

Near critical dynamics 2

January 25, 2017

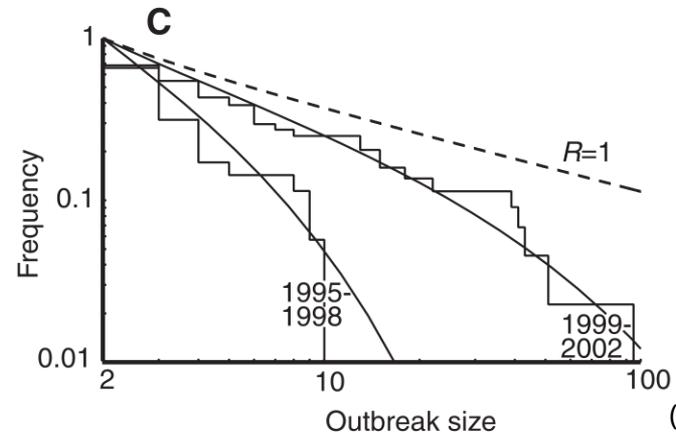
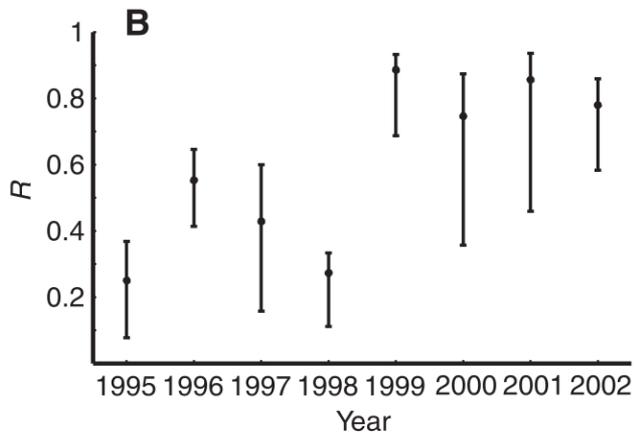
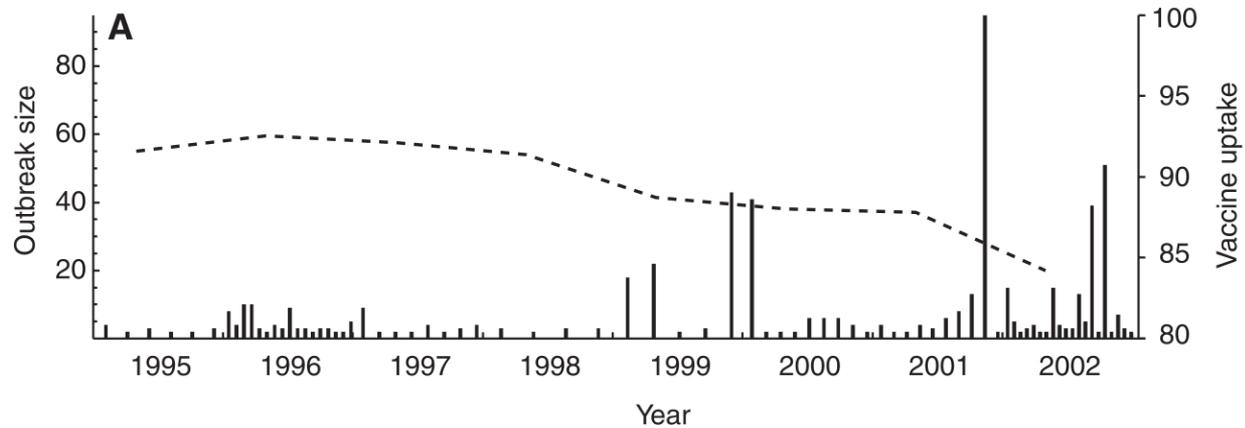
After this class, you should be able to:

1. Explain the methods and results in the assigned readings
2. Use understanding of near-critical dynamics (and R) to evaluate whether an increase in reported cases corresponds to a threshold being approached

Reading 1:

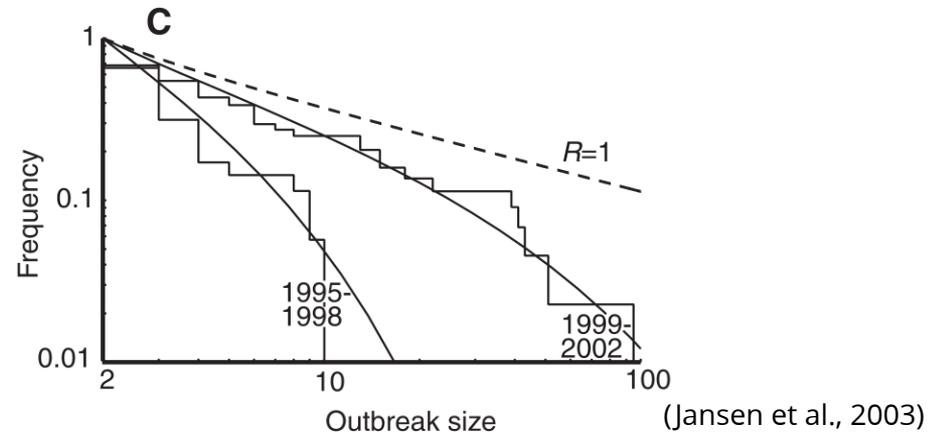
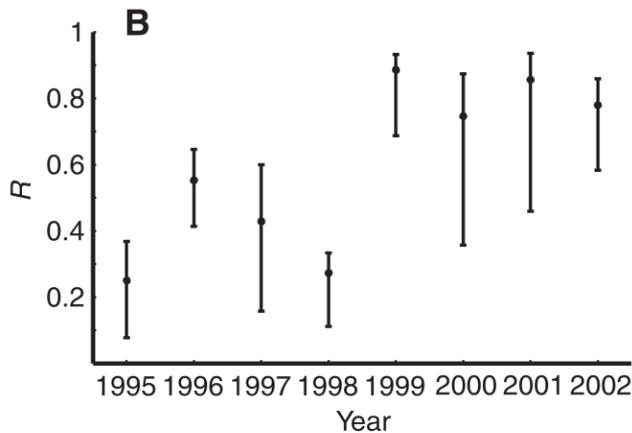
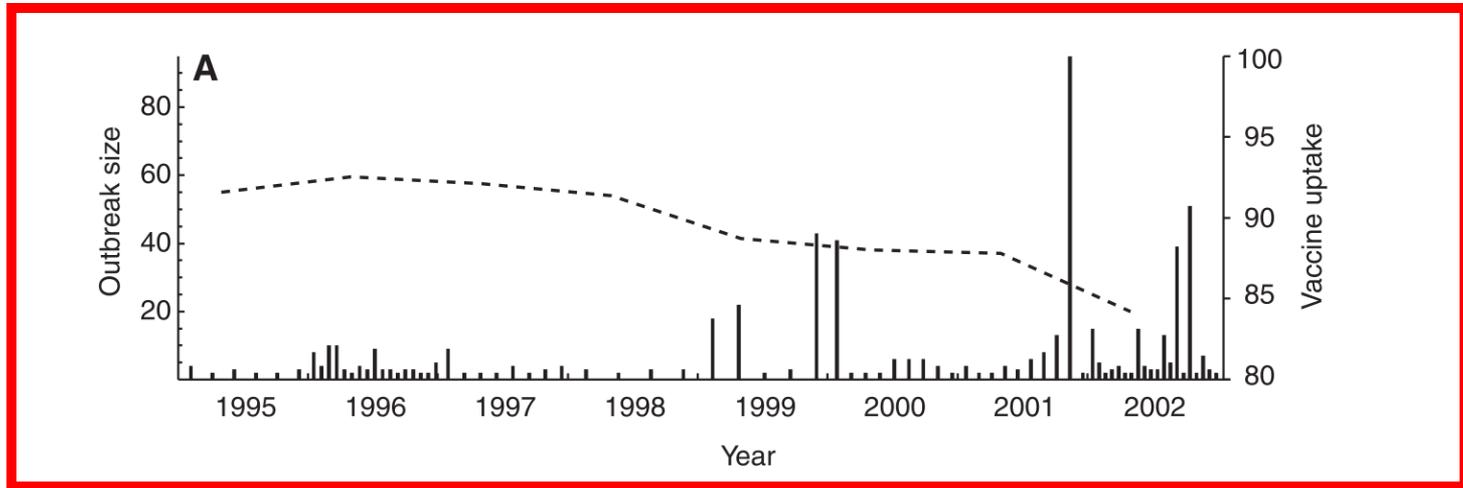
Measles Outbreaks in a Population with
Declining Vaccine Uptake

Measles in England and Wales

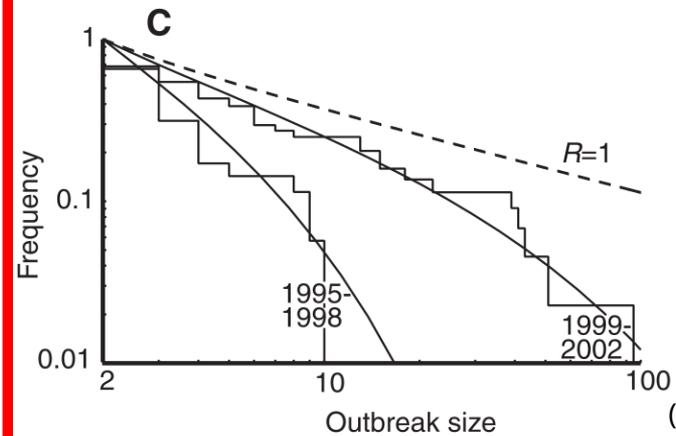
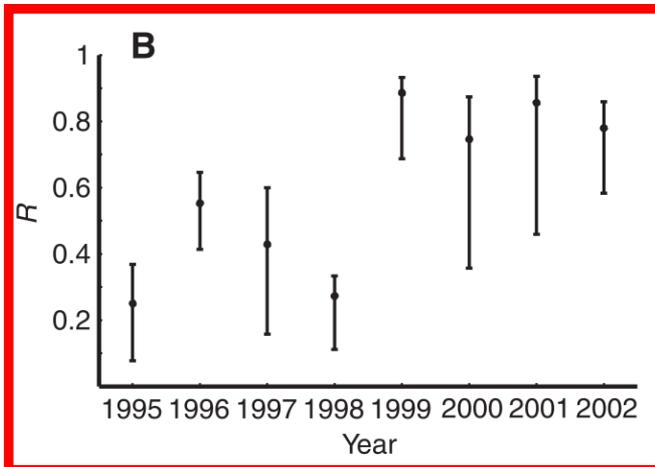
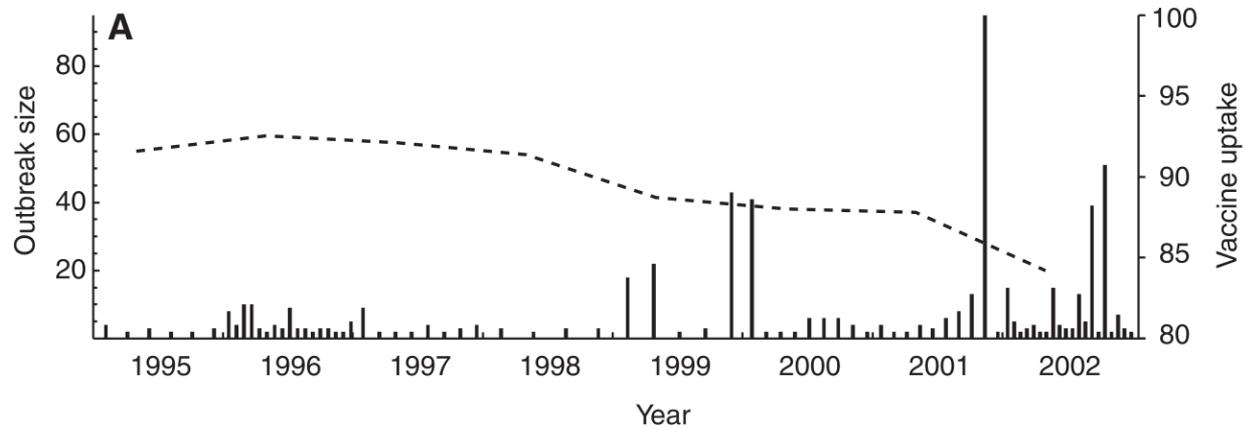


