Biological Contagion

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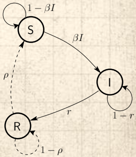
Principles of Complex Systems, Vols. 1, 2, & 3D
CSYS/MATH 6701, 6713, & a pretend number, 2024–2025

Prof. Peter Sheridan Dodds

Computational Story Lab | Vermont Complex Systems Center
Santa Fe Institute | University of Vermont



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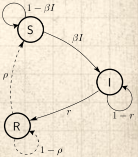

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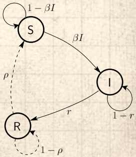
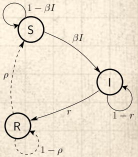


Outline




THE SUN
THE GOLDEN AGE OF REDUCTIONISM
THE MANIFESTO
WELL OF SCALES
THE LAWS OF DECAYING POWER
THE UNEXPECTED TRANSFIGURATION
MINISTRY OF RANDOM WALKS
THE RICH GET RICHER
THE DREAM OF EFFICIENT LANGUAGE
THE LAW OF DIGITS FIRST
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THE MISREADING OF THE BOOK OF SAND
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THE POURING DATA
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THE EMERGENCE OF DESTRUCTION
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THE TRUTHICIDE
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THE IMPROBABLE PACHYDERM
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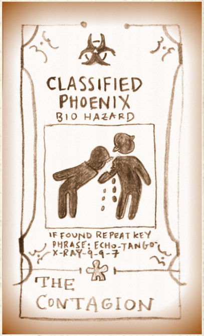
CLASSIFIED
PHOENIX
BIO HAZARD
IF FOUND REPEAT KEY PHRASE: ECHO-TANGO X-RAY-9-4-7
THE CONTAGION


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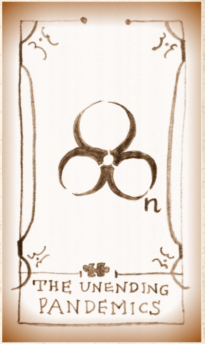
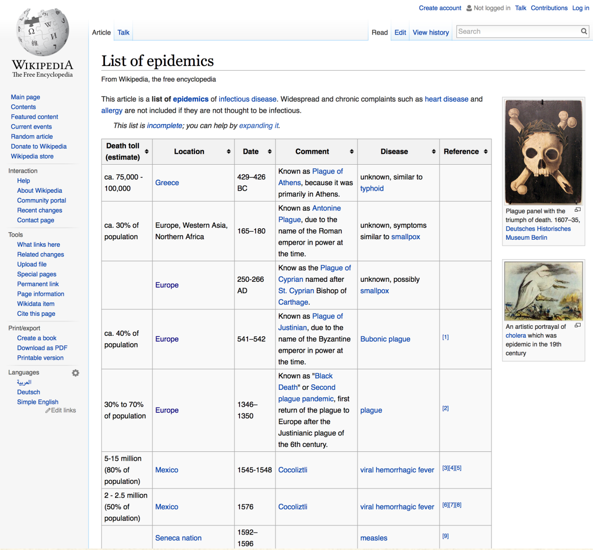

THE UNENDING PANDEMICS

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



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List of epidemics

From Wikipedia, the free encyclopedia

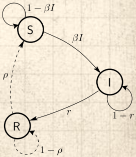
This article is a **list of epidemics** of infectious disease. Widespread and chronic complaints such as heart disease and allergy are not included if they are not thought to be infectious.

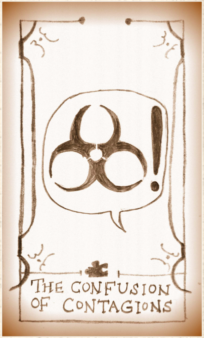
This list is incomplete; you can help by expanding it.

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	Know 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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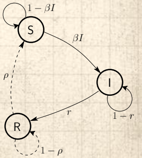
Contagion

A confusion of contagions:



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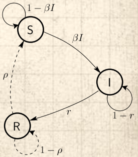

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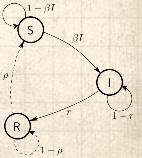

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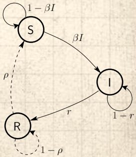

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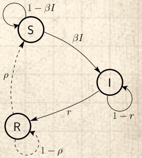

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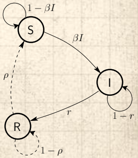

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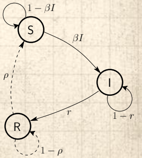

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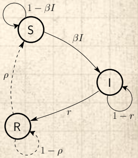

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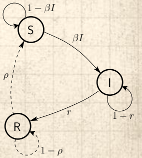

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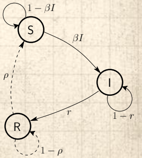

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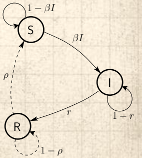

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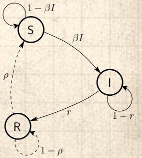

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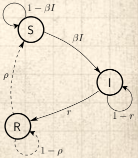

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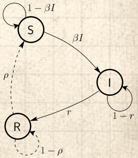

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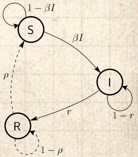
Optimism according to Ambrose Bierce:

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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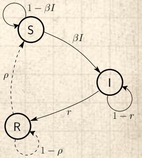

Social contagion

Eric Hoffer, 1902–1983

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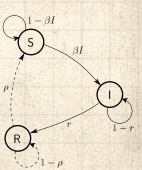

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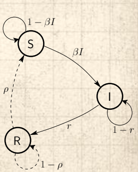

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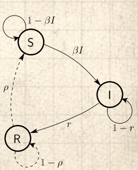

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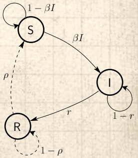

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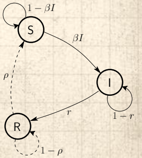

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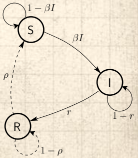

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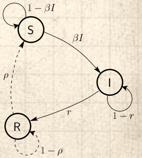

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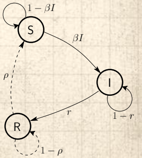

The spread of fanaticism

Hoffer's most famous work: "The True Believer: Thoughts On The Nature Of Mass Movements" (1951) [12]

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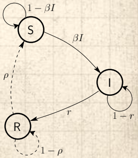

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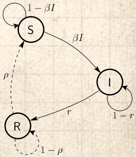

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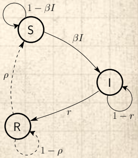

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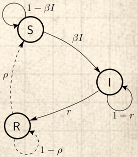
- "Where freedom is real, equality is the passion of the masses.

  "

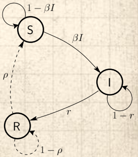


The spread of fanaticism

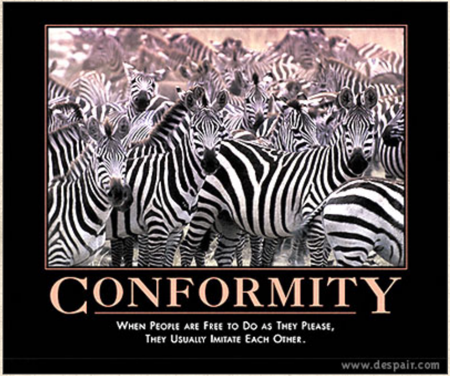
Hoffer's most famous work: "The True Believer:
Thoughts On The Nature Of Mass Movements" (1951) [12]

Aphorisms-aplenty:

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



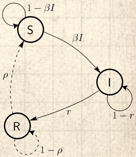
Imitation



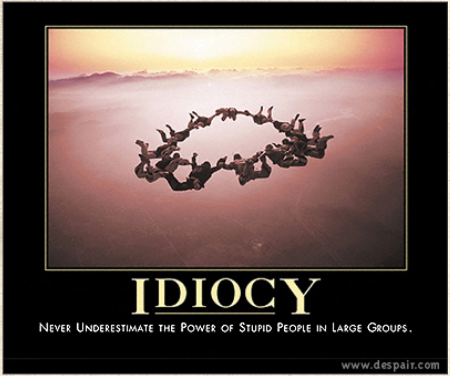
despair.com

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

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

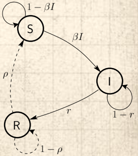


The collective...

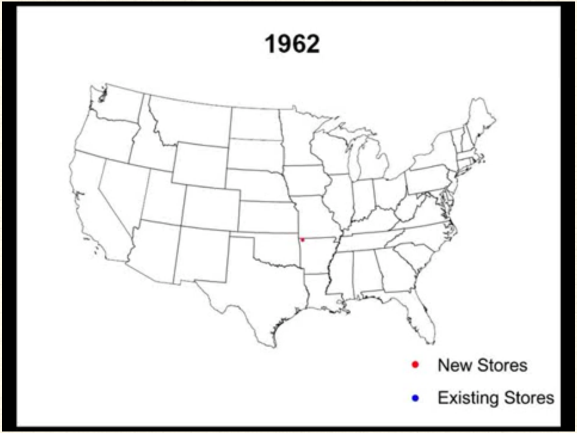


despair.com

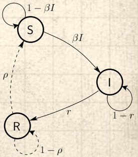
"Never Underestimate the Power of Stupid People in Large Groups."



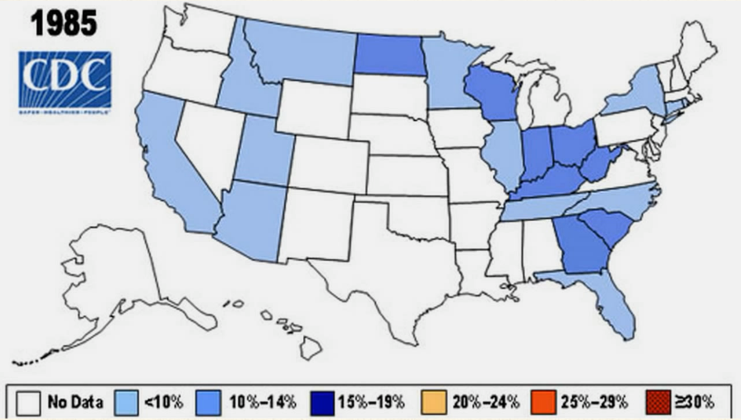
Examples of non-disease spreading:



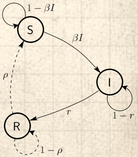
Spreading of certain buildings in the US.



