce similar distributions

Example model output: size distributions
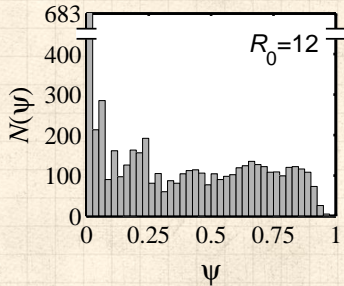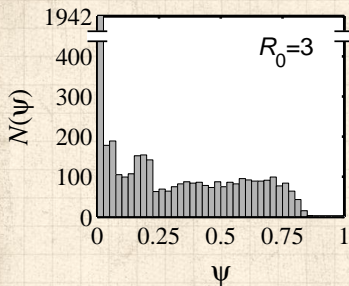
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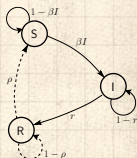Background
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- Flat distributions are possible for certain ξ and P.
- Different R_0's may produce similar distributions
- Same epidemic sizes may arise from different R_0's
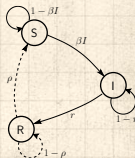
Model output—resurgence

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Standard model with transport:

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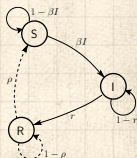Background
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Simple multiscale population structure

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Simple multiscale population structure
+
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The upshot

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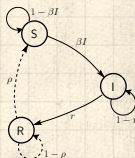Model output
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⟡ For the hierarchical movement model, epidemic size is highly unpredictable

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- For the hierarchical movement model, epidemic size is highly unpredictable
- Model is more complicated than SIR but still simple.

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- For the hierarchical movement 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.

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- For the hierarchical movement 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 terribly useful.

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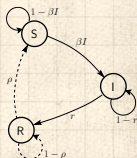Background
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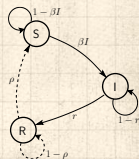models
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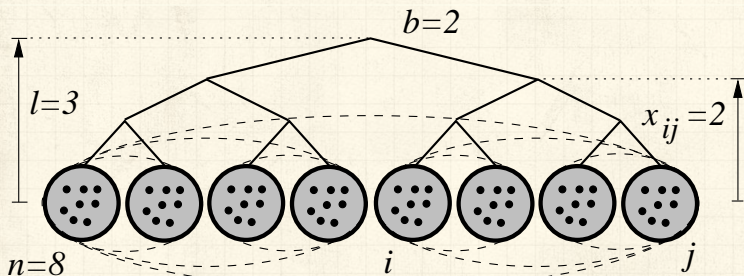
References

Nutshelling

- For the hierarchical movement 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 terribly useful.

- R_0, however measured, is not informative about

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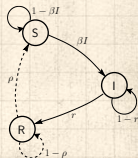Background
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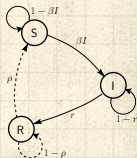Other kinds of prediction
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- For the hierarchical movement model, epidemic size is highly unpredictable
- Model is more complicated than SIR but still simple.
- We haven't even included normal social responses such as travel bans and self-quarantine.
- The reproduction number R_0 is not terribly useful.
- R_0, however measured, is not informative about
  1. how likely the observed epidemic size was,

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🧱 For the hierarchical movement 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 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.

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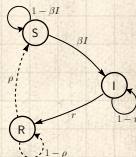Background
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- For the hierarchical movement model, epidemic size is highly unpredictable

- 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 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.
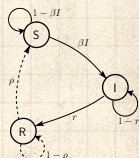
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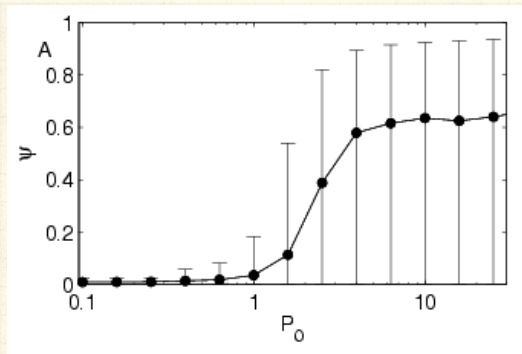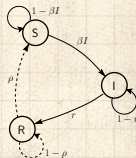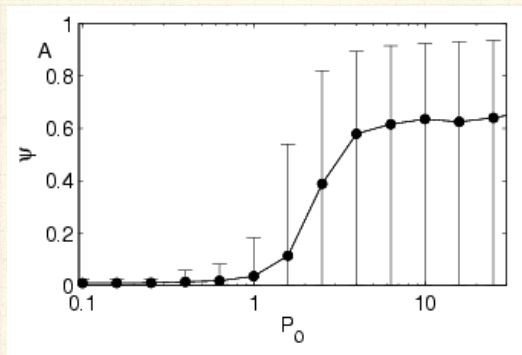Nutshell
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🎲 Disease's spread is highly sensitive to population structure.