(Jansen et al., 2003)

Measles in England and Wales



Measles in England and Wales



(Jansen et al., 2003)

Stochastic SIR model

Event	Update	Propensity
Transmission	$S \rightarrow I$	$\beta I S / N$
Recovery	$I \rightarrow R$	γI

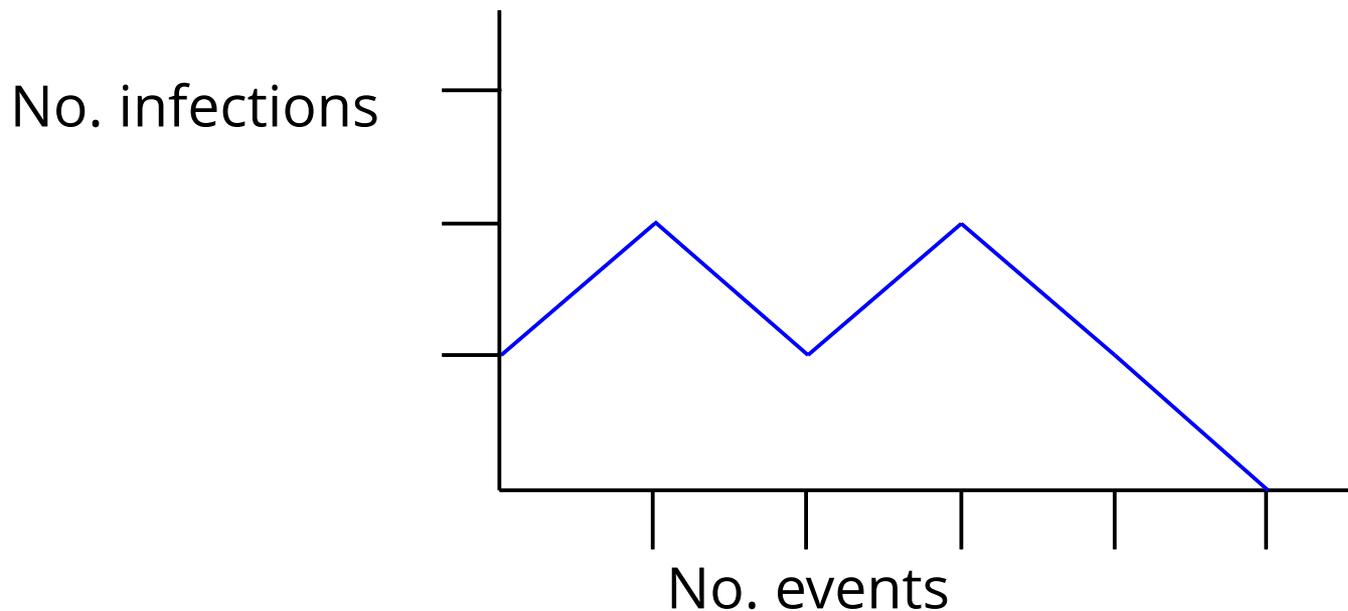
$$\text{Reproduction number} = \beta S / N \times (1 / \gamma)$$

If no major outbreaks, then: $S / N \approx 1 - c$

Random walk embedded in the SIR model

$$p = \Pr(\text{transmission} | \text{event})$$

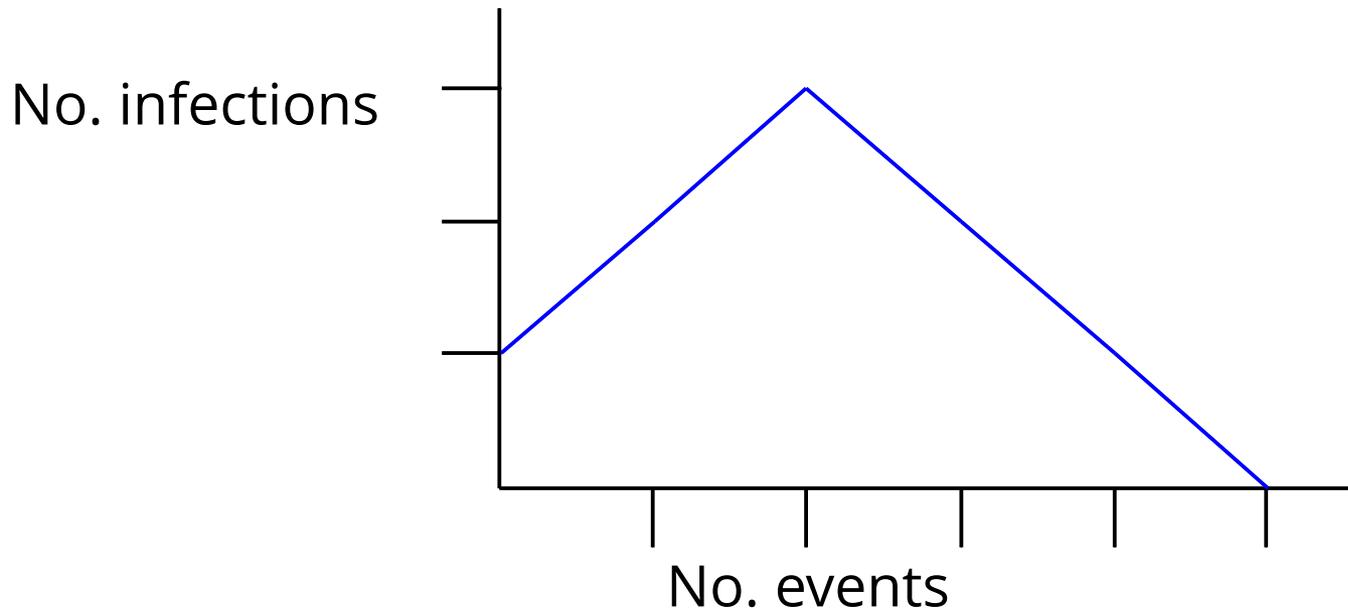
$$q = \Pr(\text{recovery} | \text{event})$$



Random walk embedded in the SIR model

$$p = \Pr(\text{transmission} \mid \text{event})$$

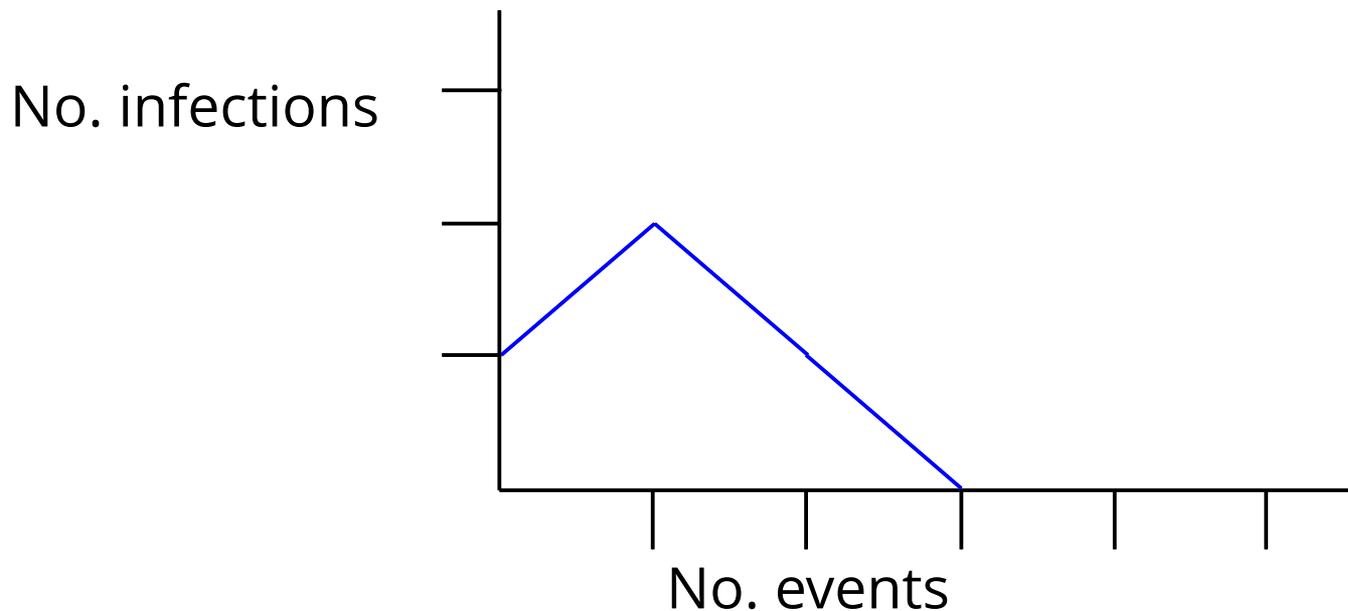
$$q = \Pr(\text{recovery} \mid \text{event})$$



