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How big will an epidemic be?

Illuminations from a simple model

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Main questions:

For novel diseases:

A. Can we predict the size of an epidemic?

B. How important is the reproduction number R_0 ?

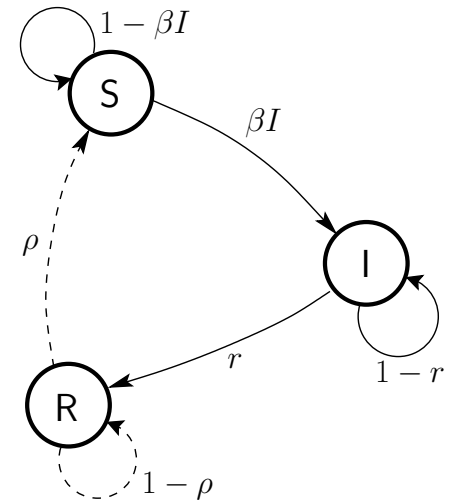
Overview:

- ① The reproduction number R_0 .
- ② Some important aspects of real epidemics:
 - 👉 peculiar distributions of epidemic size
 - 👉 resurgence
- ③ Usual simple models do not fare well regarding ②
- ④ A simple model incorporating movement does fare well.
- ⑤ Conclusion.

Compartment models:

SIR model of infectious disease dynamics:
Three basic states:

- S = Susceptible
- I = Infective/Infectious
- R = Recovered/Removed/Refractory

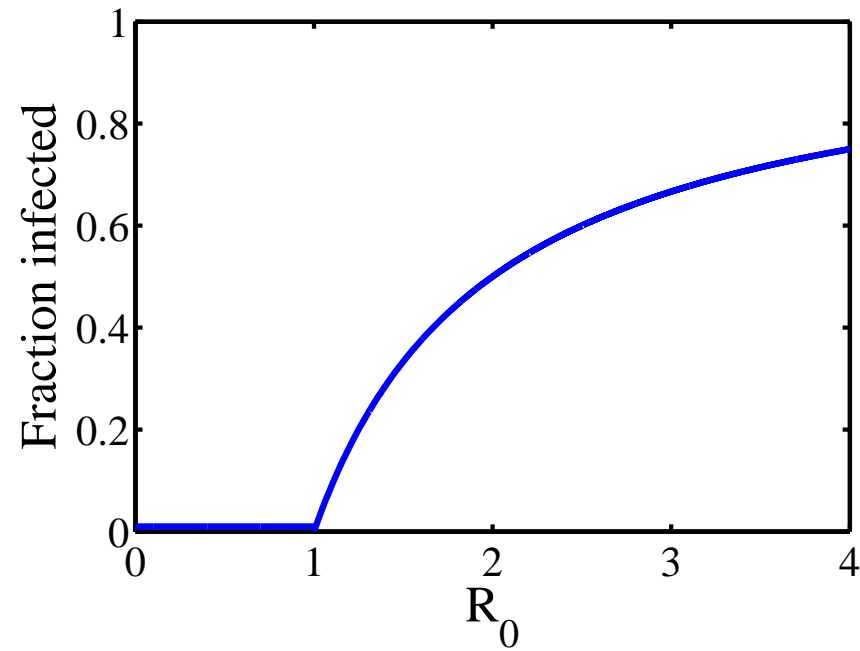


R_0 = expected number of infections due to one infective.

R_0 has become a summary statistic for epidemics.

Epidemic threshold:

If $R_0 > 1$, 'epidemic' occurs.



➤ Fine idea from a simple model.

R₀ and variation in epidemic sizes:

R₀ approximately same for all of the following:

1918-19 “Spanish Flu” ~ 500,000 deaths in US

1957-58 “Asian Flu” ~ 70,000 deaths in US

1968-69 “Hong Kong Flu” ~ 34,000 deaths in US

2003 “SARS Epidemic” ~ 800 deaths world-wide

Size distributions:

Size distributions are important elsewhere:

- earthquakes (Gutenberg-Richter law)
 - wealth distributions
 - city sizes, forest fires, war fatalities
 - 'popularity' (books, music, websites, ideas)
- (power laws distributions are common but not obligatory)