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🎲 Disease's spread is highly sensitive to population structure.

🎲 Rare events may matter enormously:

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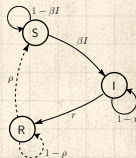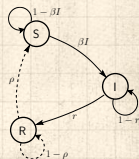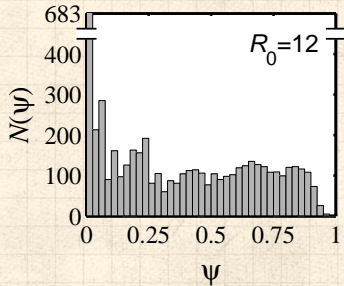Background
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🦠 Disease's spread is highly sensitive to population structure.

🦠 Rare events may matter enormously: e.g., an infected individual taking an international flight.

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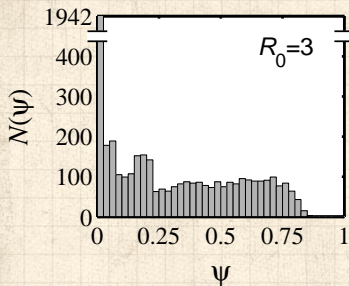Toy metapopulation
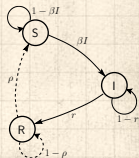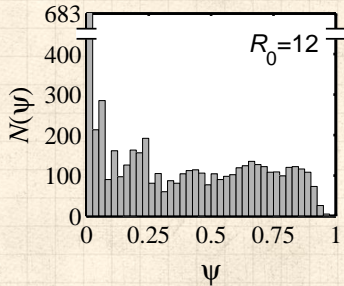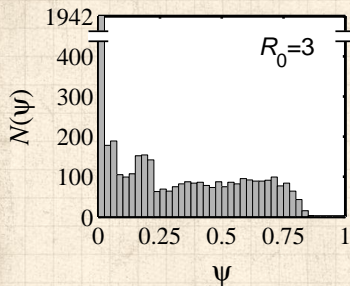models
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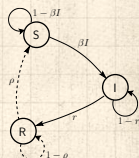
- Disease's spread is highly sensitive to population structure.
- Rare events may matter enormously: e.g., an infected individual taking an international flight.
- More support for controlling population movement:

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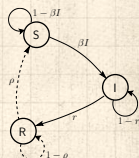
🎲 Disease's spread is highly sensitive to population structure.

🎲 Rare events may matter enormously: e.g., an infected individual taking an international flight.

🎲 More support for controlling population movement:
e.g., travel advisories, quarantine

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What to do:

🎲 Need to separate movement from disease

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What to do:

- ♻ Need to separate movement from disease
- ♻ R_0 needs a friend or two.

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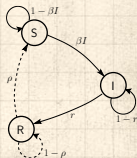More models
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What to do:

♻ Need to separate movement from disease

♻ R_0 needs a friend or two.