Random walk embedded in the SIR model

$$p = \Pr(\text{transmission} | \text{event})$$

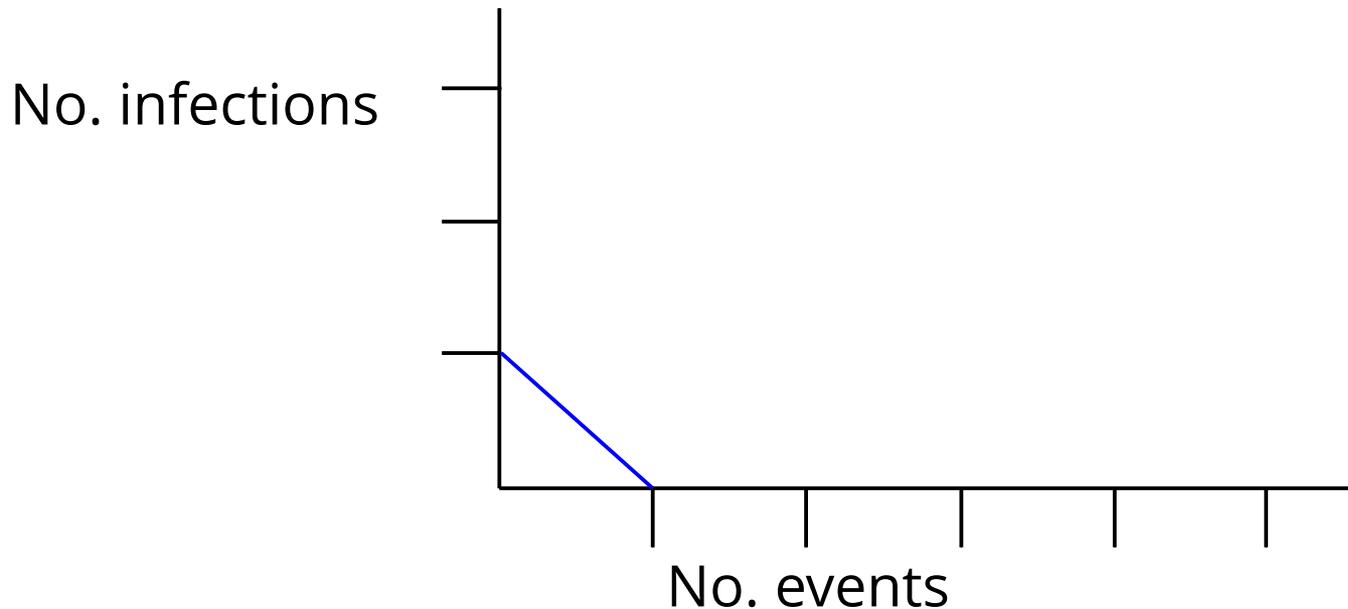
$$q = \Pr(\text{recovery} | \text{event})$$



Random walk embedded in the SIR model

$$p = \Pr(\text{transmission} \mid \text{event})$$

$$q = \Pr(\text{recovery} \mid \text{event})$$



The easy way to find the expected number of events

D_z = expected no. events given z infections

$$D_z = pD_{z+1} + qD_{z-1} + 1 \quad z > 0$$

$$D_z = 0 \quad z = 0$$

Satisfied by:

$$D_z = z / (q - p)$$

Translation to an estimator for R

x = expected outbreak size

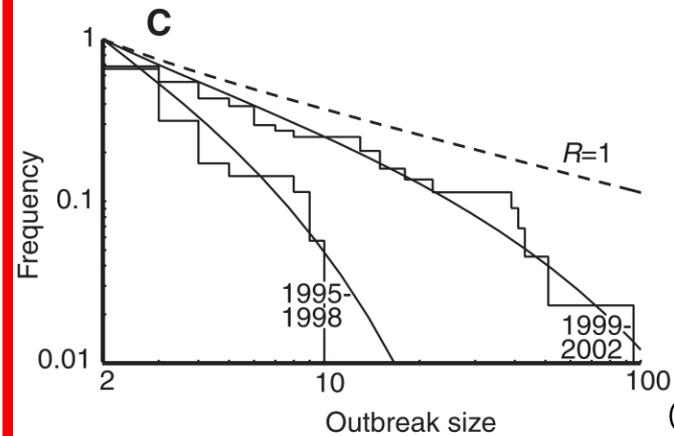
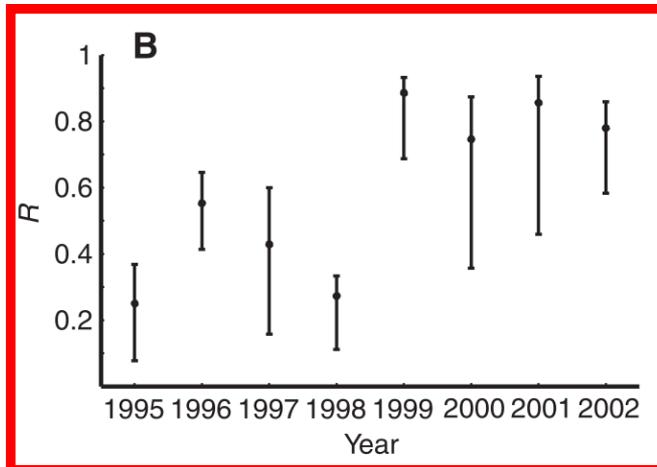
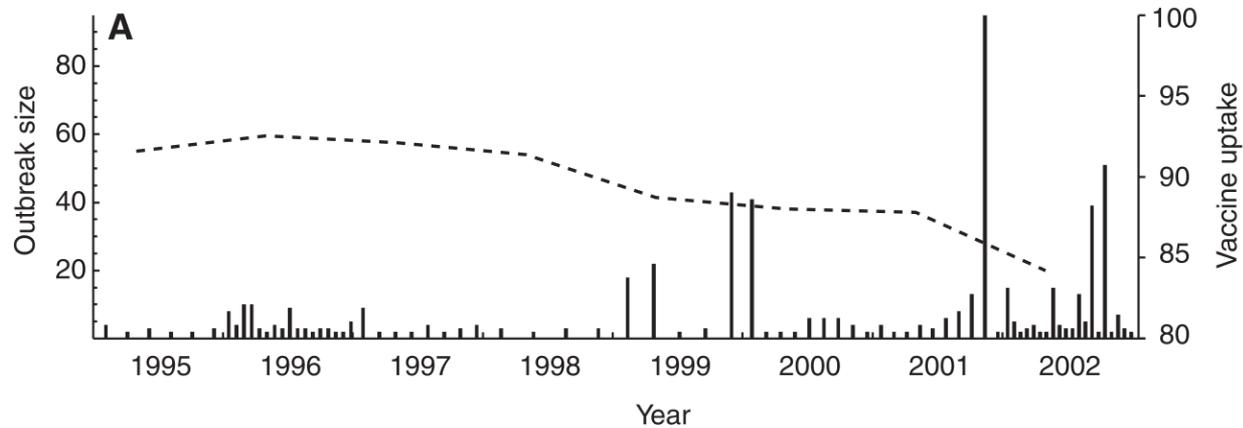
$$z = 1, \quad p = R/(1 + R), \quad q = 1/(1 + R)$$

$$D_z = z/(q - p) \rightarrow x = 1/(1 - R)$$

m = expected size, outbreaks with 2+ cases

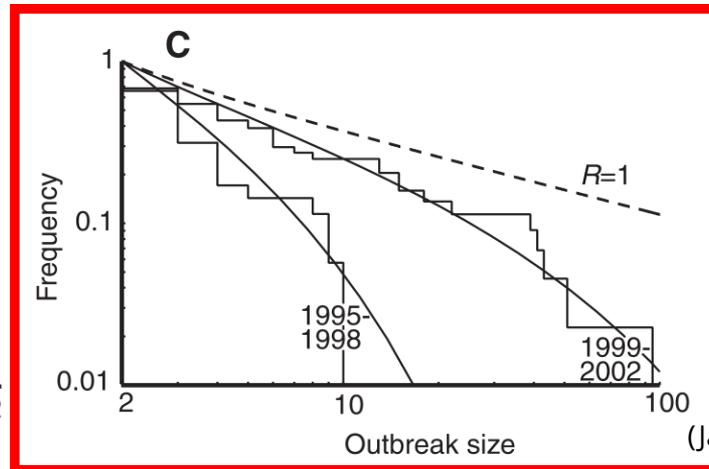
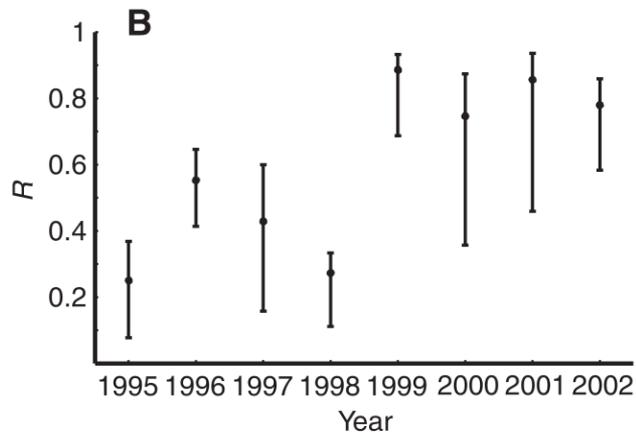
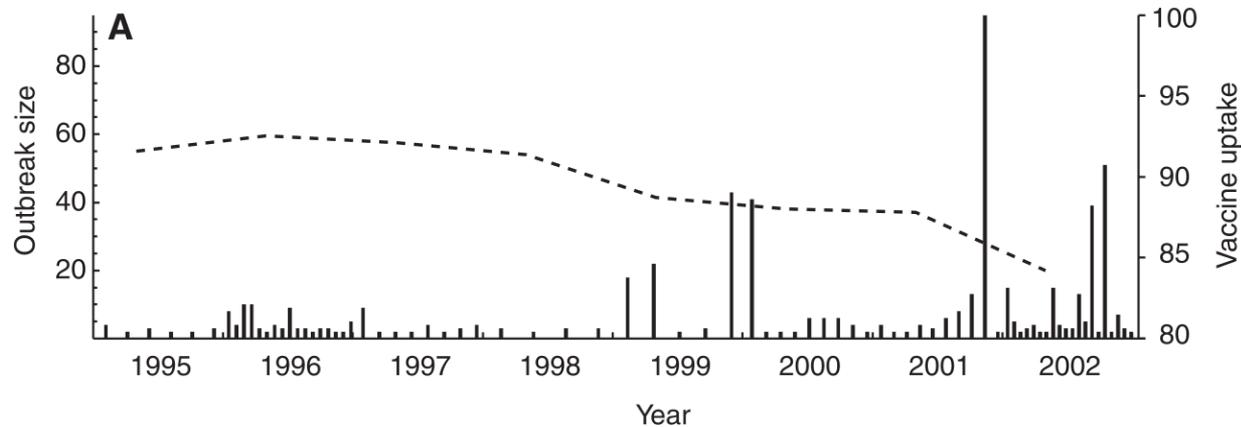
$$m = 2/(1 - R)$$

Measles in England and Wales



(Jansen et al., 2003)

Measles in England and Wales



(Jansen et al., 2003)

How to find the distribution of outbreak sizes

Probability of reaching 0 in n steps starting at z :

$$u_{z,n} = \frac{z}{n} \binom{n}{\frac{n+z}{2}} p^{(n-z)/2} q^{(n+z)/2}$$

Substitutions to get the probability that outbreak size = x :

$$z = 1, \quad n = 2x - 1, \quad p/q = R$$

$$q(x) = u_{1,(2x-1)} = \frac{R^{x-1}}{(R+1)^{2x-1}} \frac{(2x-2)!}{x!(x-1)!}$$

Simplifying the distribution when $R = 1$

$$q(x) = 2^{1-2x} \frac{(2x-2)!}{x!(x-1)!} \quad \text{Substitute } R=1 \text{ into general formula}$$

$$q(x) = 2^{1-2x} \frac{\Gamma(2x-1)}{\Gamma(x+1)\Gamma(x)} \quad \text{Write in terms of Gamma function}$$

$$q(x) = \frac{1}{2\sqrt{\pi}} \frac{\Gamma(x-1/2)}{\Gamma(x+1)} \quad \text{Use Gamma duplication formula}$$

$$q(x) \sim \frac{e^{3/2}}{2\sqrt{\pi}} \frac{(x-1/2)^{(x-1/2)}}{(x+1)^{(x+1)}} \quad \text{Use Stirling's approximation}$$