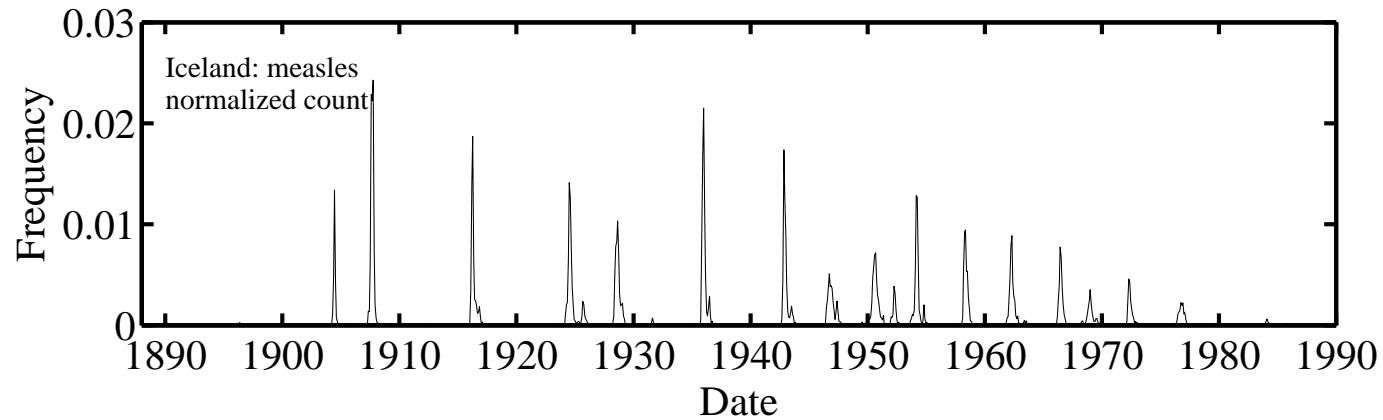
Size distributions:

What about epidemics?

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

Iceland data—monthly counts, 1888–1990:

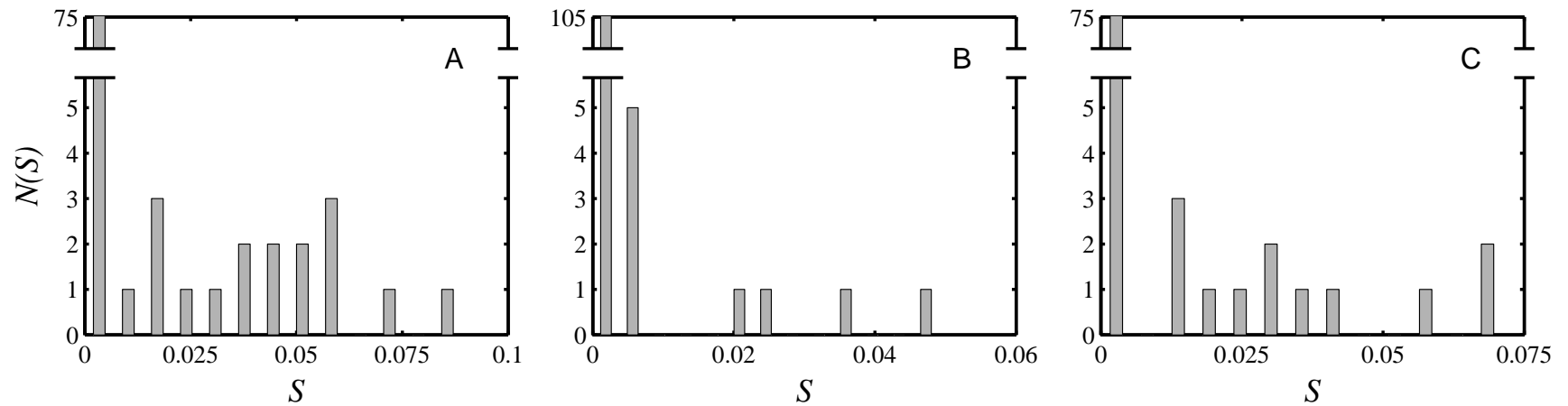
Caseload recorded monthly for range of diseases in Iceland.



Treat outbreaks separated in time as 'novel' diseases.

Iceland data—monthly counts, 1888–1990:

Epidemic size distributions for
Measles, Rubella, Whooping Cough.



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

Power law distributions:

X = event size.