♻ Need $R_0 > 1$ and $P_0 > 1$ and ξ sufficiently large for disease to have a chance of spreading

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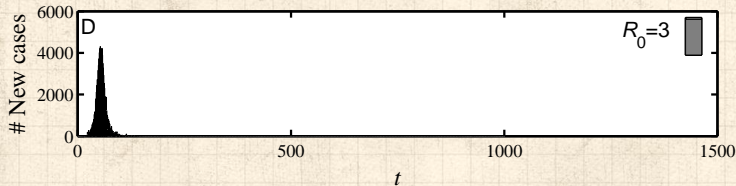Toy metapopulation
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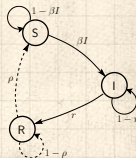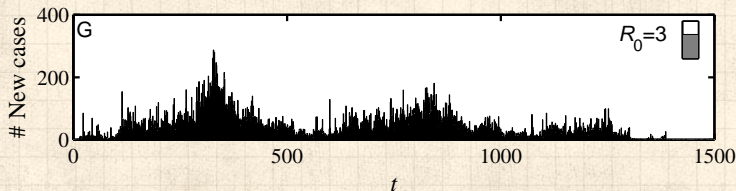Model output
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What to do:

- Need to separate movement from disease
- R_0 needs a friend or two.
- Need $R_0 > 1$ and $P_0 > 1$ and ξ sufficiently large for disease to have a chance of spreading
- And in general: keep building up the kitchen sink models.

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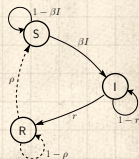More models
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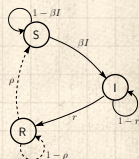
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What to do:

- ♟ Need to separate movement from disease
- ♟ R_0 needs a friend or two.
- ♟ Need $R_0 > 1$ and $P_0 > 1$ and ξ sufficiently large for disease to have a chance of spreading
- ♟ And in general: keep building up the kitchen sink models.

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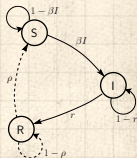Background
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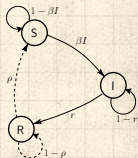Model output
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What to do:

- Need to separate movement from disease
- R_0 needs a friend or two.
- Need $R_0 > 1$ and $P_0 > 1$ and ξ sufficiently large for disease to have a chance of spreading
- And in general: keep building up the kitchen sink models.

More wondering:

- Exactly how important are rare events in disease spreading?

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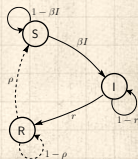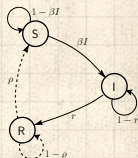Background
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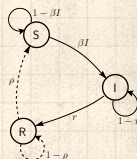
What to do:

- ♟ Need to separate movement from disease
- ♟ R_0 needs a friend or two.
- ♟ Need $R_0 > 1$ and $P_0 > 1$ and ξ sufficiently large for disease to have a chance of spreading
- ♟ And in general: keep building up the kitchen sink models.

More wondering:

- ♟ Exactly how important are rare events in disease spreading?
- ♟ Again, what is N?
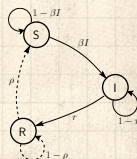
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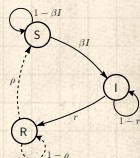models
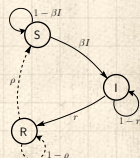Model output
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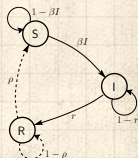Model output
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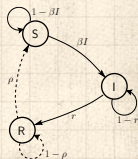Background
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[1] http://www.redherring.com/mag/issue55/economics.html

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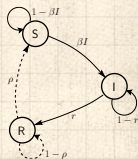Background
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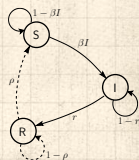Model output
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Greenspan continues:

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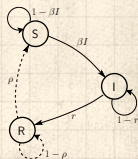Background
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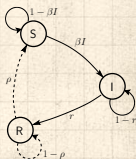models
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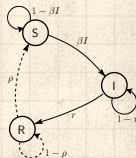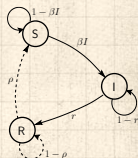models
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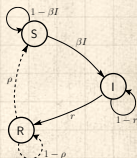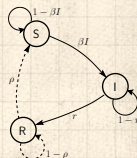Model output
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Jon Stewart:

"You just bummed the @*!# out of me."

wildbluffmedia.com
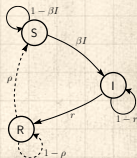
🎲 From the Daily Show ☐ (September 18, 2007)
🎲 The full episode is here:
http://www.cc.com/video-clips/cenrt5/the-daily-show-with-jon-st

Predicting social catastrophe isn't easy...