Simplifying the distribution when $R = 1$

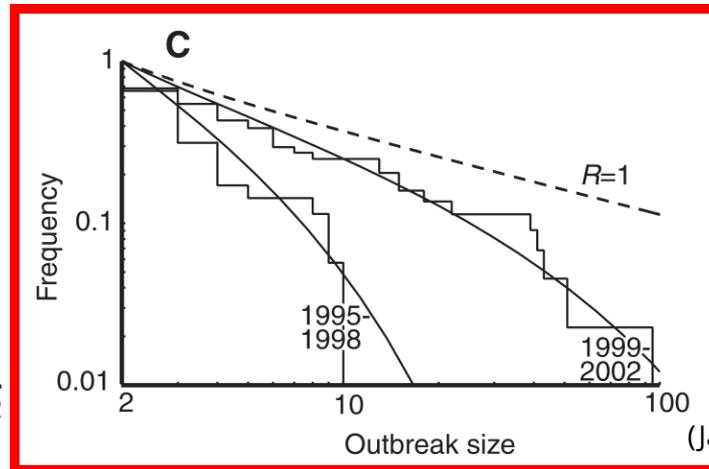
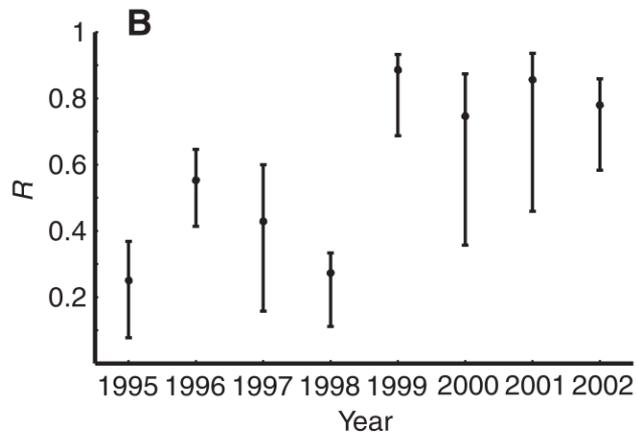
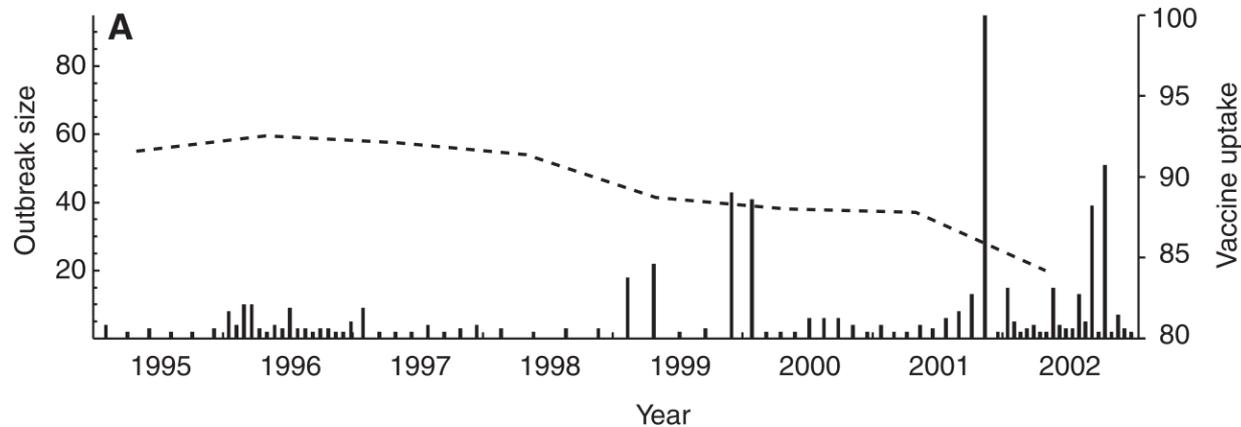
$$q(x) \sim \frac{e^{3/2}}{2\sqrt{\pi}} \frac{(x-1/2)^{(x-1/2)}}{(x+1)^{(x+1)}} \quad \text{Use Stirling's approximation}$$

$$q(x) \sim \frac{x^{-3/2}}{2\sqrt{\pi}} \quad \text{Taylor expand on log scale}$$

Integrate to obtain probability that $x > n$:

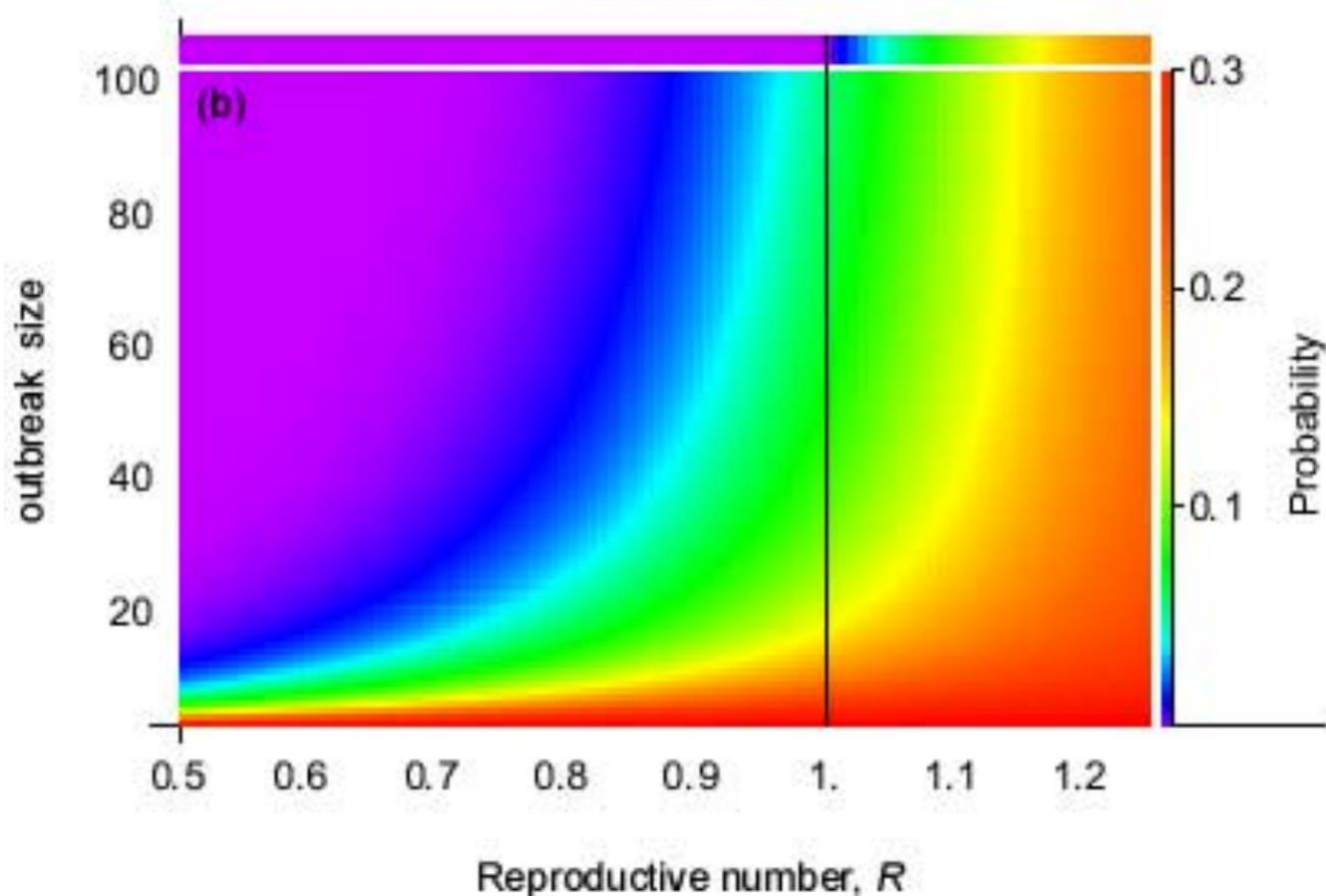
$$\int_{x=n}^{\infty} q(x) dx \sim \int_{x=n}^{\infty} \frac{x^{-3/2}}{2\sqrt{\pi}} dx = \frac{n^{-1/2}}{\sqrt{\pi}}$$

Measles in England and Wales

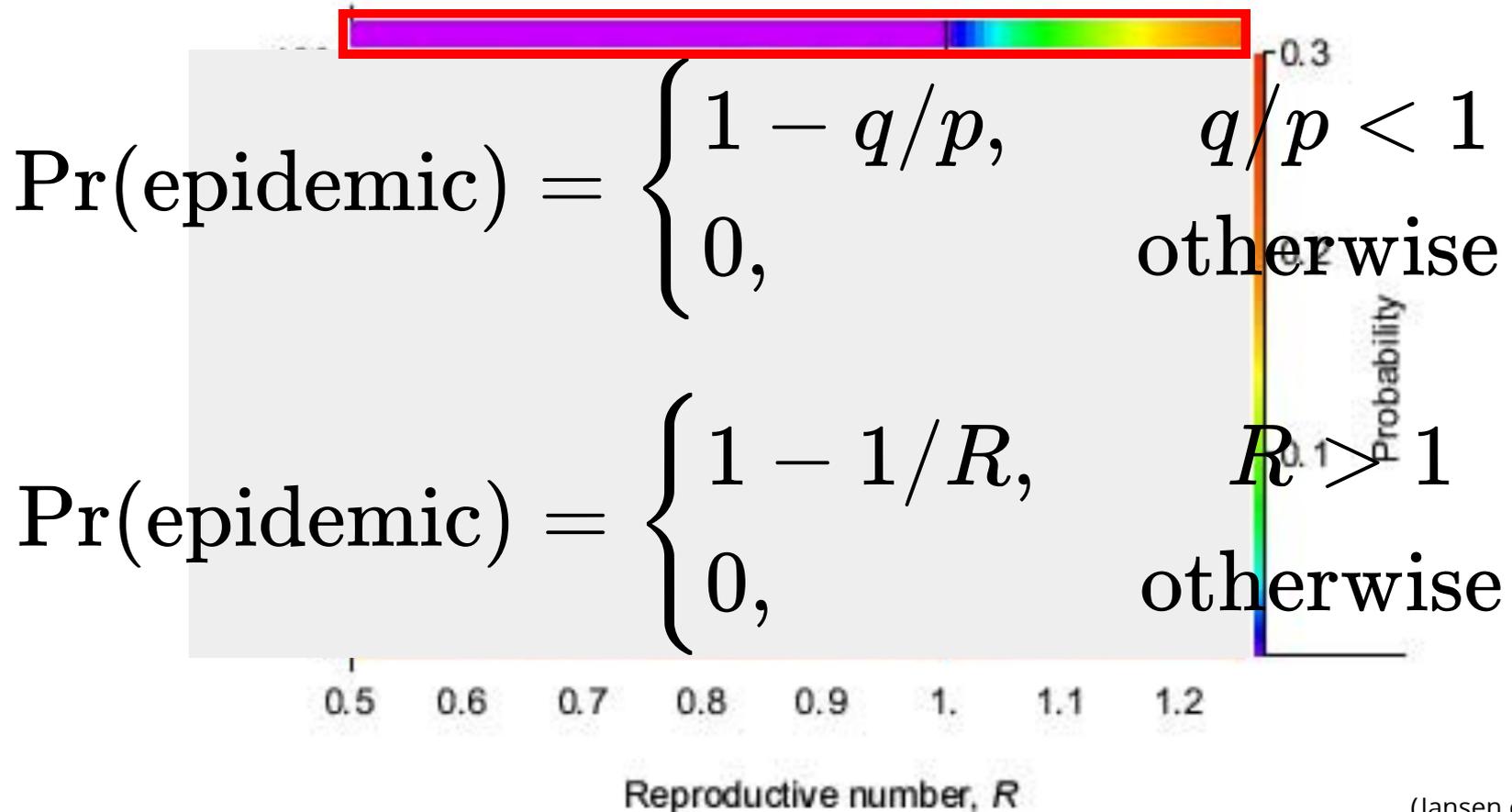


(Jansen et al., 2003)