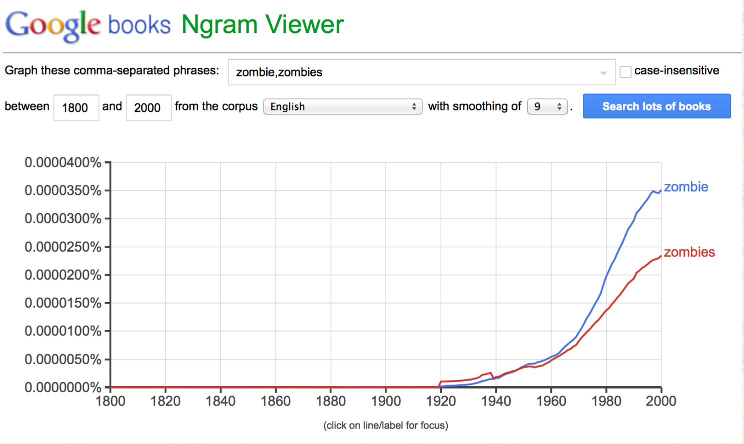
Marbleization of the US:

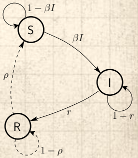


The spreading of spreading.

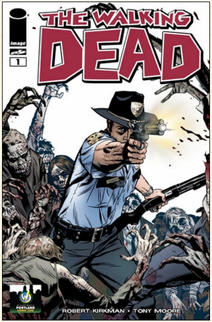


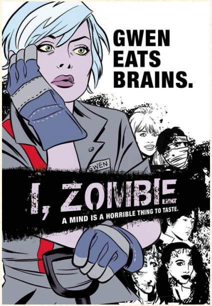
The most terrifying contagious outbreak?



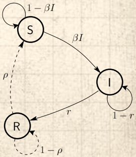



THE
WALKING DEAD


THE WALKING
DEAD
image
1
ROBERT KIRKMAN • TONY MOORE


GWEN
EATS
BRAINS.
GWEN
I, ZOMBIE
A MIND IS A HORRIBLE THING TO TASTE.


iZOMBiE


S
I
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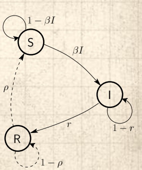
Contagion

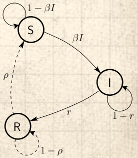
Definitions



Contagion

Definitions

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



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- (2) A disease itself:
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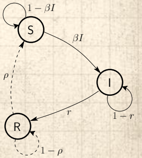

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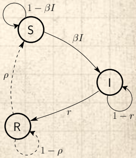

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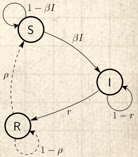
- Contagion has unpleasant overtones...



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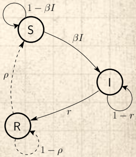

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- Contagion has unpleasant overtones...
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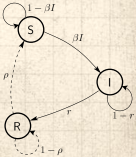
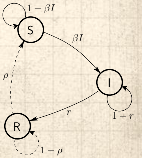
- But contagion is kind of exciting...

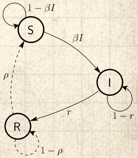


Contagions



Two main classes of contagion

Contagions



Two main classes of contagion

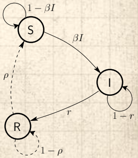
1. Infectious diseases

Contagions

Two main classes of contagion

1. Infectious diseases

2. Social contagion



Contagions

Two main classes of contagion

1. **Infectious diseases**:
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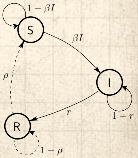
2. **Social contagion**

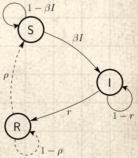


Contagions

Two main classes of contagion

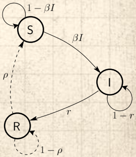
1. Infectious diseases:
   tuberculosis, HIV, ebola, SARS, influenza, zombification, ...

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



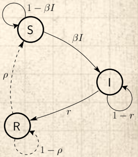
Archival footage from the Black Plague:

Bring out your dead.

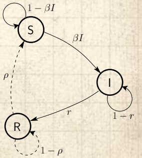


Community—S2E06: Epidemiology

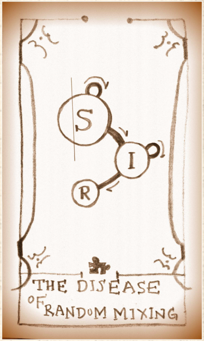
“I thought I was special”



Outline




THE SUN
THE GOLDEN AGE OF REDUCTIONISM
THE MANIFESTO
THE WELL OF SCALES
THE LAWS OF DECAYING POWER
THE UNEXPECTED TRANSFIGURATION
MINISTRY OF RANDOM WALKS
THE RICH GET RICHER
THE DREAM OF EFFICIENT LANGUAGE
THE LAW OF DIGITS FIRST
THE SURPRISE OF BEING ROBUST YET FRAGILE
THE MISREADING OF THE BOOK OF SAND
THE MANY TAILS OF MANY TAILS
THE MEASURING
THE DATA POOR
THE POURING DATA
THE CHARMS OF THE MANY WRONG PATHS
THE BOOKS THAT SHOULD NOT BE OPENED
THE KNOWLEDGE OF DEAD MONKS
THE EMERGENCE OF STRUCTURE
THE EMERGENCE OF DESTRUCTION
THE EMERGENCE OF THINKING
THE EMERGENCE OF STORIES
THE MECHANICS STATISTICAL
THE THRESHOLDS OF PERCOLATION
THE NETWORKS COMPLEX
THE ELEMENTS OF WEBS
THE BIRDS OF A FEATHER
THE BIRDS OF NOT A FEATHER
THE ARK OF THE RANDOM NETWORK
THE STRANGENESS OF FRIENDS
THE SMALLNESS OF WORLDS
THE THEORY OF SIX DEGREES
THE NETWORKS FREE OF SCALE
THE CONTAGION
THE CONFUSION OF CONTAGIONS
THE UNENDING PANDEMICS
THE THRESHOLDS OF THE MIND
THE SOCIAL WILD
THE SOCIAL CONTAGION
THE RATIO OF GAIN
THE MECHANICS OF FAME
THE TALK OF FAME
THE STORIES CONTAGIOUS
THE JOHN DORY
THE ADJACENT NARRATIVES
THE STORYTELLERS
THE FATED ASTRAL PATH
THE PATHS OF UNIVERSALITY
THE DEPENDENT PATHS
THE TROUSERS OF BIFURCATING REALITIES
THE UNKNOWN MECHANISM
THE LANDSCAPES OF FORKING PATHS
THE NETWORKS OF BLOOD
THE TREES OF REALITY
THE ORDERS OF STREAMS
THE LAWS OF BRANCHING
THE SCALING OF BROKEN HIERARCHIES
THE BRAID OR THE BRANCH
THE LAW OF OPTIMAL FORKS
THE CHURCH OF QUARTEROLOGY
THE TRUTHICIDE
THE FAMILY OF PANCAKE COWS
THE FAMILY OF SPHERICAL COWS
THE IMPROBABLE PACHYDERM
THE ILLSCALING OF ALLOMETRIC BODIES
THE SUPPLY MOST FAIR
THE SUPPLY TO THE MOST
THE DARK ART OF GENERATING FUNCTIONS
THE RANDOM SUM OF RANDOMNESS
THE TWO-SIDED WORLDS
THE STORIES AND THE TROPES
THE TRUTH OF DIFFUSION
THE UNVEILING OF HIDDEN POWERS
THE SCRYING FOR THE SHAPES OF THINGS
THE LIMITS OF ORGANIZATIONS


S
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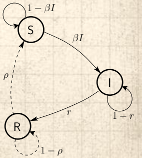
THE DISEASE OF RANDOM MIXING

Mathematical Epidemiology

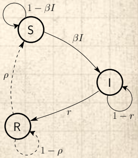
The standard SIR model [18]



Mathematical Epidemiology

The standard SIR model [18]

- = basic model of disease contagion



Mathematical Epidemiology

The standard SIR model [18]

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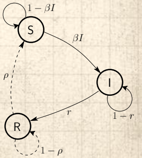
- Three states:



Mathematical Epidemiology

The standard SIR model [18]

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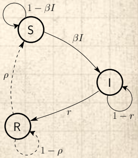
  1. S = Susceptible



Mathematical Epidemiology

The standard SIR model [18]

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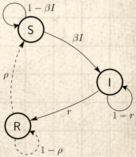
  2. I = Infective/Infectious



Mathematical Epidemiology

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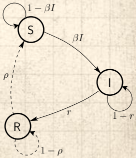
  2. I = Infective/Infectious
  3. R = Recovered



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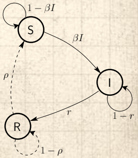
  2. I = Infective/Infectious
  3. R = Recovered or Removed or Refractory



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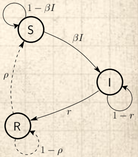
- $S(t) + I(t) + R(t) = 1$



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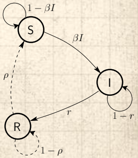

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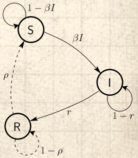

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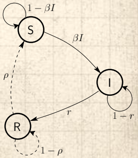
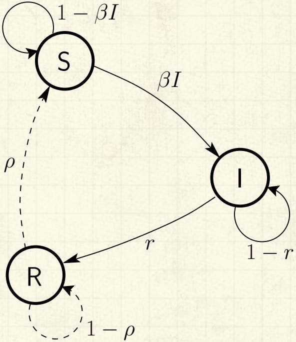
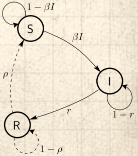
- Discrete and continuous time versions



Mathematical Epidemiology

Discrete time automata example:





Mathematical Epidemiology

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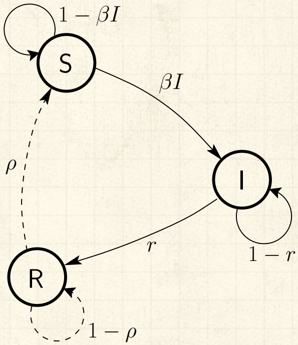
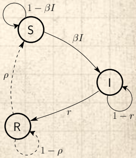


Transition Probabilities:



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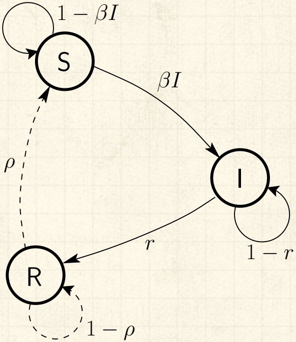
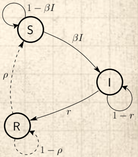


Transition Probabilities:

β for being infected given contact with infected



Mathematical Epidemiology

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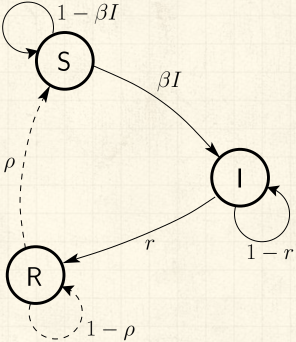

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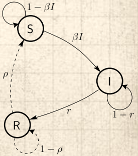
r for recovery



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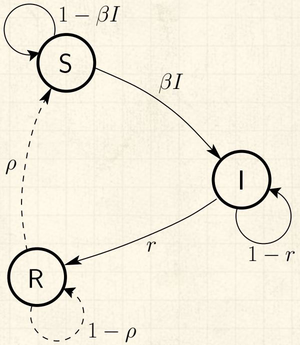

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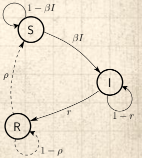
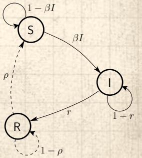
β for being infected given contact with infected
r for recovery
ρ for loss of immunity



Mathematical Epidemiology

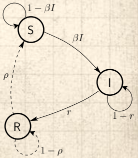
Original models attributed to



Mathematical Epidemiology

Original models attributed to

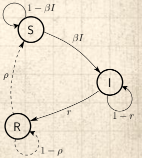
- 1920's: Reed and Frost



Mathematical Epidemiology

Original models attributed to

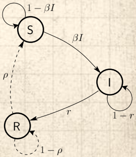
- 1920's: Reed and Frost
- 1920's/1930's: Kermack and McKendrick [14, 16, 15]



Mathematical Epidemiology

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

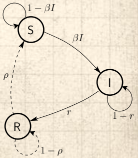
Differential equations for continuous model

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

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

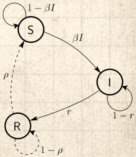
$$\frac{\mathrm{d}}{\mathrm{d}t}R = r I - \rho R$$

β, r, and ρ are now rates.