"Greenspan Concedes Error on Regulation"

New York Times, October 23, 2008 ⌧

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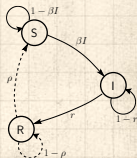Background
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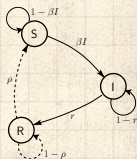Background
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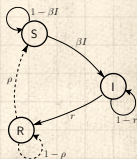Model output
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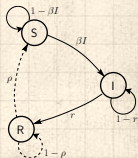Other kinds of prediction
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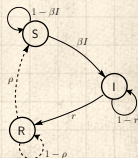Background
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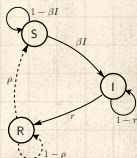Background
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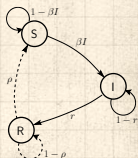Model output
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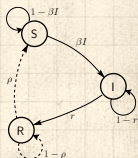Background
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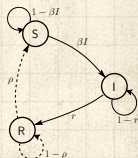Background
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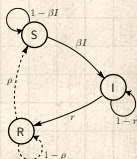
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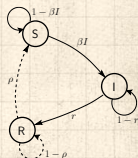Background
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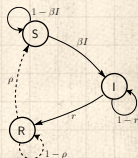models
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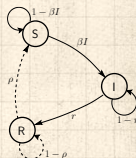Other kinds of prediction
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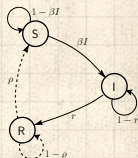Background
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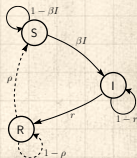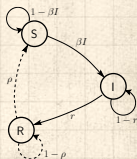More models
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Social contagion:

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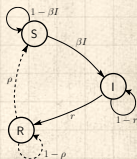Model output
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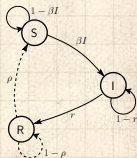
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Social contagion:

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- But we need new fundamental models.

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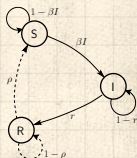
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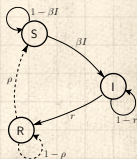🎲 Spread of Feynmann diagrams (Bettencourt et al., 2006)
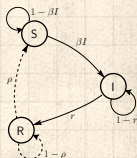
Social contagion:

🎲 SIR may apply sometimes ...

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🎲 Next up: Thresholds.

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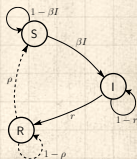
We really should know social contagion is different but …

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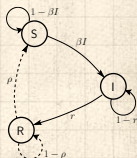
☐ "Facebook will lose 80% of users by 2017, say Princeton researchers" ☐ (Guardian, 2014)
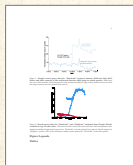
"Epidemiological modeling of online social network dynamics" ☐
Spechler and Cannarella,
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http://arxiv.org/abs/1401.4208, 2014. [21]

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The Facebook Data Science team's response🗗:
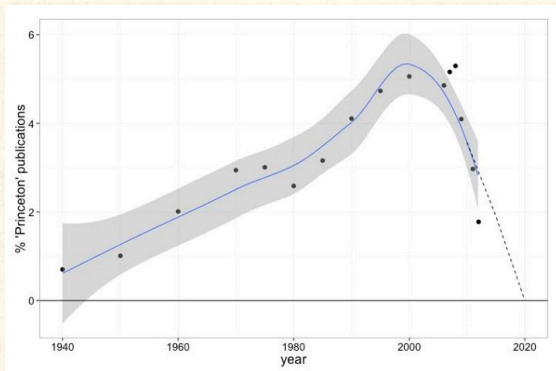
🎲 Mike Develin, Lada Adamic, and Sean Taylor.

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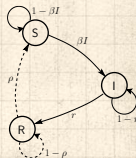
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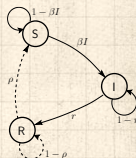
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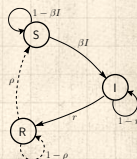
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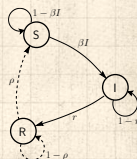
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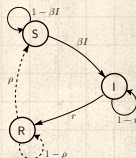endemicity.
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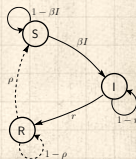More models
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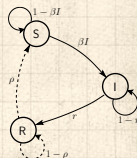
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