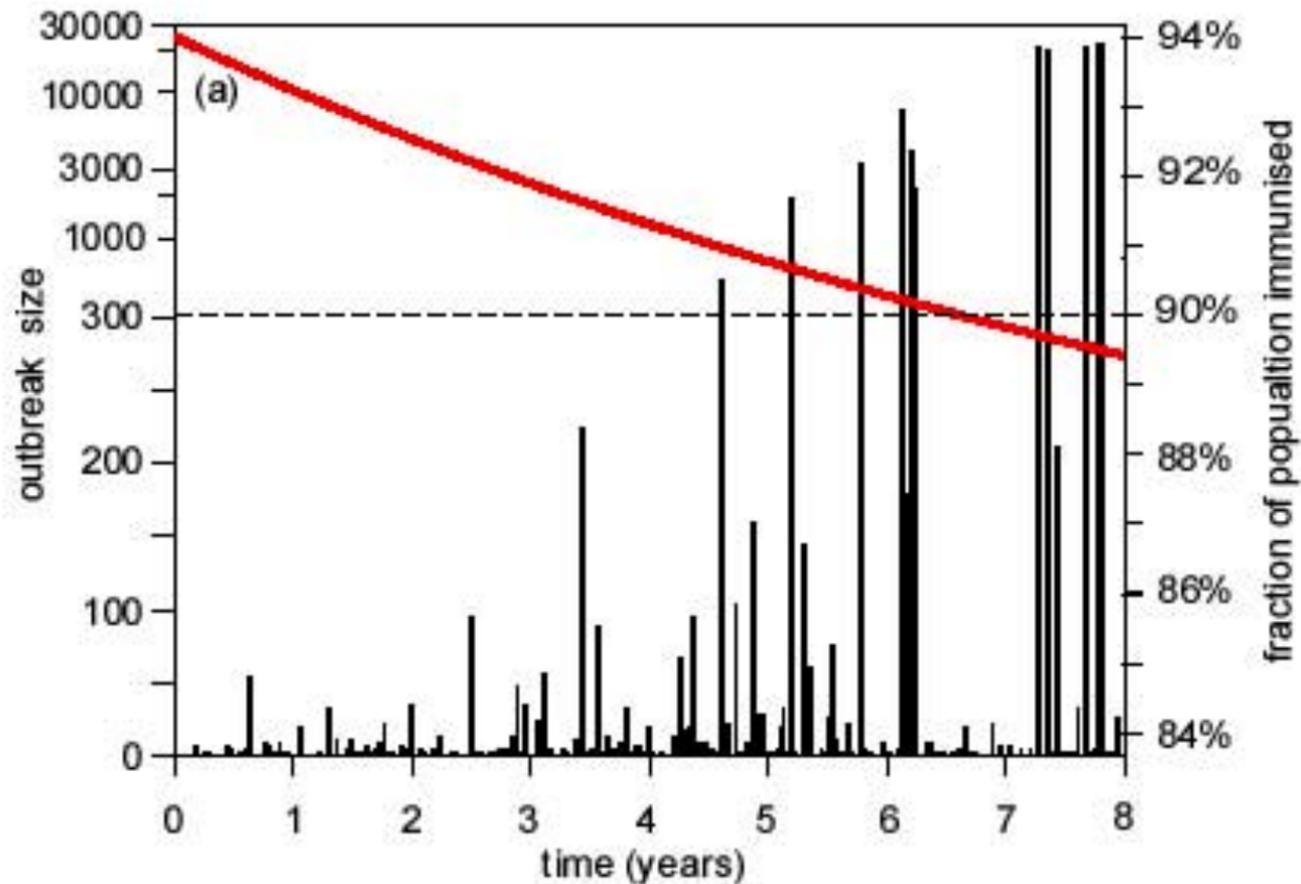
The distribution of outbreak sizes changes smoothly



Pr(epidemic) also follows from random walk results



Models with declining vaccination resemble data

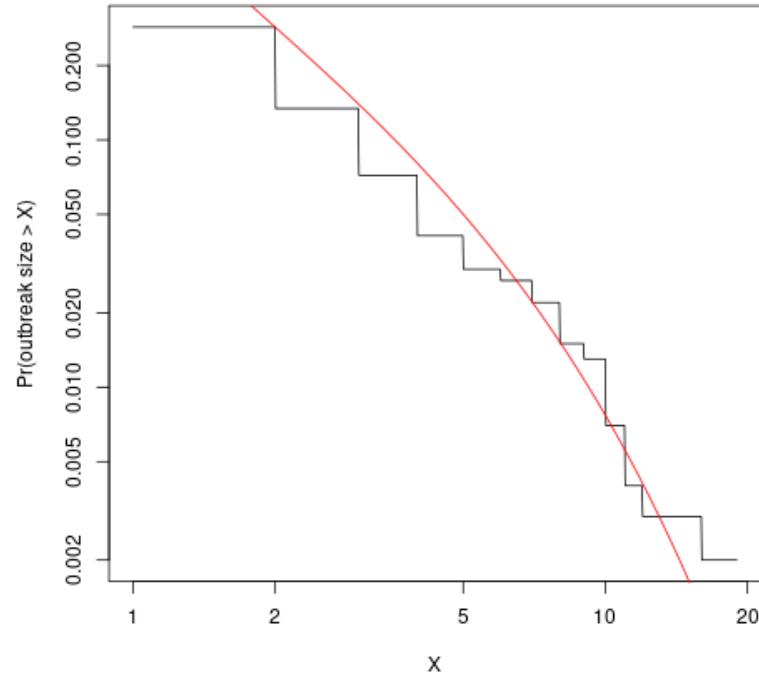


How would the time series of the number infected also indicate declining vaccination?

Suggested method of investigation? Try this in R:

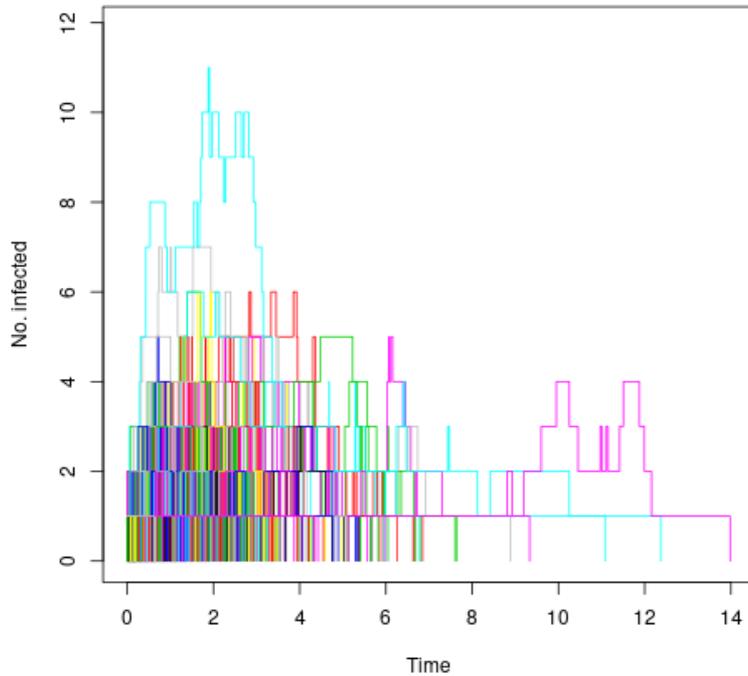
```
source("http://ebodea.name/obplots.R")  
  
make_outbreak_plots(R = 0.1, nsims = 1000)  
make_outbreak_plots(R = 0.9, nsims = 1000)
```

Simulations verify theory for outbreak size distribution

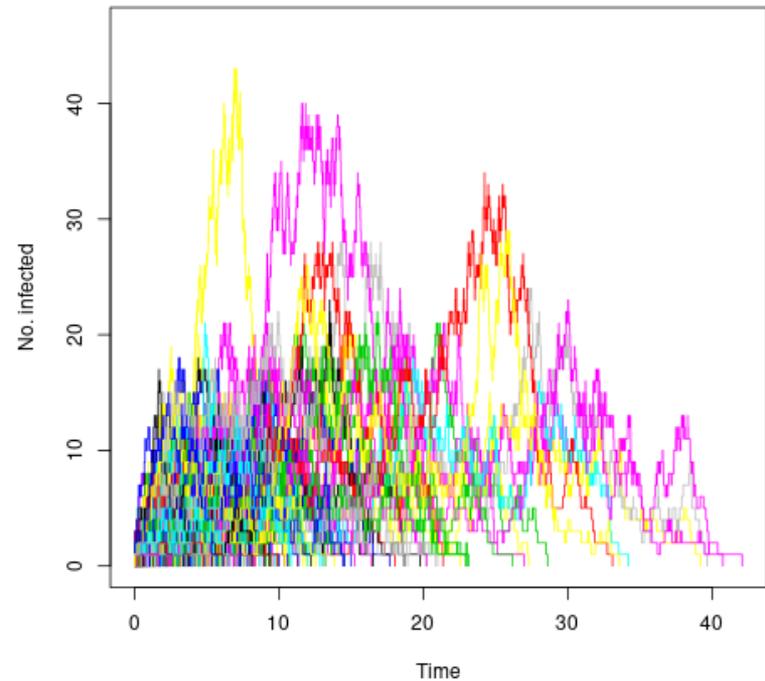


How might we quantify the change in trajectories?