Reproduction Number R_0

Reproduction Number R_0



Reproduction Number R_0

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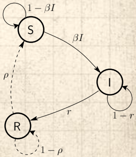
- R_0 = expected number of infected individuals resulting from a single initial infective



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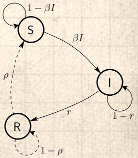
- Epidemic threshold: If $R_0 > 1$, 'epidemic' occurs.



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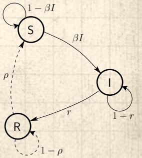

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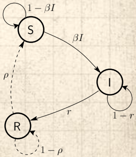
- Exponential take off: R_0^n where n is the number of generations.
- Fantastically awful notation convention: R_0 and the R in SIR.



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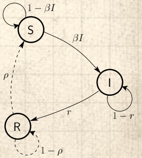
Discrete version:

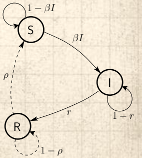
- Set up: One Infective in a randomly mixing population of Susceptibles



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



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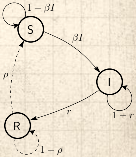
Discrete version:

- 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



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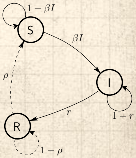
- At time $t = 1$, single Infective remains infected with probability $1 - r$



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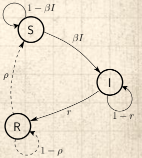
- Set up: One Infective in a randomly mixing population of Susceptibles
- At time $t = 0$, single infective random bumps into a Susceptible
- Probability of transmission = β
- At time $t = 1$, single Infective remains infected with probability $1 - r$
- At time $t = k$, single Infective remains infected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

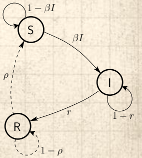


Reproduction Number R_0

Discrete version:

- Expected number infected by original infective:

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



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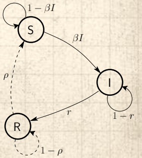
$$= \beta\left(1 + (1-r) + (1-r)^2 + (1-r)^3 + \ldots\right)$$



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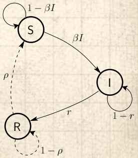
$$= \beta\left(1 + (1-r) + (1-r)^2 + (1-r)^3 + \dots\right)$$

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



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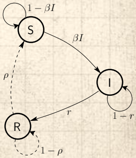
$$= \beta \frac{1}{1-(1-r)} = \beta/r$$



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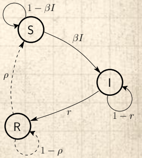
$$= \beta\left(1 + (1-r) + (1-r)^2 + (1-r)^3 + \ldots\right)$$

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

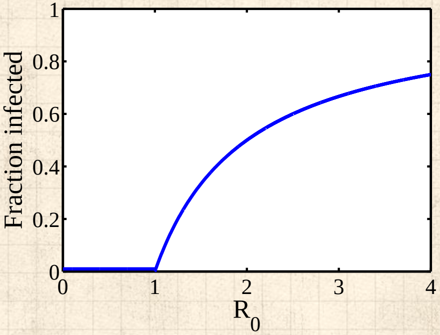
For $S(0) \simeq 1$ initial susceptibles ($1 - S(0) = R(0)$ = fraction initially immune):

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

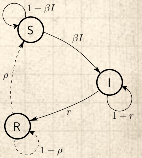


Independent Interaction models

Example of epidemic threshold:



- Continuous phase transition.
- Fine idea from a simple model.

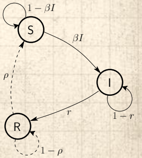


Independent Interaction models

For the continuous version

- Second equation:

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



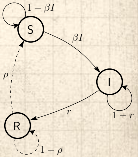
Independent Interaction models

For the continuous version

- Second equation:

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

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



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

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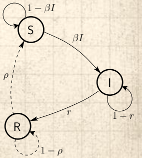
- Number of infectives grows initially if

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

where $S(0) \simeq 1$.



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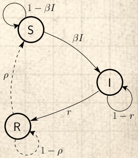

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- Number of infectives grows initially if

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

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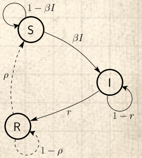

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- Number of infectives grows initially if

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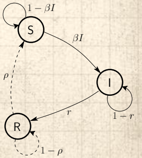
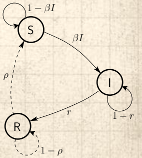
where $S(0) \simeq 1$.

- Same story as for discrete model.



Independent Interaction models

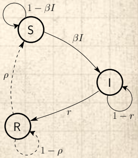
Many variants of the SIR model:



Independent Interaction models

Many variants of the SIR model:

- SIS: susceptible-infective-susceptible



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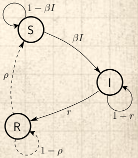
- SIRS: susceptible-infective-recovered-susceptible



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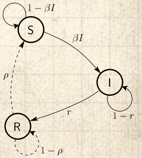
- compartment models (age or gender partitions)



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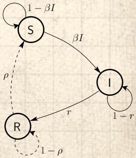
- compartment models (age or gender partitions)
- more categories such as ‘exposed’ (SEIRS)



Independent Interaction models

Many variants of the SIR model:

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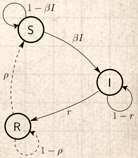
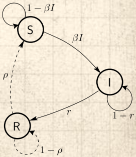
- SIRS: susceptible-infective-recovered-susceptible
- compartment models (age or gender partitions)
- more categories such as 'exposed' (SEIRS)
- recruitment (migration, birth)

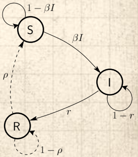


Watch someone else pretend to save the world:

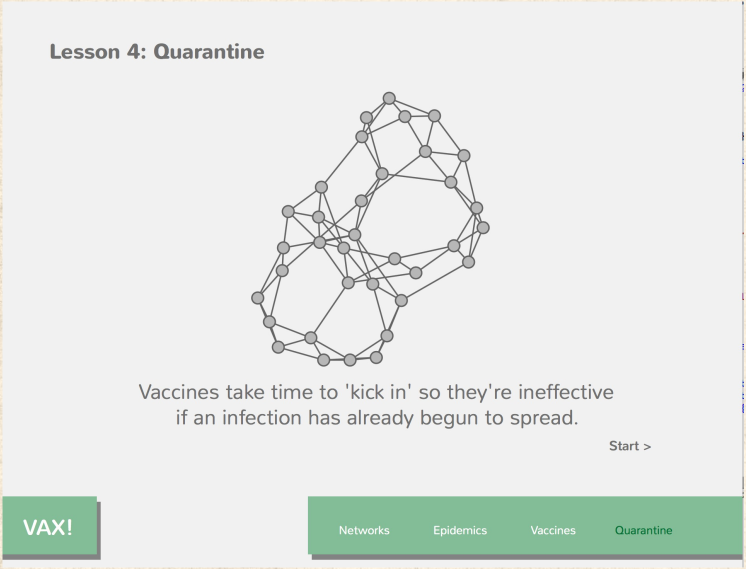


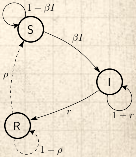
Save the world yourself:

- And you can be the virus.
- Also contagious?: Cooperative games ...

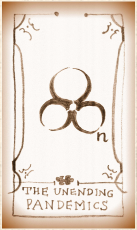


Neural reboot—Save another pretend world with Vax:



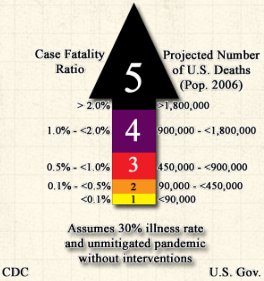


Outline

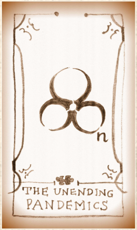


Pandemic severity index (PSI)

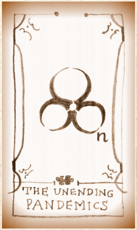
- Classification during/post pandemic:



- Category based.
- 1–5 scale.
- Modeled on the Saffir-Simpson hurricane scale.

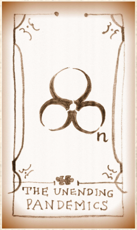


For novel diseases:



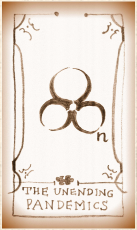
For novel diseases:

1. Can we predict the size of an epidemic?



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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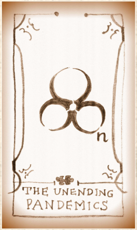
R_0 approximately same for all of the following:



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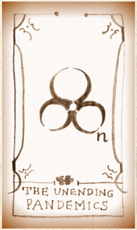
R_0 approximately same for all of the following:

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



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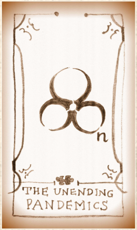
- 1957-58 "Asian Flu" $\sim$ 2,000,000 world-wide, 70,000 deaths in US.



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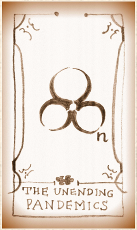
- 1968-69 “Hong Kong Flu” $\sim$ 1,000,000 world-wide, 34,000 deaths in US.



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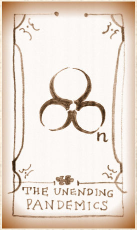
- 1968-69 “Hong Kong Flu” $\sim$ 1,000,000 world-wide, 34,000 deaths in US.
- 2003 “SARS Epidemic” $\sim$ 800 deaths world-wide.