Probability distribution function's tail for large x :

$$\Pr(X = x) \propto x^{-\theta-1}$$

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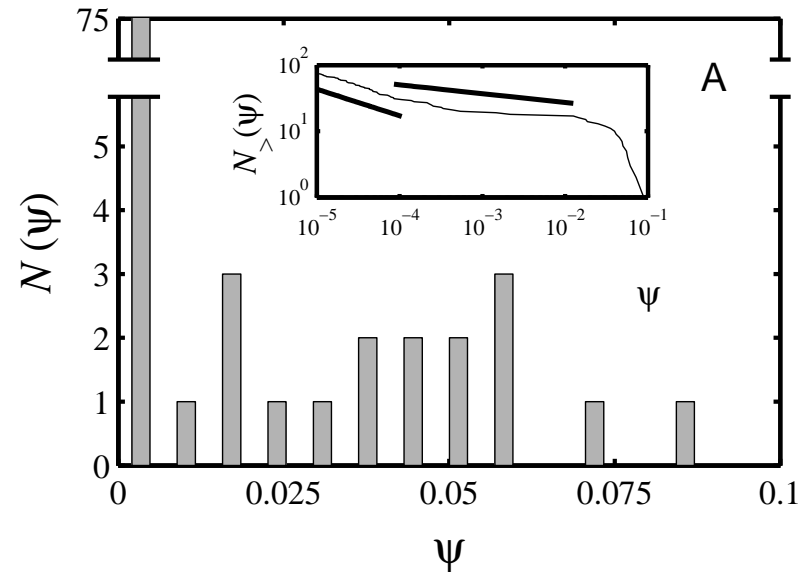
Complementary cumulative distribution function:

$$\Pr(X > x) = \int_x^{\infty} \Pr(X = x') dx' \propto x^{-\theta}$$

Expect $1 \leq \theta < 2$ (finite mean, infinite variance)

Iceland data—monthly counts, 1888–1990:

Measles:

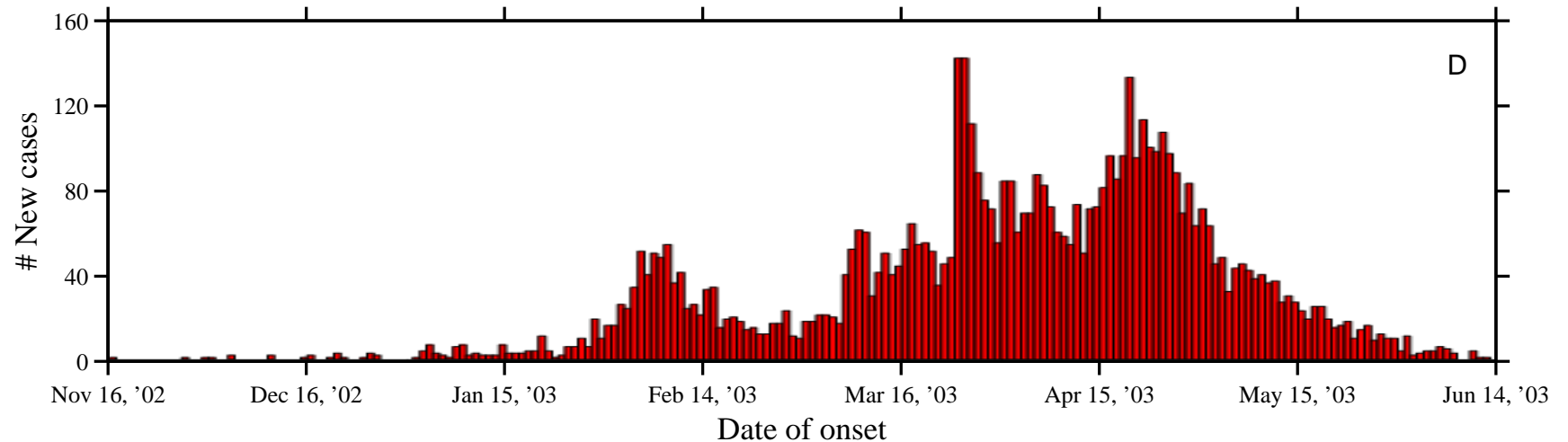


Complementary cdf: $\Pr(X > x) \propto x^{-\theta}$

$\theta = 0.40$ and 0.13 , both outside of range $1 \leq \theta < 2$.

⇒ Distribution seems 'flat.'

Resurgence—example of SARS:



Epidemic slows... Then an infective moves to a new context.

Epidemic discovers new 'pools' of susceptibles: [Resurgence](#).

➤ Importance of rare, stochastic events.

So...