$R = 0.4$



$R = 0.9$



Reading 2:

Early warning signals of dynamic bifurcation in the emergence of monkeypox virus

SIR model with repeated introductions and demography

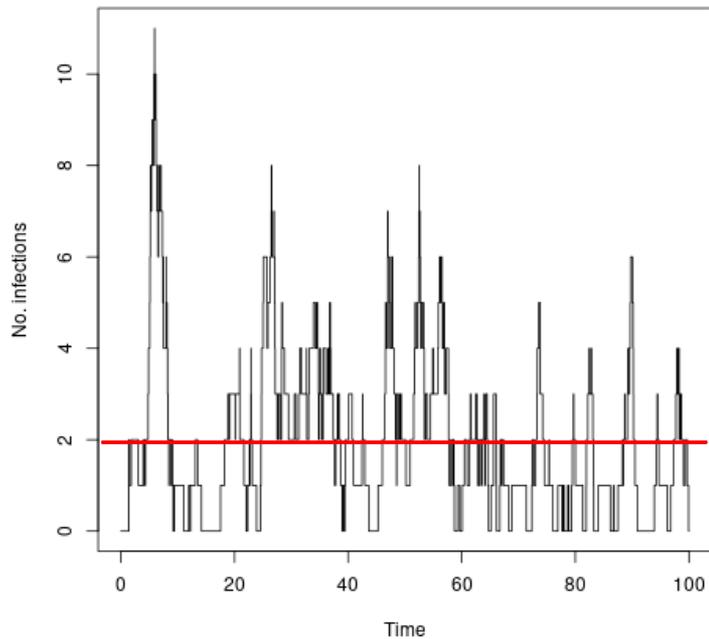
Event	Update	Propensity
Transmission	$S \rightarrow I$	$\beta I S$
Recovery	$I \rightarrow R$	γI
Introduction	$S \rightarrow I$	ξS
Birth	$\emptyset \rightarrow S$	$\mu(S + I + R)$
Death of S, I, or R	$S, I \text{ or } R \rightarrow \emptyset$	$\mu S, \mu I, \text{ or } \mu R$

Reproduction number $\approx \beta S / \gamma$

Variance of model with multiple introductions also indicates criticality

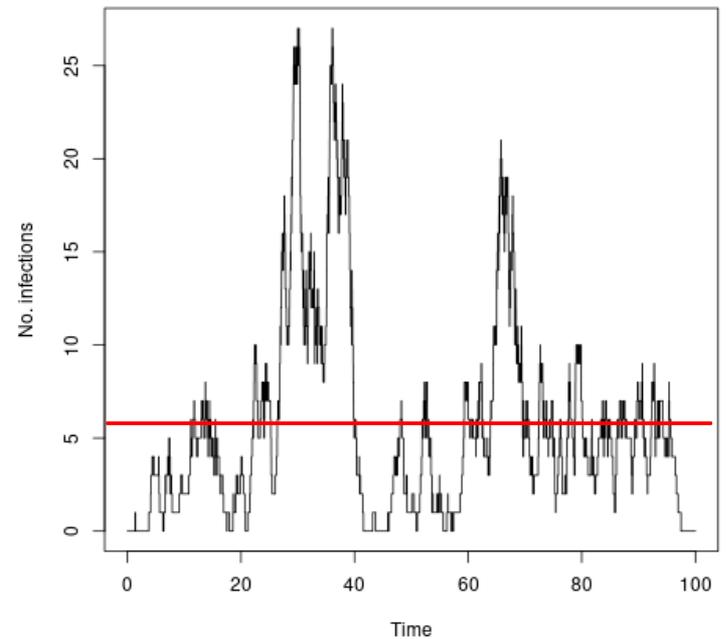
$R = 0.4$

Variance = 3



$R = 0.9$

Variance = 30

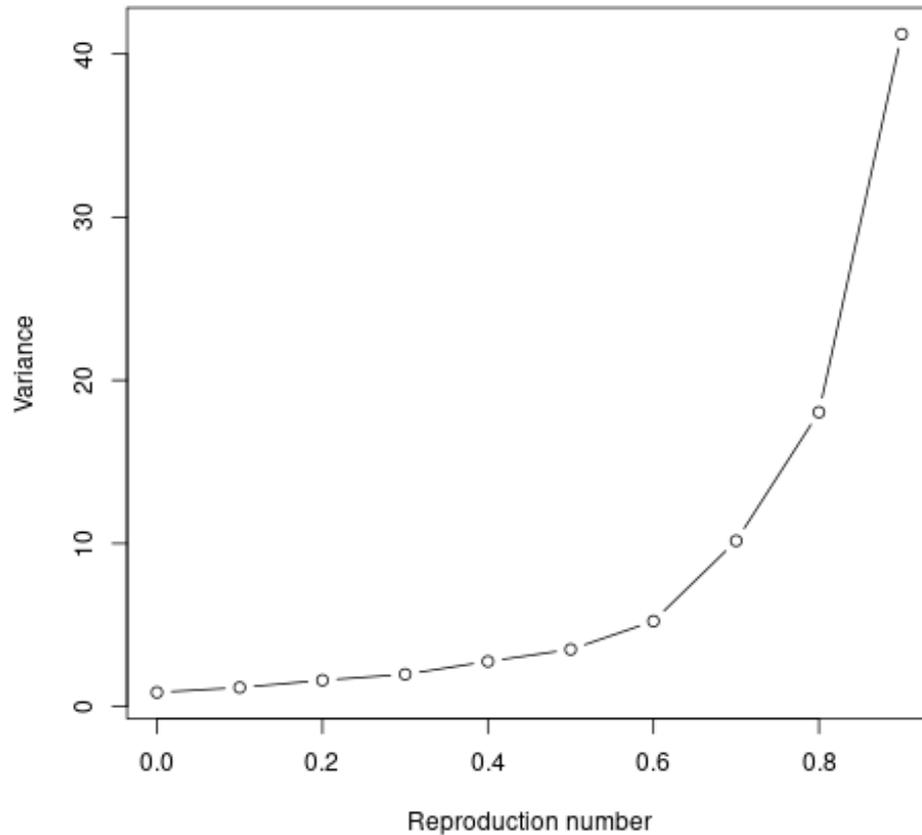


Mean

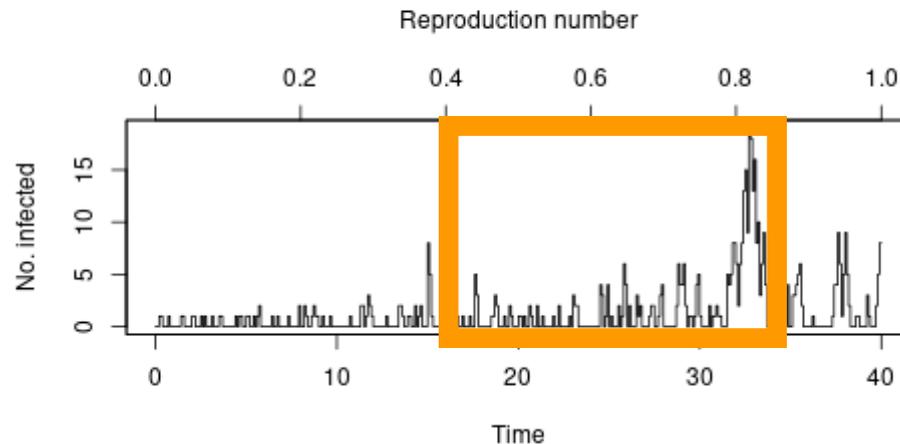
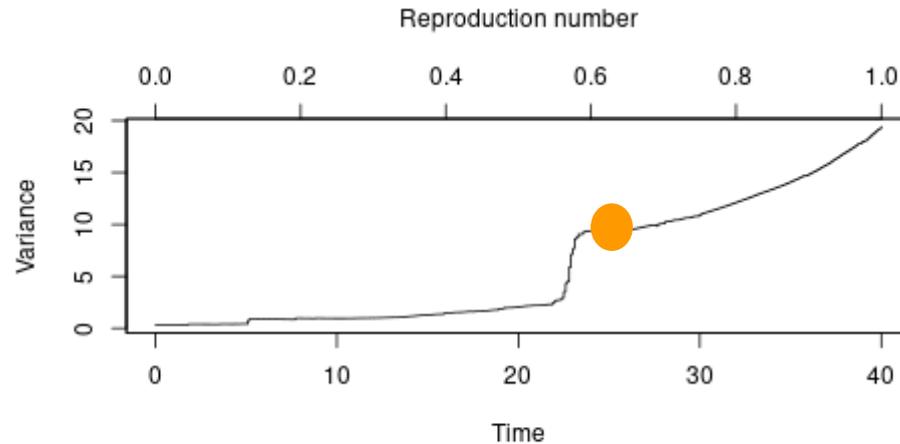
Variance is inversely proportional to $1 - R$

As R approaches 1 from below:

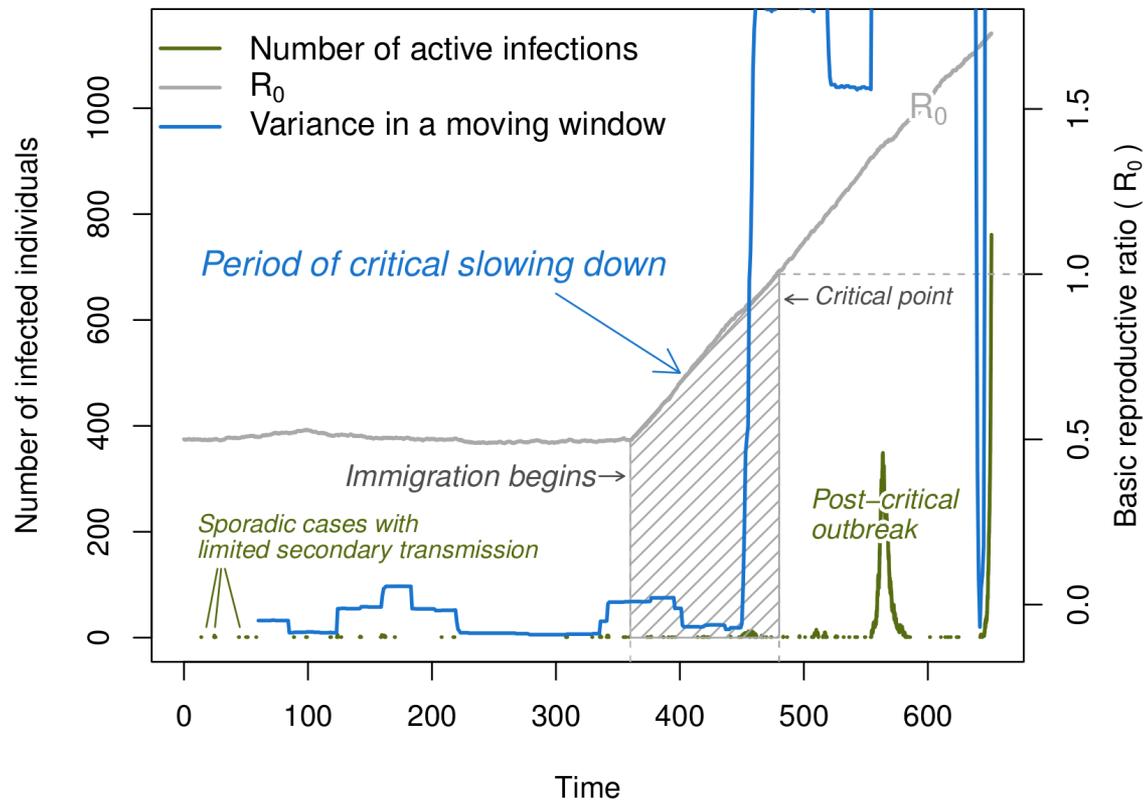
- Variance increases
- Rate of increase increases