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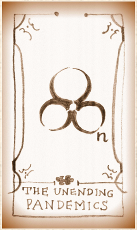
As we know, heavy-tailed size distributions are somewhat prevalent in complex systems:



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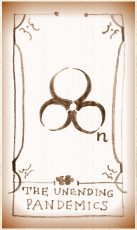

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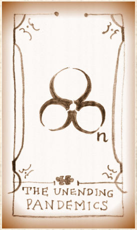

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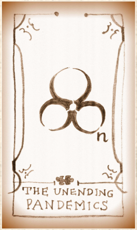

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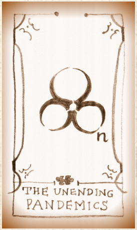

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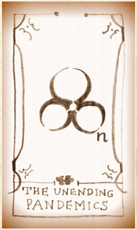

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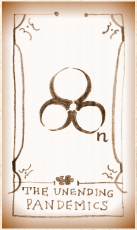
Power law distributions are common but not obligatory...



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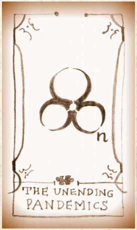

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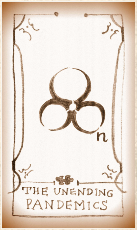

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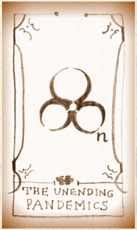
Power law distributions are common but not obligatory...

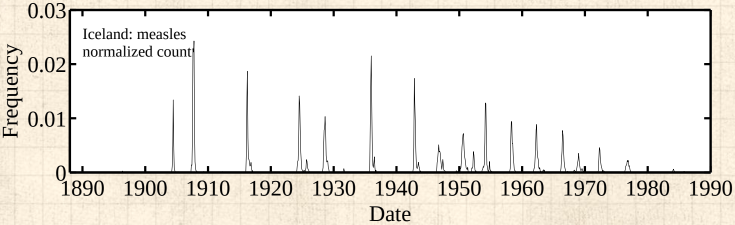
Really, what about epidemics?

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

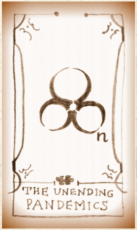


Feeling Ill in Iceland

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

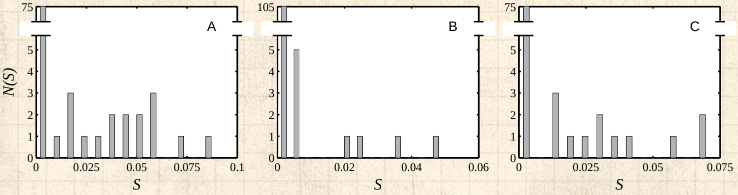


- Treat outbreaks separated in time as 'novel' diseases.

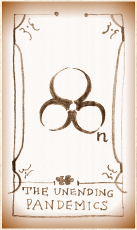


Really not so good at all in Iceland

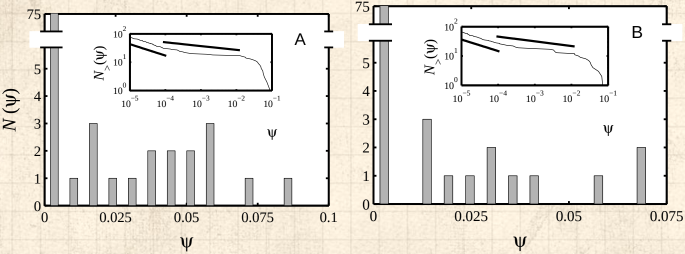
Epidemic size distributions $N(S)$ for Measles, Rubella, and Whooping Cough.

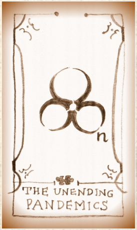


Spike near $S = 0$, relatively flat otherwise.



Measles & Pertussis





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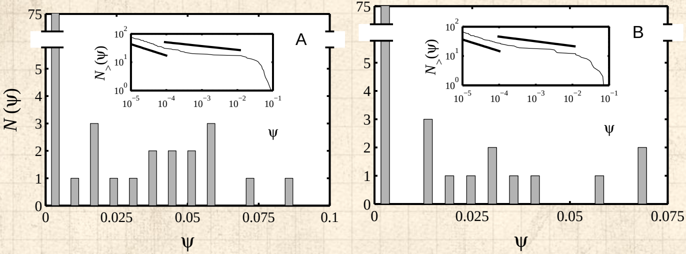
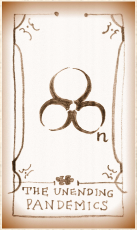


Insert plots:

Complementary cumulative frequency distributions:

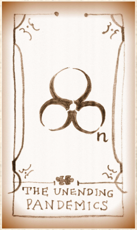
$$N(\Psi' > \Psi) \propto \Psi^{-\gamma+1}$$

Limited scaling with a possible break.



Power law distributions

Measured values of γ:



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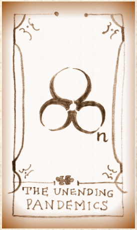

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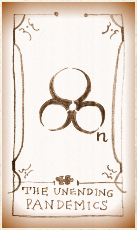

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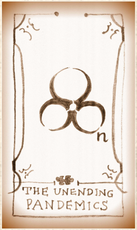

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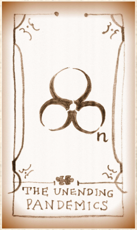

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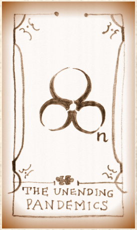
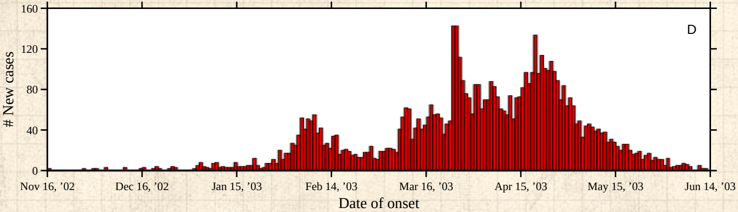
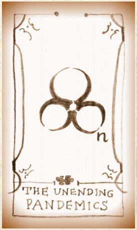
- Expect $2 \leq \gamma < 3$ (finite mean, infinite variance)
- When $\gamma < 1$, can't normalize
- Distribution is quite flat.



Resurgence—example of SARS





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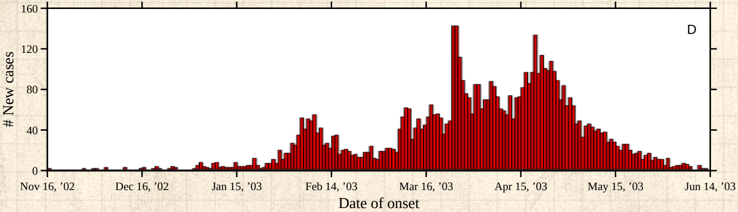
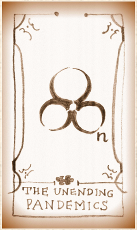


- Epidemic slows...



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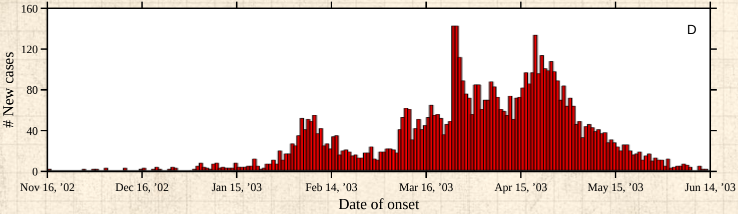
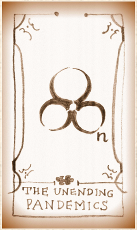


- Epidemic slows...
  then an infective moves to a new context.



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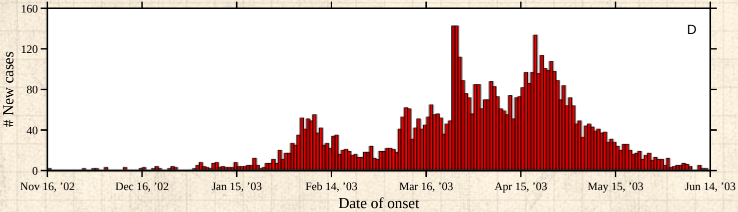

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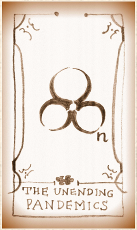
- Epidemic discovers new 'pools' of susceptibles: Resurgence.



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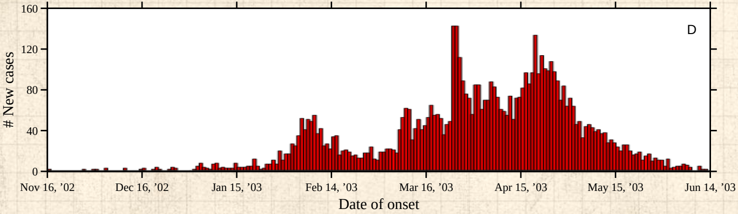
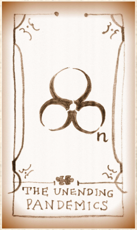
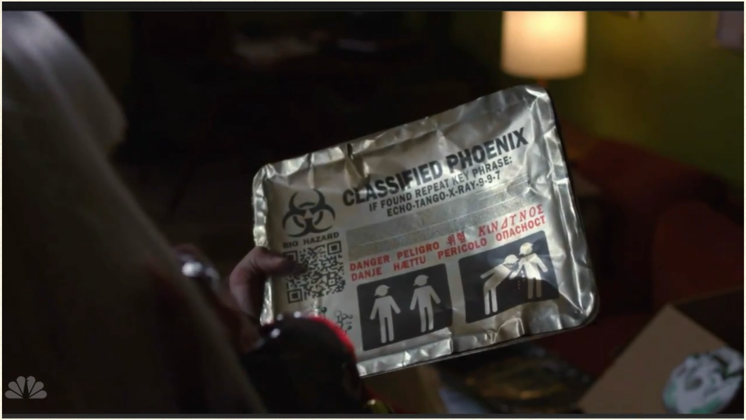


- Epidemic slows... then an infective moves to a new context.
- Epidemic discovers new 'pools' of susceptibles: Resurgence.
- Importance of rare, stochastic events.

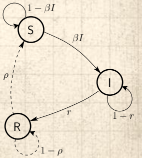


Community—S2E06: Epidemiology



Classified Phoenix.

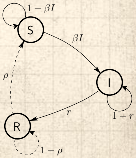
Outline



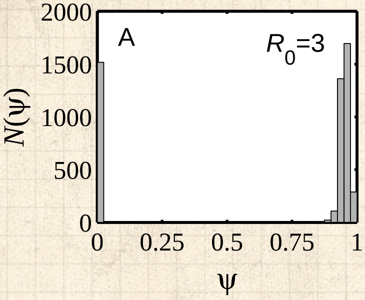
The challenge

So... can a simple model produce

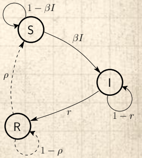
1. broad epidemic distributions
   and
2. resurgence ?