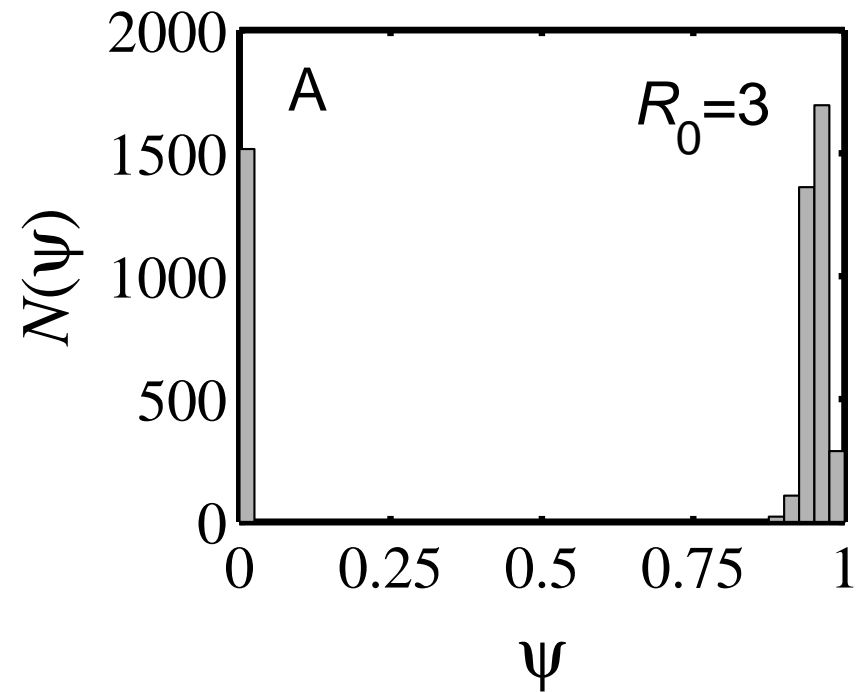
Can existing simple models produce

broad epidemic distributions + resurgence?

Size distributions:

No: Simple models typically produce bimodal or unimodal size distributions.

Including network models: random, small-world, scale-free, . . .



Burning through the population:

Forest fire models: (Rhodes & Anderson, 1996).

The physicist's approach:

“if it works for magnets, it'll work for people...”

Bit of a stretch:

1. epidemics \equiv forest fires

spreading on 3-d and 5-d lattices.

2. Claim Iceland and Faroe Islands exhibit power law distributions for outbreaks.

3. Original model not completely understood.

Sophisticated metapopulation models:

Community based mixing: Longini (two scales).

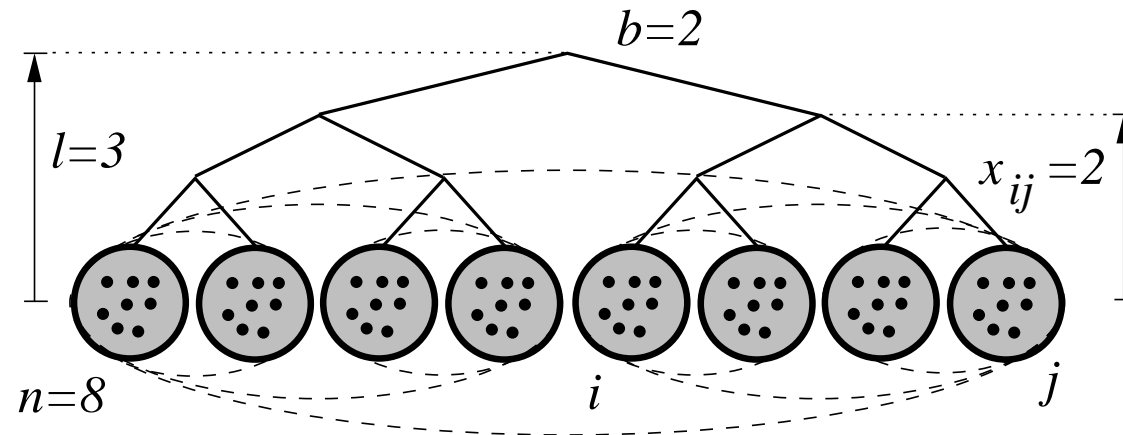
Eubank et al.'s EpiSims/TRANSIMS—city simulations.

Spreading through countries—Airlines: Germann et al.,

Vital work but perhaps hard to generalize from...

⇒ Create a simple model involving multiscale travel.