Windowed variance can detect slow trends in R

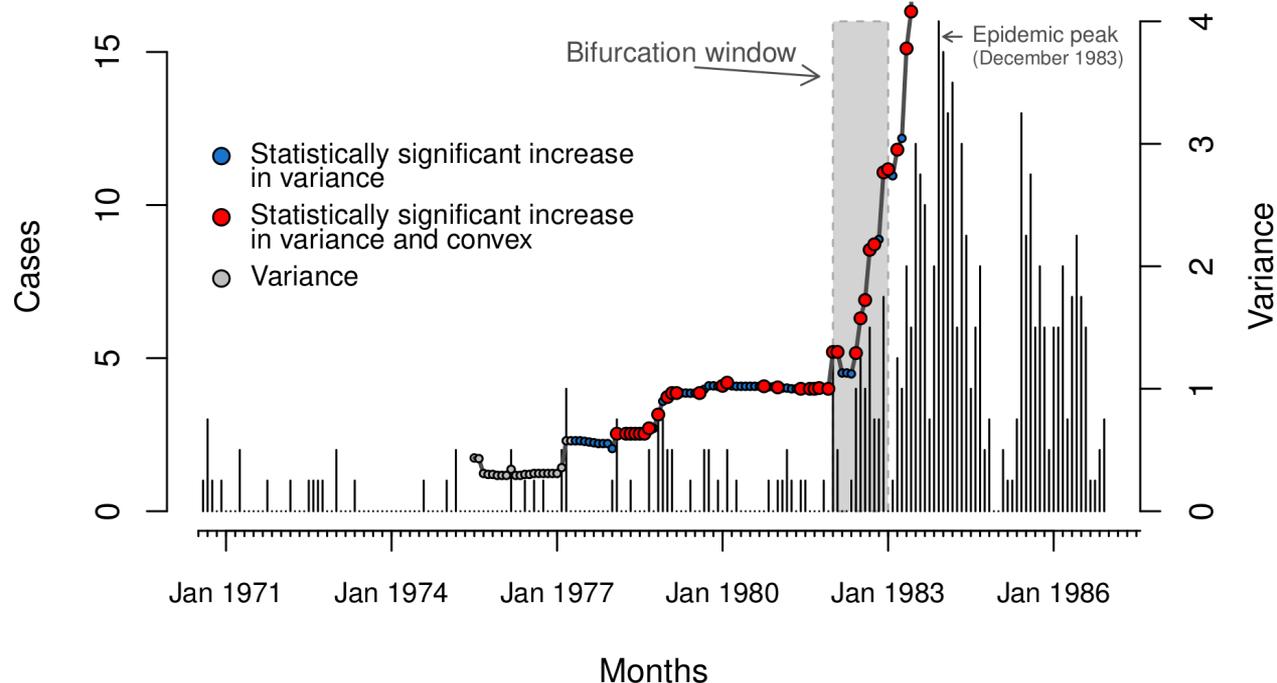


Simulation results supported MKXV application



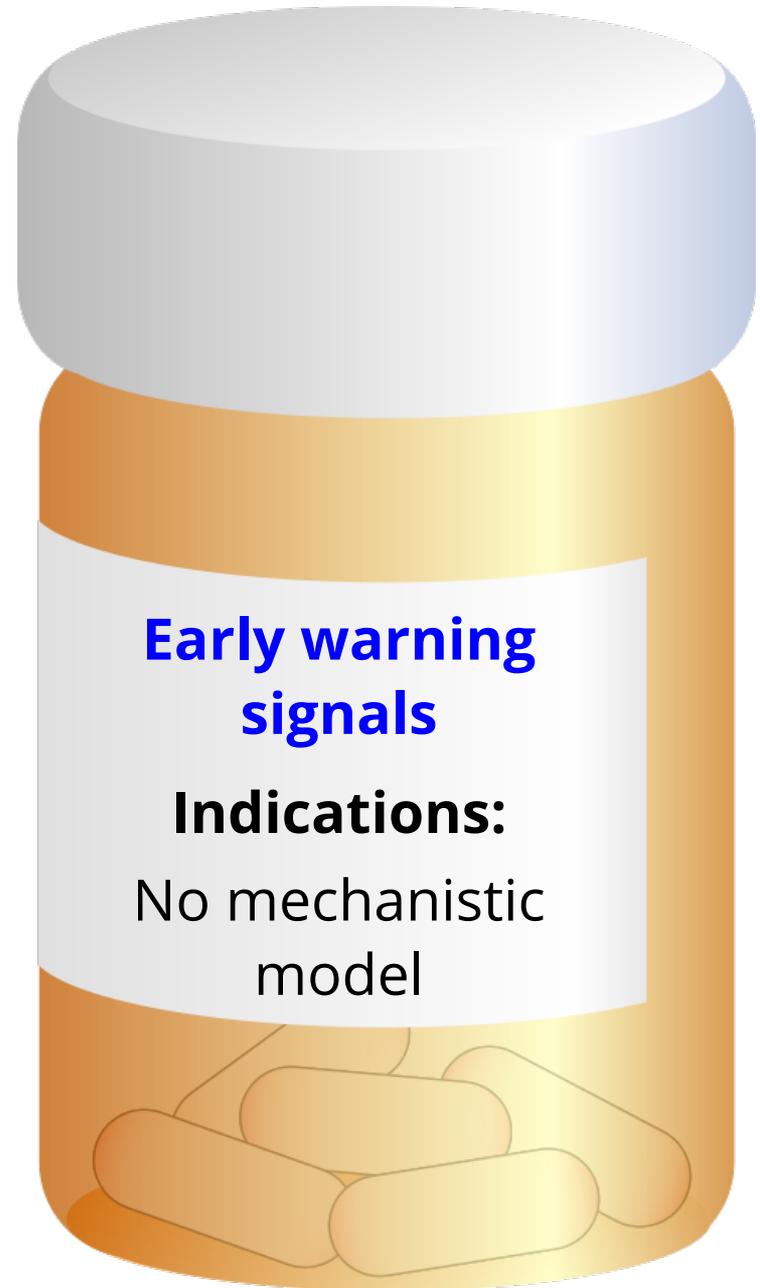
Variance of real data does accelerate up before epidemic

Monkeypox in Central and West Africa



This approach may improve predictability of epidemics

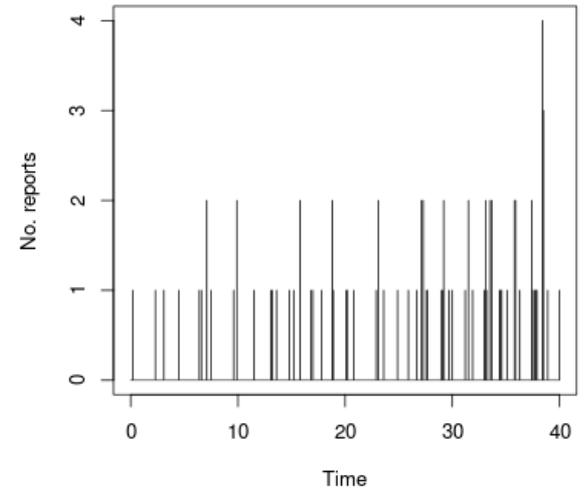
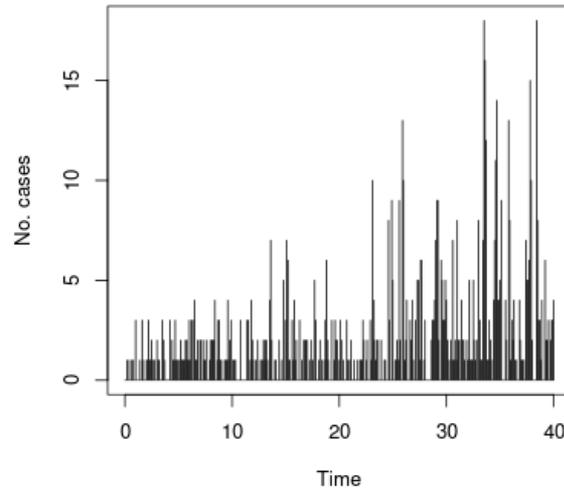
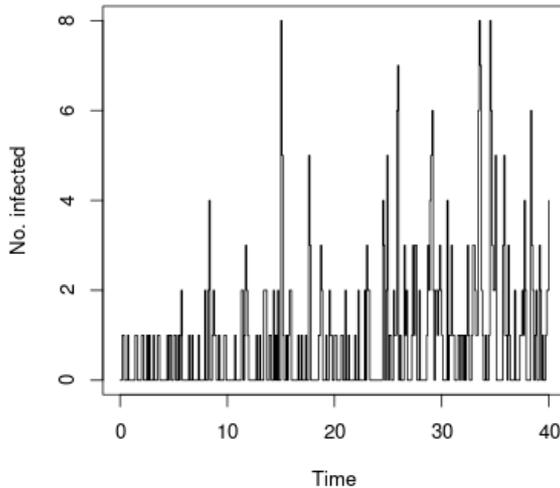
We are investigating the conditions under which variance and other statistics may allow for emergence of infectious diseases to be better predicted.



Evaluating an approach to a threshold

We rarely observe the actual number infected

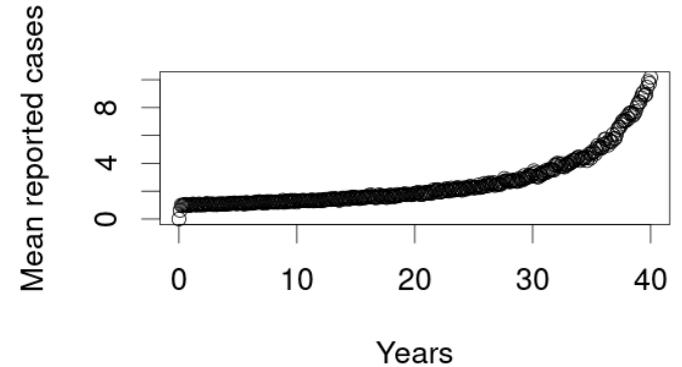
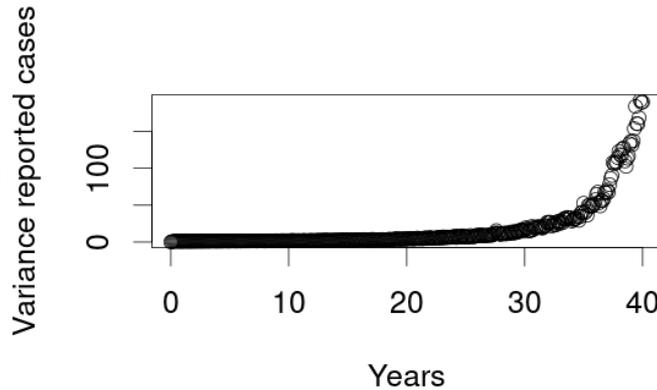
- More likely to observe the count of removals per reporting period
- Counts are usually incomplete



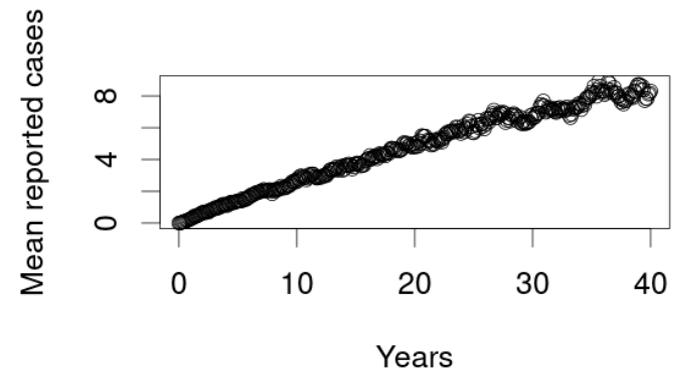
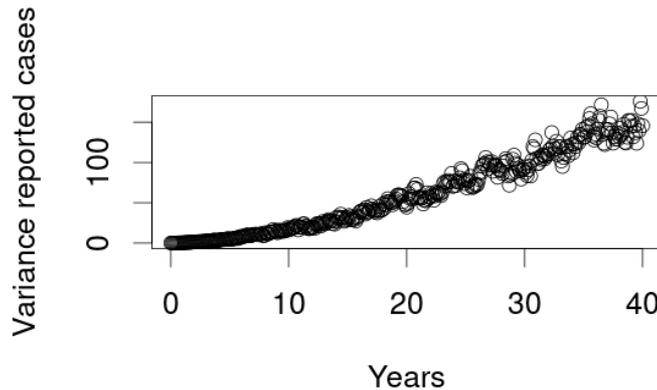
Can we distinguish between an increase in cases and reporting?