Size distributions



Simple models typically produce bimodal or unimodal size distributions.



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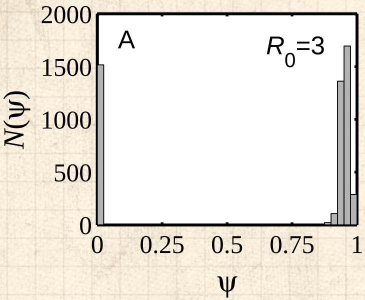

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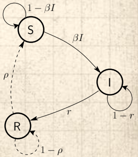

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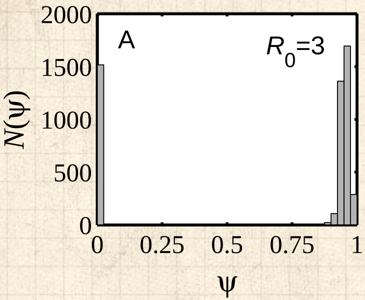

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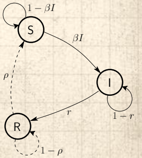

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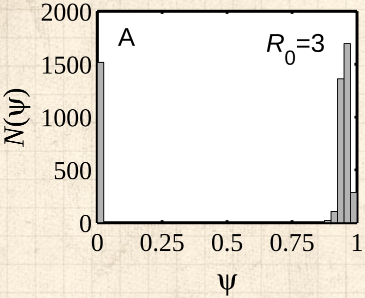

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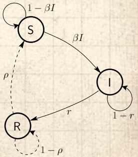

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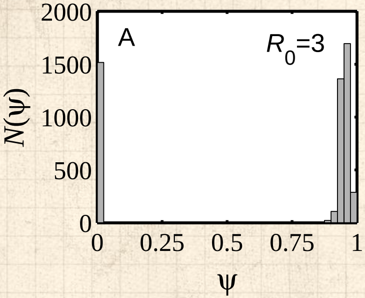

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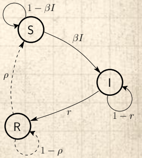


Burning through the population

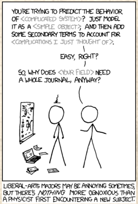
Forest fire models: [19]

LIBERAL-ARTS MAJORS MAY BE ANNOYING SOMETIMES, BUT THERE'S *NOTHING* MORE OBNOXIOUS THAN A PHYSICIST FIRST ENCOUNTERING A NEW SUBJECT.

Burning through the population

Forest fire models: [19]

- Rhodes & Anderson, 1996



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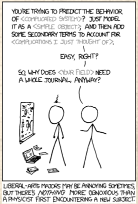

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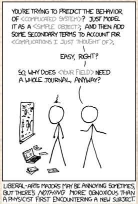

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A bit of a stretch:

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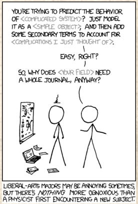
3. Original forest fire model not completely understood.



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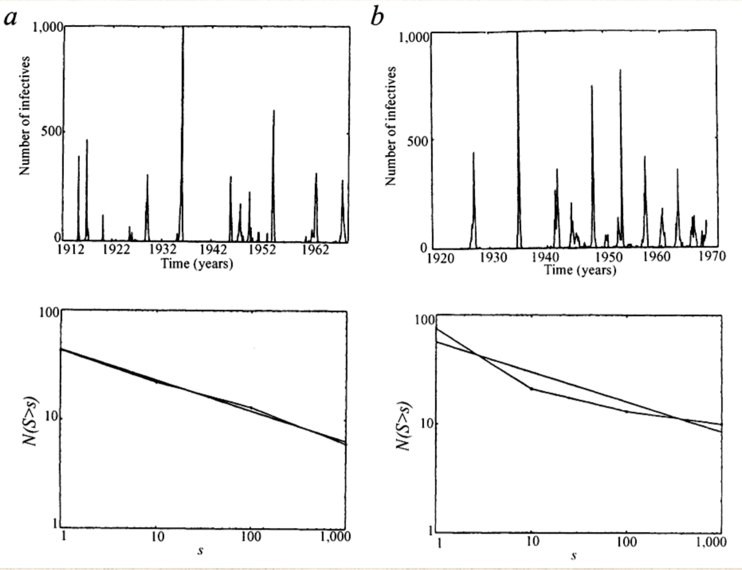
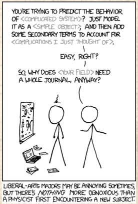
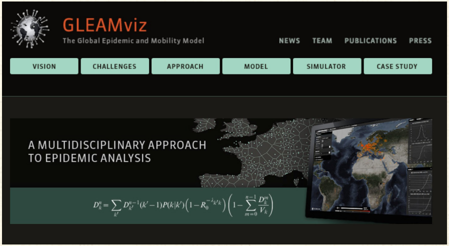


From Rhodes and Anderson, 1996.

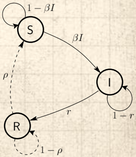


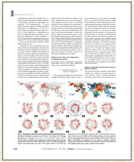
Sophisticated metapopulation models:

- 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]

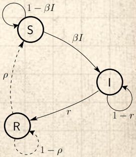


- GLEAM: Global pandemic simulations by Vespignani et al.





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



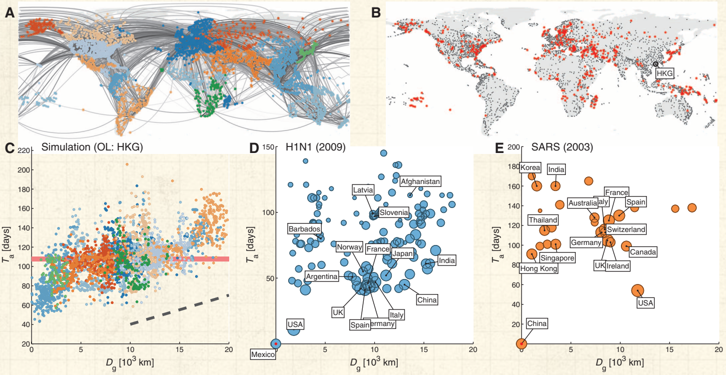
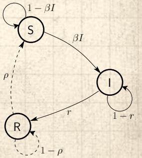


Fig. 1. Complexity in global, network-driven contagion phenomena. (**A**) The global mobility network (GMN). Gray lines represent passenger flows along direct connections between 4069 airports worldwide. Geographic regions are distinguished by color [classified according to network modularity maximization (*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}, $\varepsilon = 10^{-6}$. 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 epidemic 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.



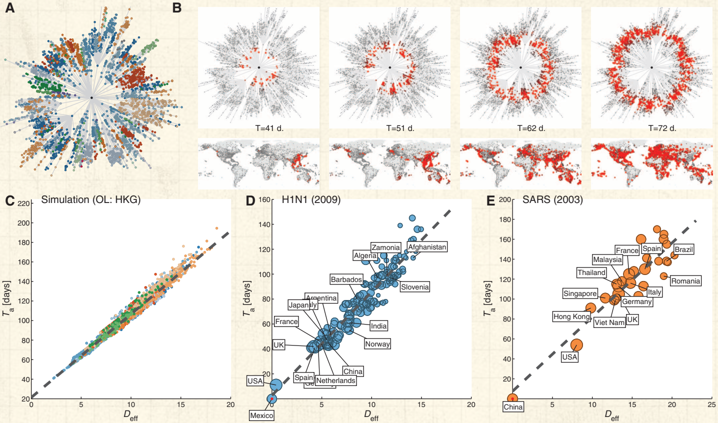
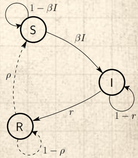


Fig. 2. Understanding global contagion phenomena using effective distance. (**A**) The structure of the shortest path tree (in gray) from Hong Kong (central node). Radial distance represents effective distance D_{eff} as defined by Eqs. 4 and 5. Nodes are colored according to the same scheme as in Fig. 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 a 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.



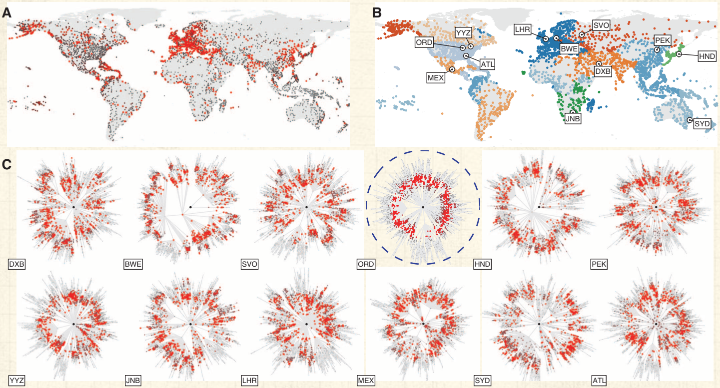
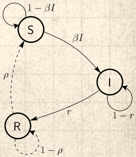
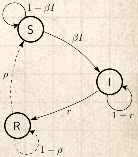


Fig. 3. Qualitative outbreak reconstruction based on effective distance. (**A**) Spatial distribution of prevalence $j_n(t)$ at time $T = 81$ days for OL Chicago (parameters $\beta = 0.28$ day^{-1}, $R_0 = 1.9$, $\gamma = 2.8 \times 10^{-3}$ day^{-1}, and $\varepsilon = 10^{-6}$). After this time, it 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.



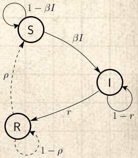
Community—S2E06: Epidemiology

Scenario B.



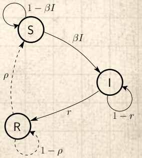
Size distributions

Vital work but perhaps hard to generalize from...



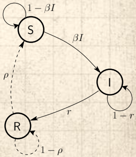
Size distributions

- Vital work but perhaps hard to generalize from...
- ⇒ Create a simple model involving multiscale travel



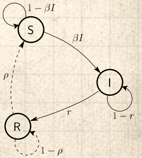
Size distributions

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



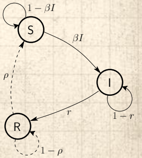
Size distributions

- 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?

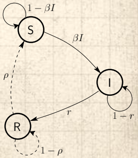


Size distributions

- 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...