A toy agent-based model:



Locally: standard SIR model with random mixing

β = infection probability

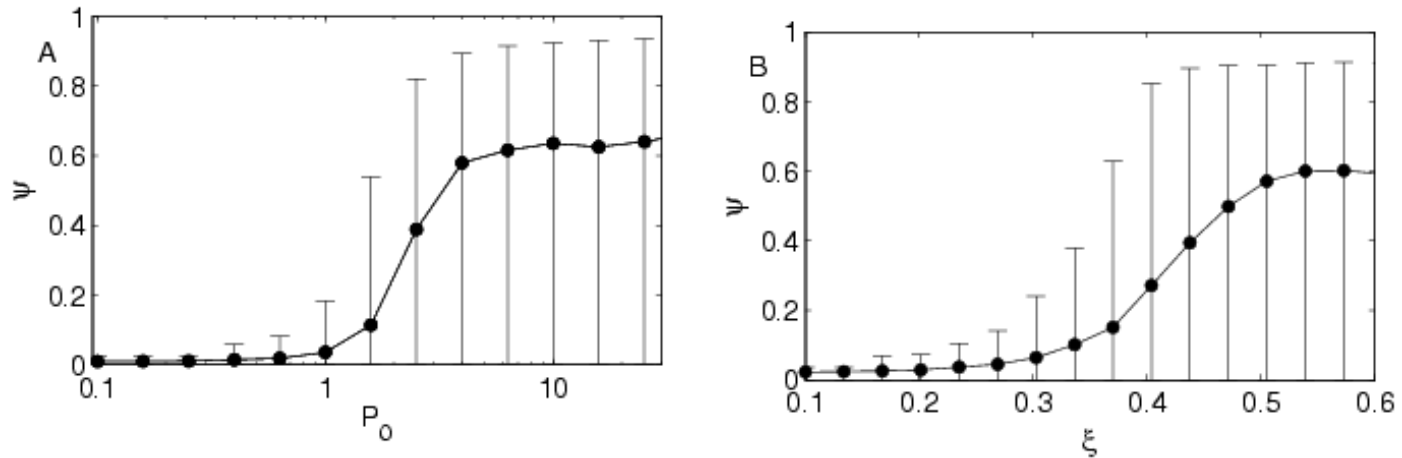
discrete time simulation

γ = recovery probability

P = probability of travel

Movement distance: $\Pr(d) \propto \exp(-d/\xi)$

Model output: varying P_0 (left) and ξ (right):

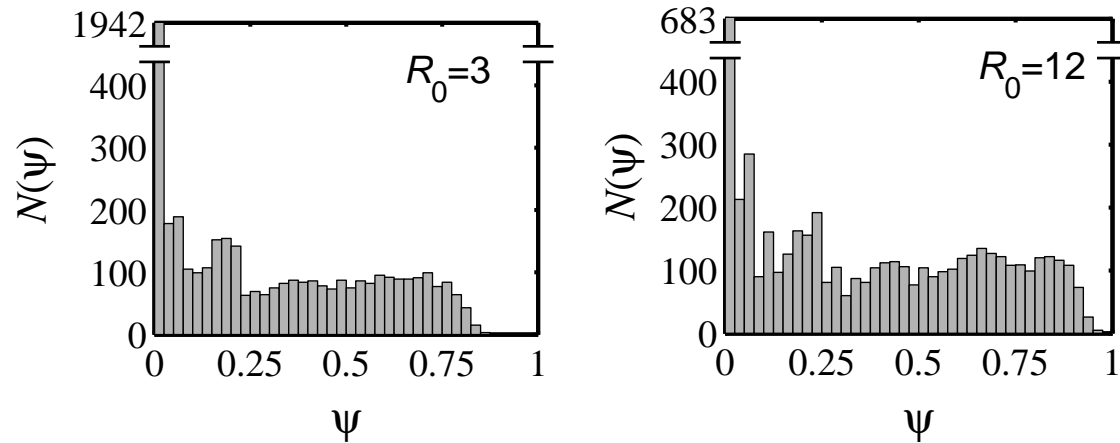


$P_0 =$ Expected number of infected individuals leaving initially infected context.

Need $P_0 > 1$ for disease to spread (independent of R_0).

Restricting frequency of travel
and/or range limits epidemic size.