These explanations predict different time trends in variance

Increase in transmission rate

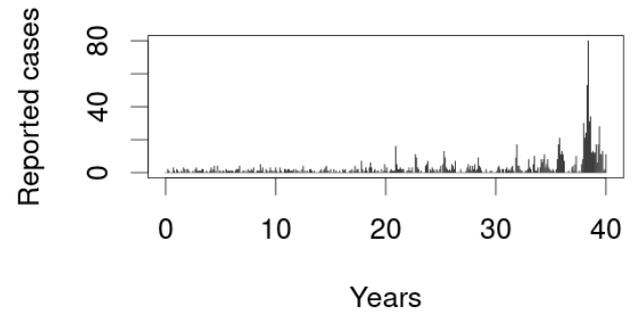
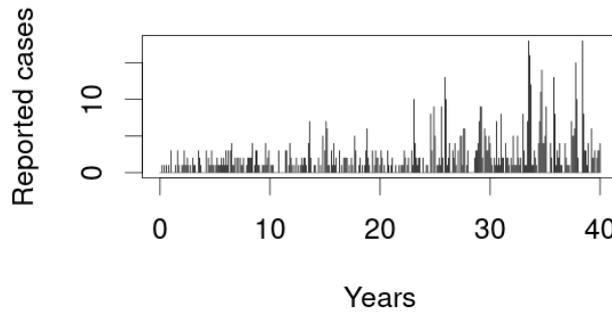


Increase in reporting probability

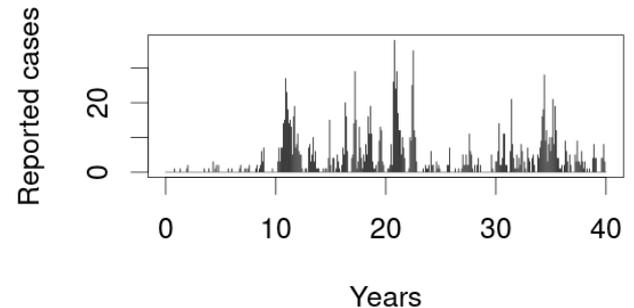
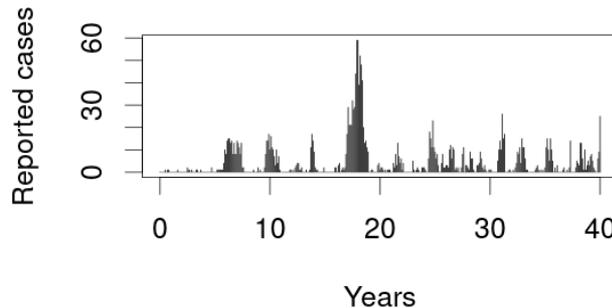


Rolling variance estimates could be used to classify time series

Increase in transmission rate



Increase in reporting probability



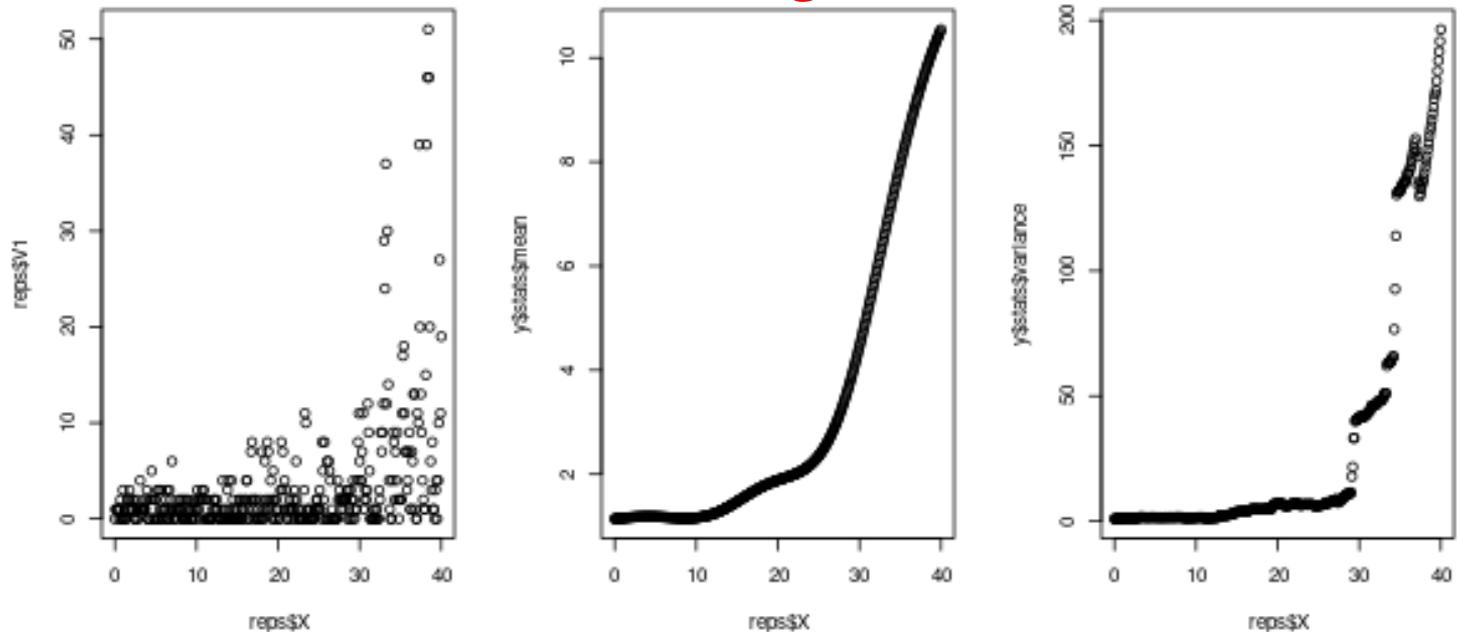
Example in R

```
library(spaero) ## load package for calculating moving window statistics
reps <- read.csv("http://ebodea.name/reports.csv") ## load time series data

y <- get_stats(x = reps$V1, ## time series to use as input
              center_trend = "local_constant", ## estimate mean using moving window
              center_bandwidth = 40, ## window size for mean
              stat_bandwidth = 40) ## window size for other statistics

plot(reps$X, reps$V1) ## plot input time series
plot(reps$X, y$stats$mean) ## plot rolling mean
plot(reps$X, y$stats$variance) ## plot rolling variance
```

Looks like increasing transmission.



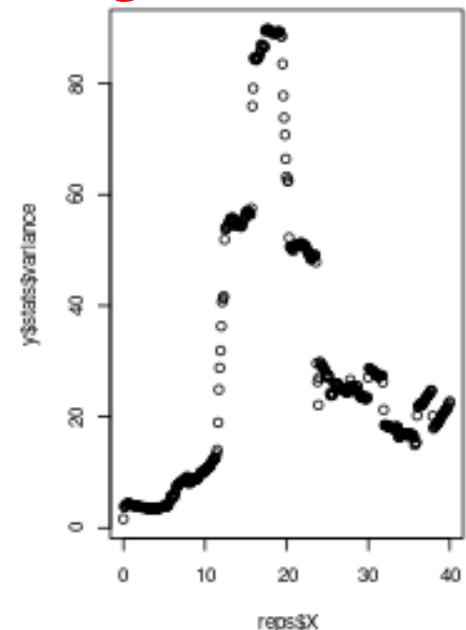
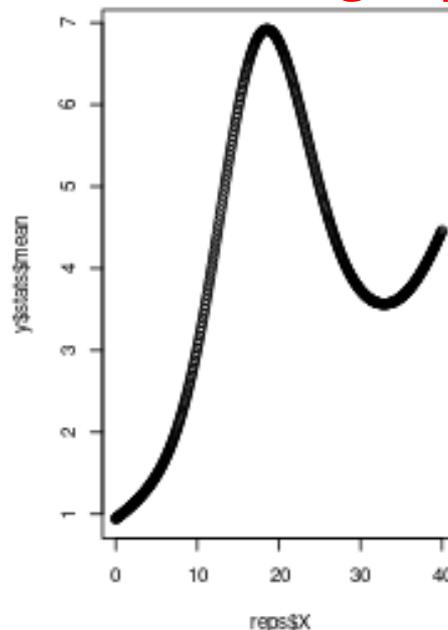
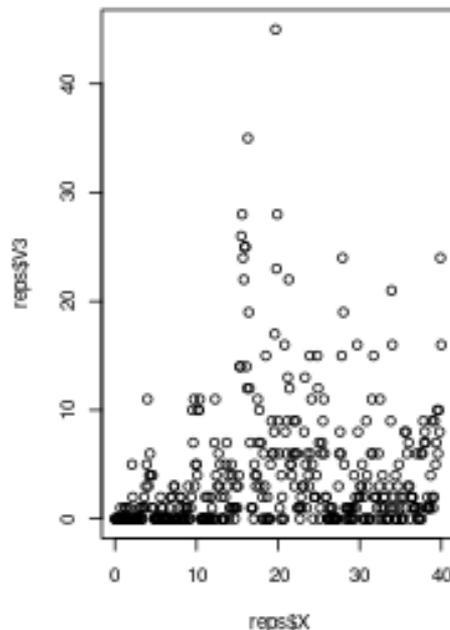
Example in R

```
library(spaero) ## load package for calculating moving window statistics
reps <- read.csv("http://ebodea.name/reports.csv") ## load time series data

y <- get_stats(x = reps$V3, ## time series to use as input
              center_trend = "local_constant", ## estimate mean using moving window
              center_bandwidth = 40, ## window size for mean
              stat_bandwidth = 40) ## window size for other statistics

plot(reps$X, reps$V3) ## plot input time series
plot(reps$X, y$stats$mean) ## plot rolling mean
plot(reps$X, y$stats$variance) ## plot rolling variance
```

Looks like increasing reporting.



The WHO urgently needs your help!

1. There are 2000 time series in the file at <http://ebodea.name/reports.csv>
2. Write an R script that produces a logical vector of length 2000. If element i of the vector is TRUE, it means you have classified V_i as having increasing transmission rate. Work in groups if you'd like.
3. Email your script to ebodea@uga.edu to find out how many you got right.

For documentation of spaero:

```
?get_stats ## read documentation of get_stats  
vignette("spaero-introduction") ## extended documentation of spaero
```