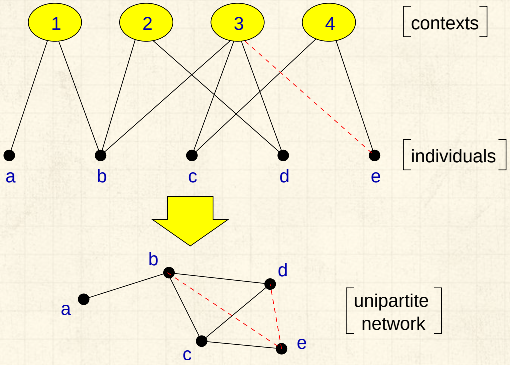


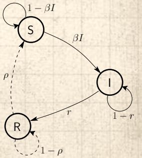
Outline



Improving simple models

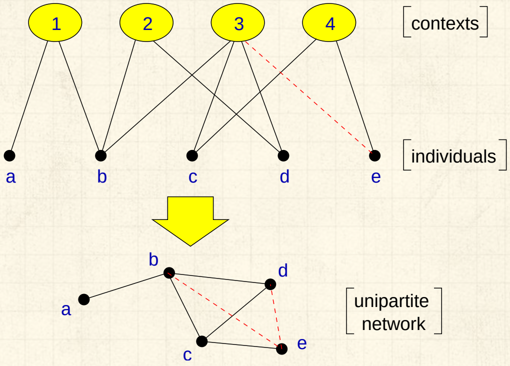
Contexts and Identities—Bipartite networks



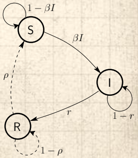


Improving simple models

Contexts and Identities—Bipartite networks

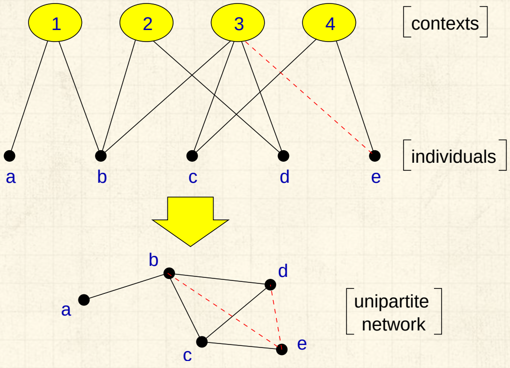


- boards of directors

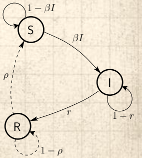


Improving simple models

Contexts and Identities—Bipartite networks

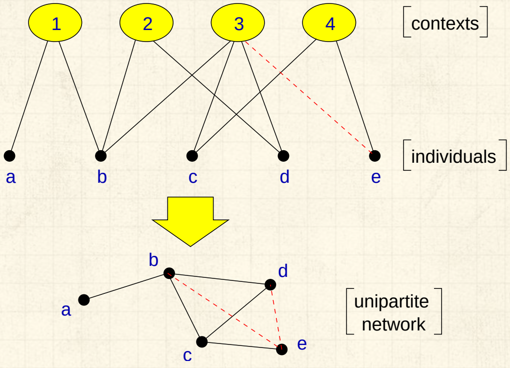


- boards of directors
- movies

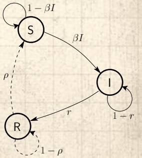


Improving simple models

Contexts and Identities—Bipartite networks

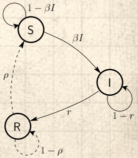


- boards of directors
- movies
- transportation modes (subway)



Improving simple models

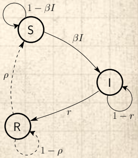
Idea for social networks: incorporate identity



Improving simple models

Idea for social networks: incorporate identity

Identity is formed from attributes such as:

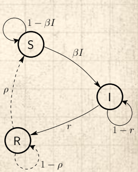


Improving simple models

Idea for social networks: incorporate identity

Identity is formed from attributes such as:

- Geographic location

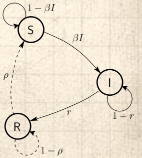


Improving simple models

Idea for social networks: incorporate identity

Identity is formed from attributes such as:

- Geographic location
- Type of employment

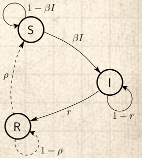


Improving simple models

Idea for social networks: incorporate identity

Identity is formed from attributes such as:

- Geographic location
- Type of employment
- Age

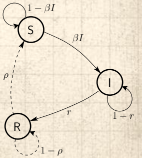


Improving simple models

Idea for social networks: incorporate identity

Identity is formed from attributes such as:

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



Improving simple models

Idea for social networks: incorporate identity

Identity is formed from attributes such as:

- Geographic location
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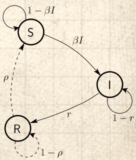
Groups are crucial...



Improving simple models

Idea for social networks: incorporate identity

Identity is formed from attributes such as:

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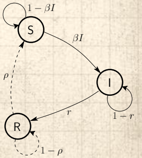
- Recreational activities

Groups are crucial...

- formed by people with at least one similar attribute



Improving simple models

Idea for social networks: incorporate identity

Identity is formed from attributes such as:

- Geographic location
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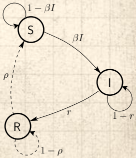
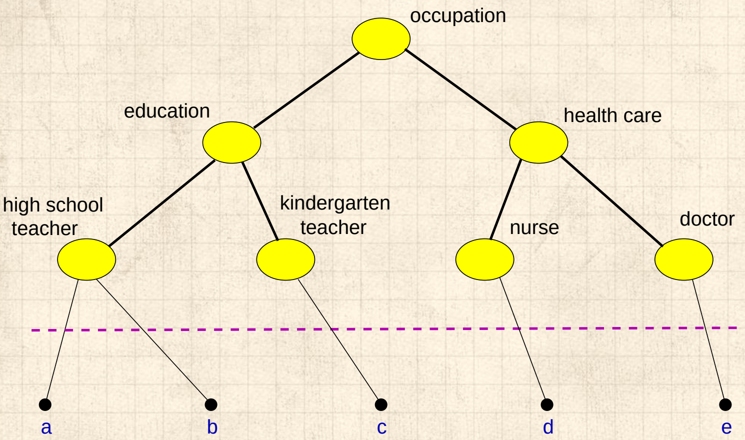
- Age
- Recreational activities

Groups are crucial...

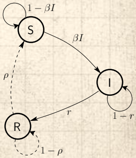
- formed by people with at least one similar attribute
- Attributes ⇔ Contexts ⇔ Interactions ⇔ Networks. [23]



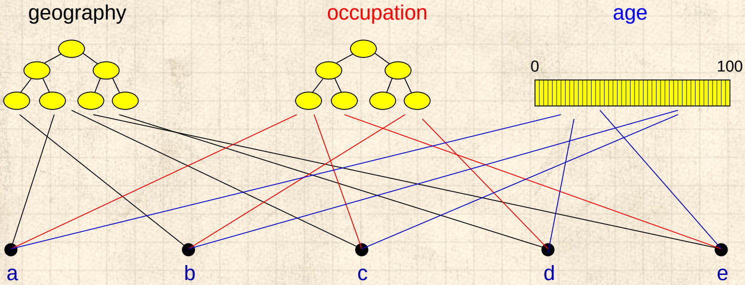
Infer interactions/network from identities



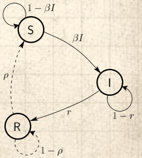
Distance makes sense in identity/context space.



Generalized context space



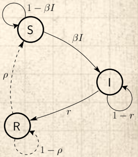
(Blau & Schwartz [3], Simmel [20], Breiger [4])



A toy agent-based model:

"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



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Multiscale, resurgent epidemics in a hierarchical metapopulation model

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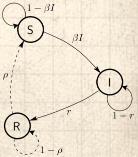
Geography: allow people to move between contexts

- Locally: standard SIR model with random mixing



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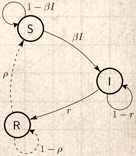
Geography: allow people to move between contexts

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



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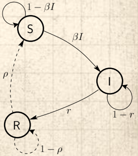
Geography: allow people to move between contexts

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



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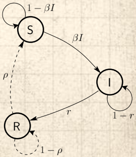
Geography: allow people to move between contexts

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



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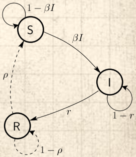
Geography: allow people to move between contexts

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



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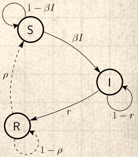
Geography: allow people to move between contexts

- 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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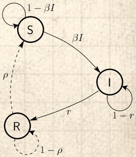
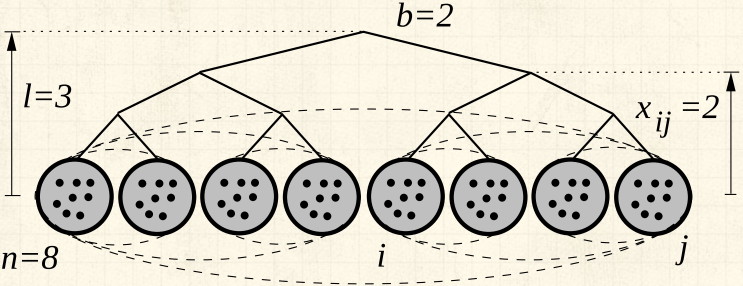
Geography: allow people to move between contexts

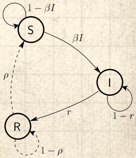
- Locally: standard SIR model with random mixing
- discrete time simulation
- β = infection probability
- γ = recovery probability
- P = probability of travel
- Movement distance: $\Pr(d) \propto \exp(-d/\xi)$
- ξ = typical travel distance



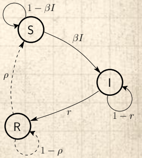
A toy agent-based model

Schematic:



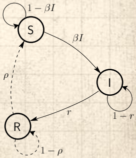


Outline



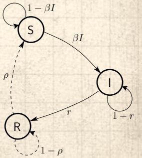
Model output

Define P_0 = Expected number of infected individuals leaving initially infected context.