Model output: size distributions:

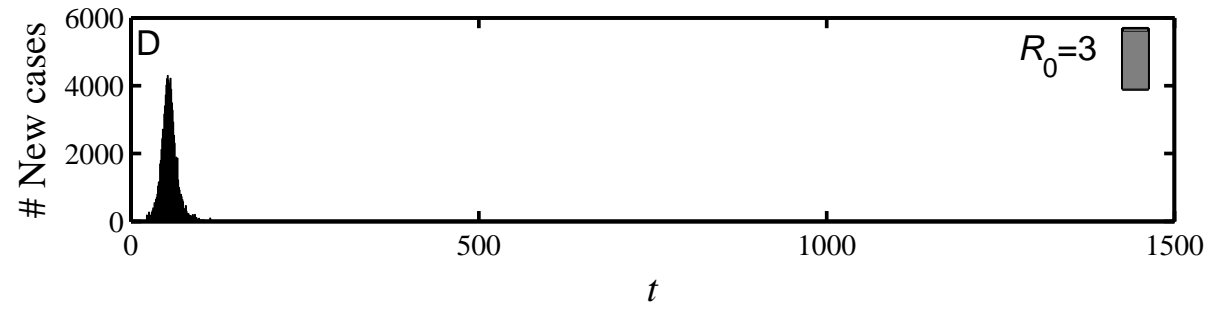


Flat distributions are possible for certain ξ and P_0 .

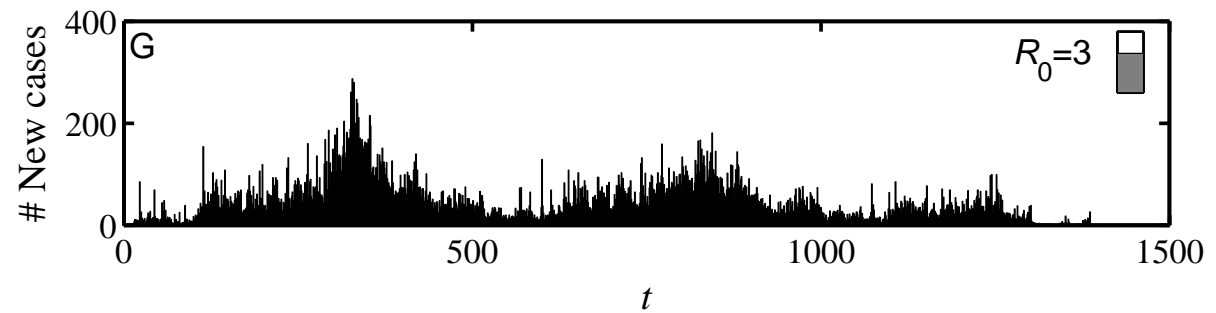
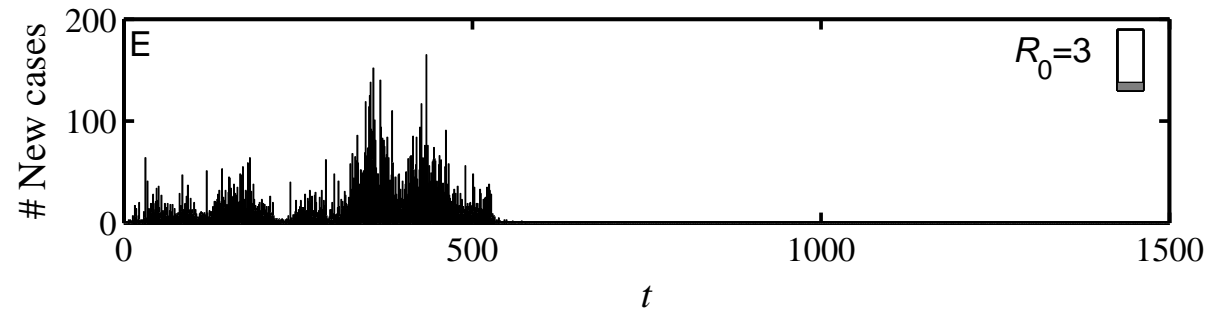
- Different R_0 's may produce similar distributions.
- Same epidemic sizes may arise from different R_0 's.

Model output—resurgence:

Standard
model



Standard
model with
transport:



Conclusions-I:

Results suggest that for novel diseases:

A. Epidemic size unpredictable.

B. The reproduction number R_0 is not overly useful.

R_0 summarises **one** epidemic after the fact and enfolds transport, everything.

R_0 , however measured, is not informative about (A) how likely the observed epidemic size was or (B) how likely future epidemics will be.

Conclusions—II:

Disease spread 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).

Reference:

“Multiscale, resurgent epidemics in a hierarchical metapopulation model.”

D.J. Watts, R. Muhamad, D. Medina, and P.S. Dodds

Proc. Natl. Acad. Sci., Vol. 102(32), pp. 11157-11162.