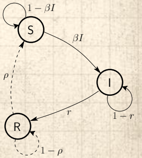
Model output

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



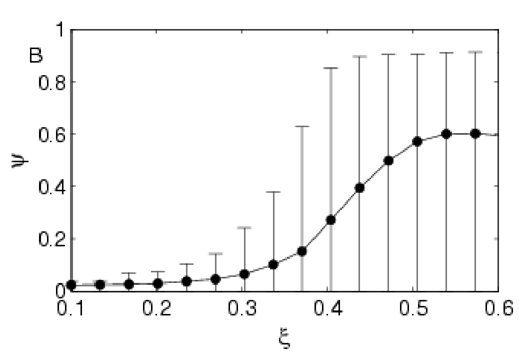
Model output

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

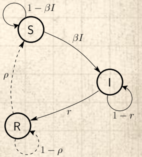


Model output

Varying ξ:



- Transition in expected final size based on typical movement distance



Model output

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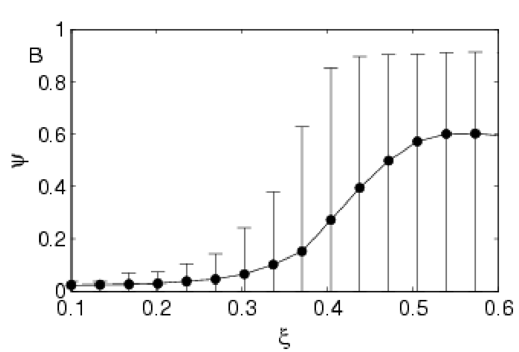
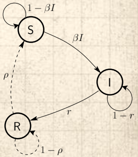
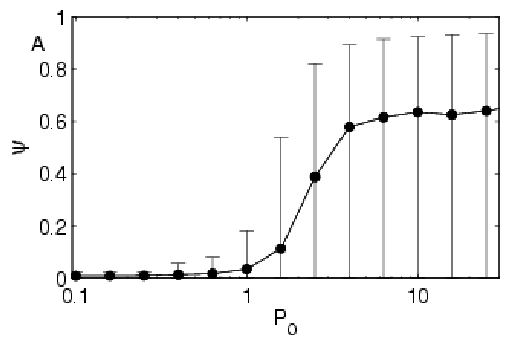


- Transition in expected final size based on typical movement distance (sensible)

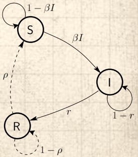


Model output

Varying P_0:

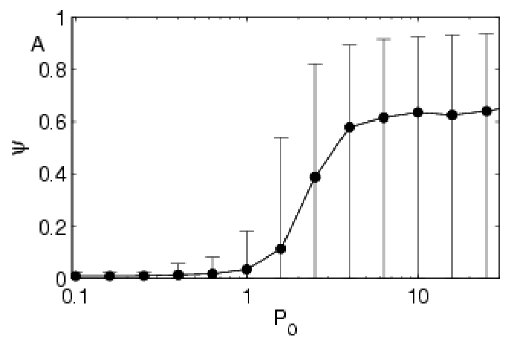


- Transition in expected final size based on typical number of infectives leaving first group

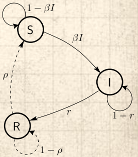


Model output

Varying P_0:

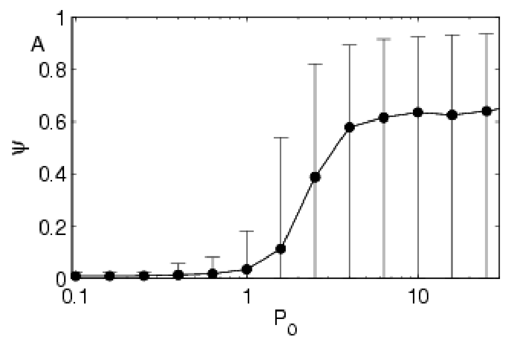


- Transition in expected final size based on typical number of infectives leaving first group (also sensible)

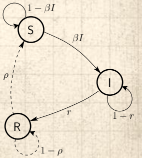


Model output

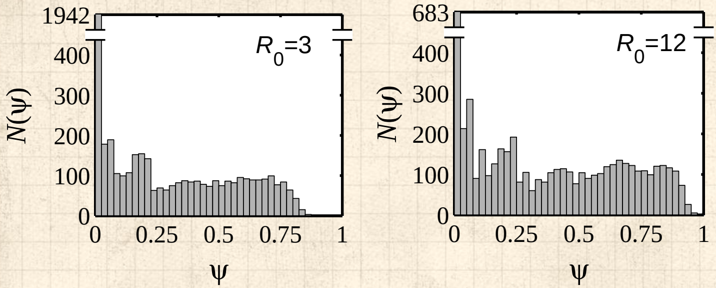
Varying P_0:

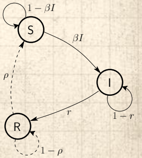


- Transition in expected final size based on typical number of infectives leaving first group (also sensible)
- Travel advisories: ξ has larger effect than P_0.



Example model output: size distributions





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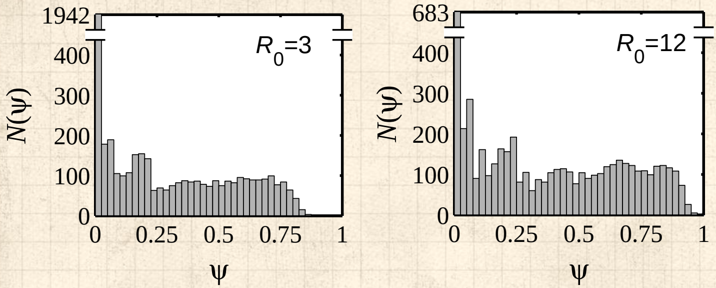

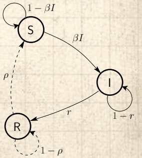

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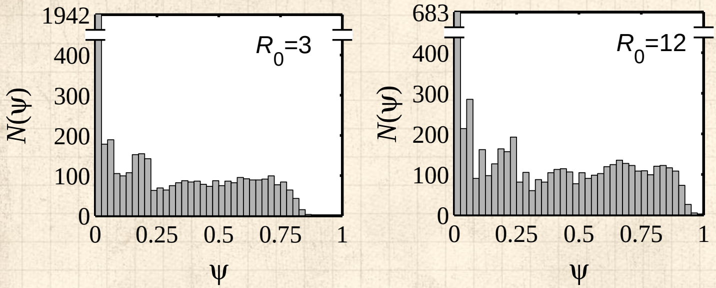
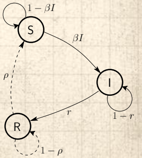


- Flat distributions are possible for certain ξ and P.



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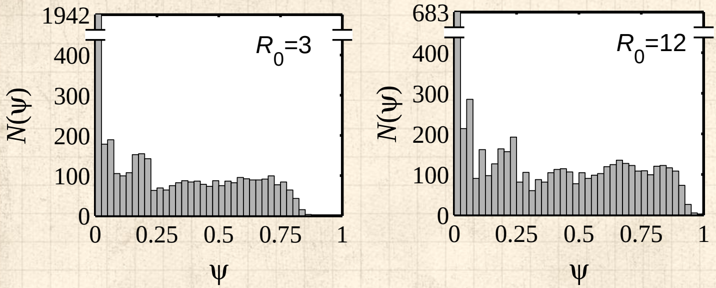

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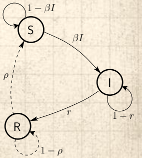

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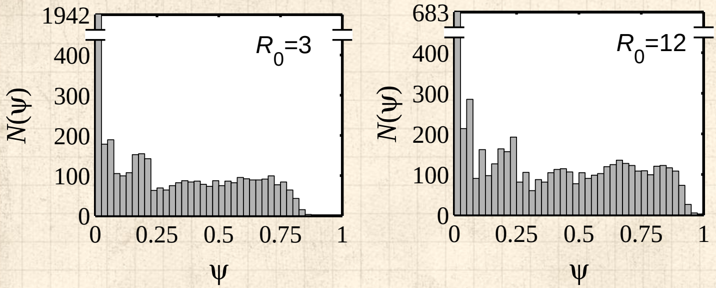
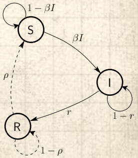
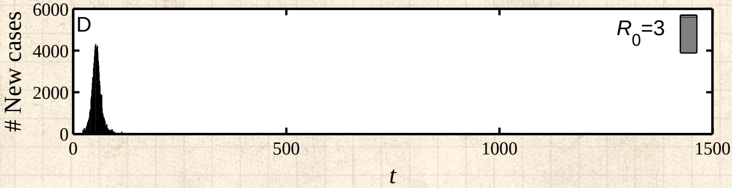


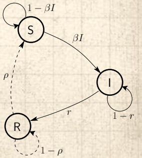
- Flat distributions are possible for certain ξ and P.
- Different R_0's may produce similar distributions
- Same epidemic sizes may arise from different R_0's



Model output—resurgence

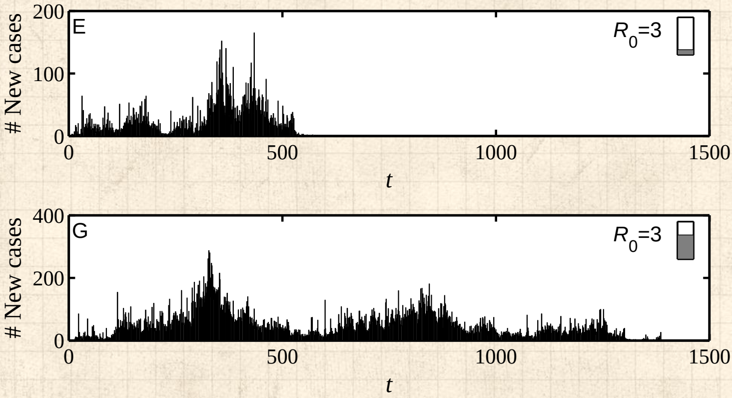
Standard model:

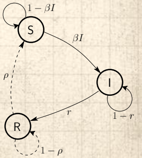




Model output—resurgence

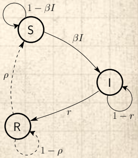
Standard model with transport:





The upshot

Simple multiscale population structure



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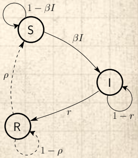
+

stochasticity



The upshot

Simple multiscale population structure

+

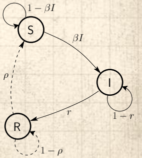
stochasticity

leads to

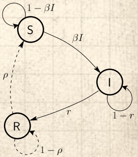
resurgence

+

broad epidemic size distributions



The Last of Us: Groups



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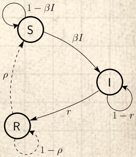

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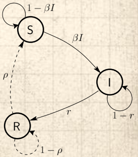

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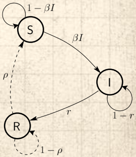

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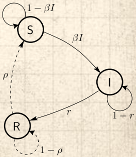

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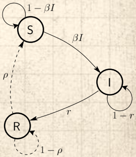

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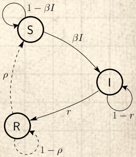

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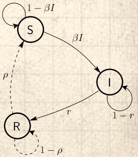

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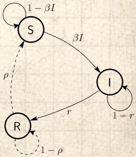

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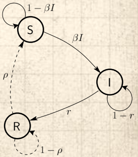

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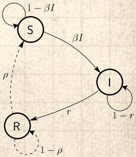

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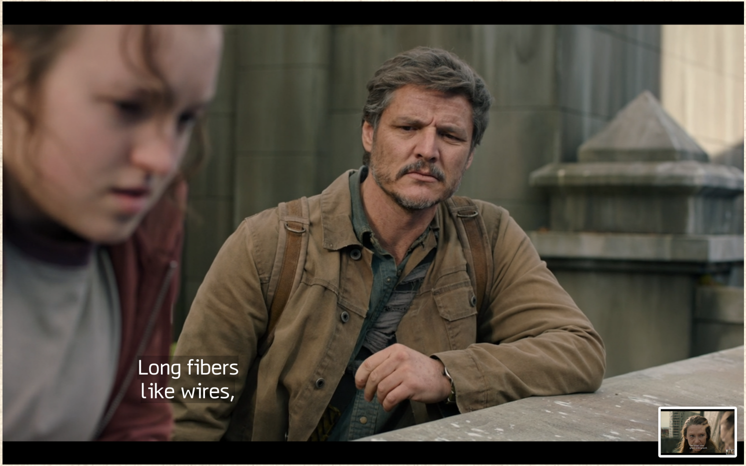

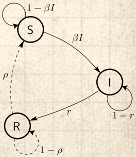

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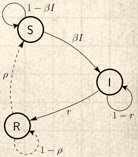

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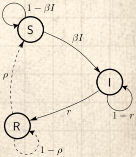

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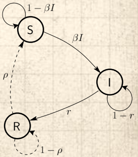

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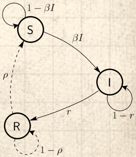
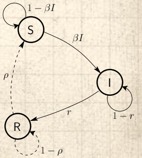
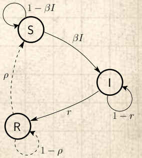


Outline



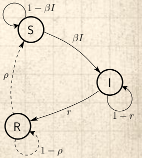
Nutshelling

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



Nutshelling

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



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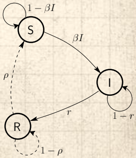

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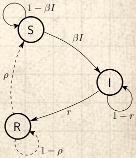

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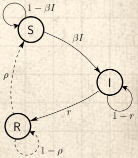

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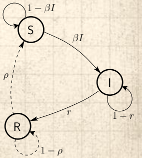

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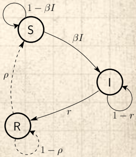

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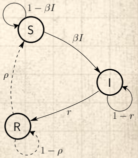
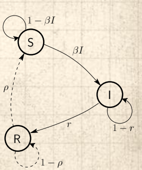
  2. and how likely future epidemics will be.
- Problem: R_0 summarises one epidemic after the fact and enfolds movement, the price of bananas, everything.



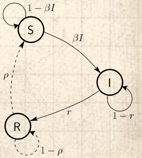
Conclusions

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



Conclusions

- Disease's spread is highly sensitive to population structure.
- Rare events may matter enormously:



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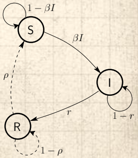

Conclusions

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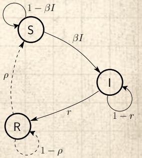
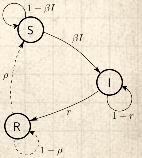
- More support for controlling population movement:



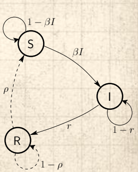
Conclusions

- 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



Nutshelling

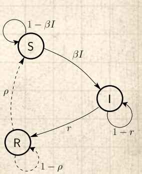
What to do:



Nutshelling

What to do:

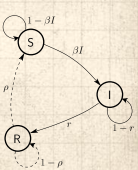
- Need to separate movement from disease



Nutshelling

What to do:

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



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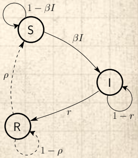

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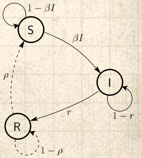

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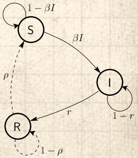

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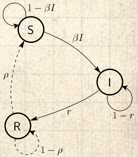

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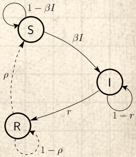


THE SUN
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THE MECHANICS STATISTICAL
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THE ELEMENTS OF WEBS
THE BIRDS OF A FEATHER
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THE ARK OF THE RANDOM NETWORK
THE STRANGENESS OF FRIENDS
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THE THEORY OF SIX DEGREES
THE NETWORKS FREE OF SCALE
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THE THRESHOLDS OF THE MIND
THE SOCIAL WILD
THE RATIO OF GAIN
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THE TALK OF FAME
THE STORIES CONTAGIOUS
THE JOHN DORY
THE ADJACENT NARRATIVES
THE STORYTELLERS
THE FATED ASTRAL PATH
THE PATHS OF UNIVERSALITY
THE DEPENDENT PATHS
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THE UNKNOWN MECHANISM
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THE TRUTHICIDE
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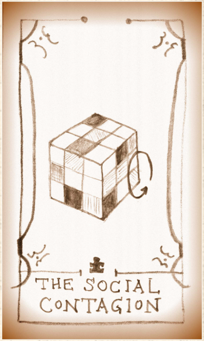
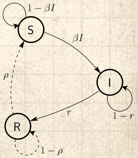

THE SOCIAL CONTAGION

Outline



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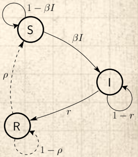

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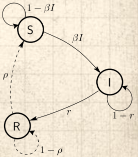

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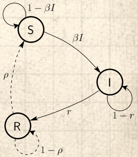

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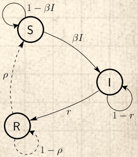

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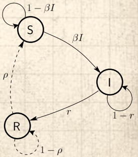

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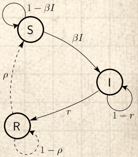

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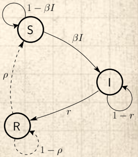

[1] http://www.redherring.com/mag/issue55/economics.html

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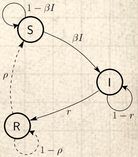

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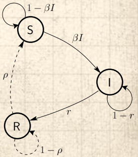

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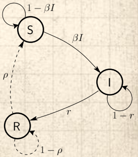

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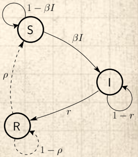

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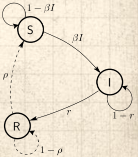

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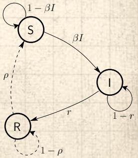

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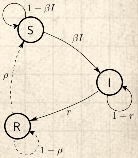

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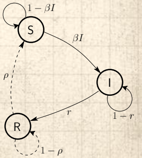

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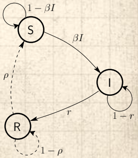

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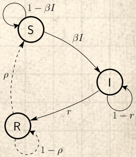

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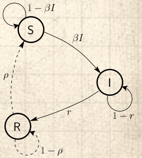

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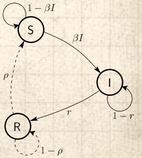

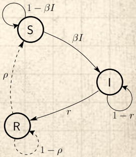

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Jon Stewart:

"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-stewart-alan-gr

Predicting social catastrophe isn't easy...

"Greenspan Concedes Error on Regulation"

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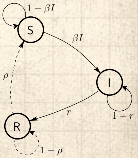

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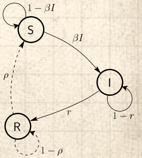

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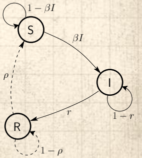

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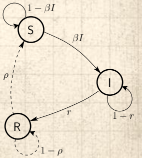

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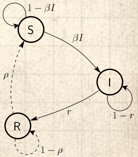

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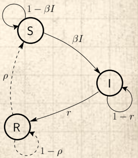

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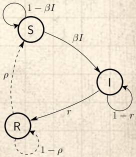

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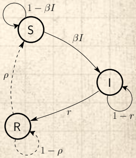

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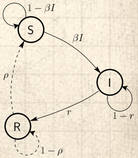

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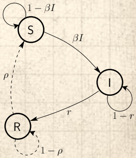

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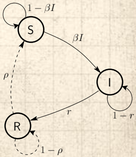

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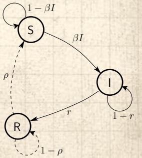
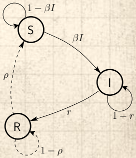


Outline



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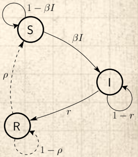

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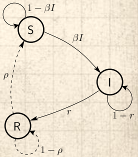

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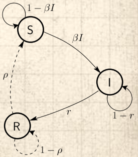

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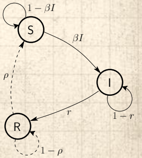

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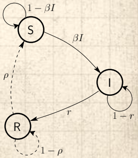

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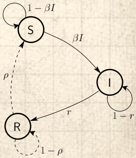

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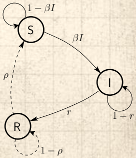

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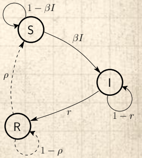

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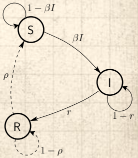

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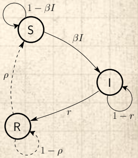

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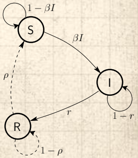
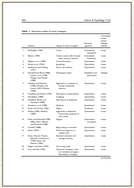


[1] Apologies sir, I'm afraid our chefs can't help themselves

We really should know social contagion is different but ...



“It’s contagious: Rethinking a metaphor dialogically”

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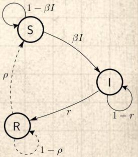

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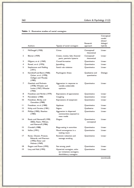

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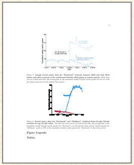

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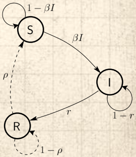
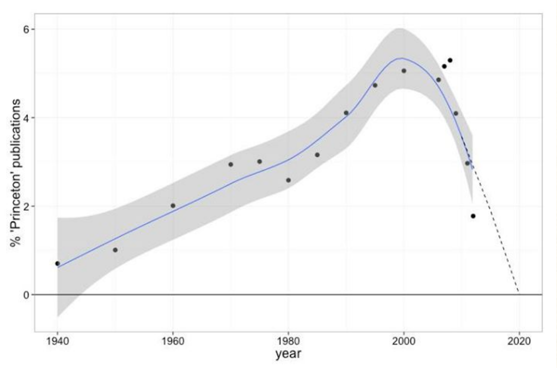
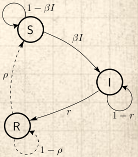


The Facebook Data Science team's response:



Mike Develin, Lada Adamic, and Sean Taylor.



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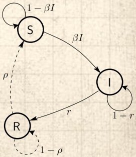

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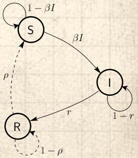

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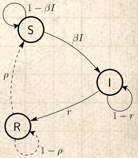

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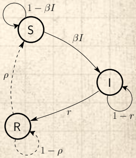

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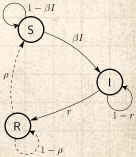

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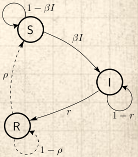

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