

CHALLENGES IN REPRESENTING SPATIAL STRUCTURE



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IDP, 5th June 2020

Five challenges for spatial epidemic models

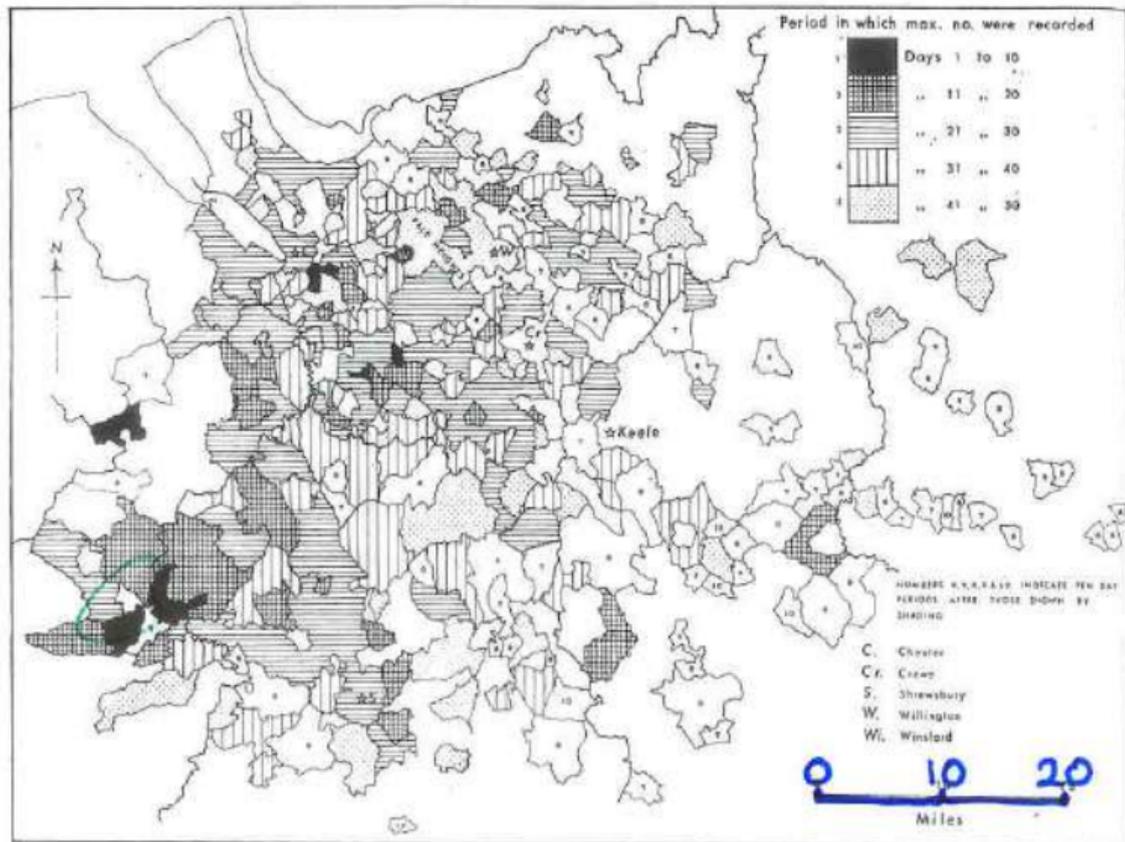
Steven Riley, Ken Eames, Valerie Isham, Denis Mollison,
Pieter Trapman

- 1: How can network models best be constructed to reflect spatial population structure?
- 2: How should we model contact structure in spatially heterogeneous populations?
- 3: How do we define a threshold parameter for spatial models?
- 4: How should we model long-distance interactions?
- 5: On what scale is intervention most effective?

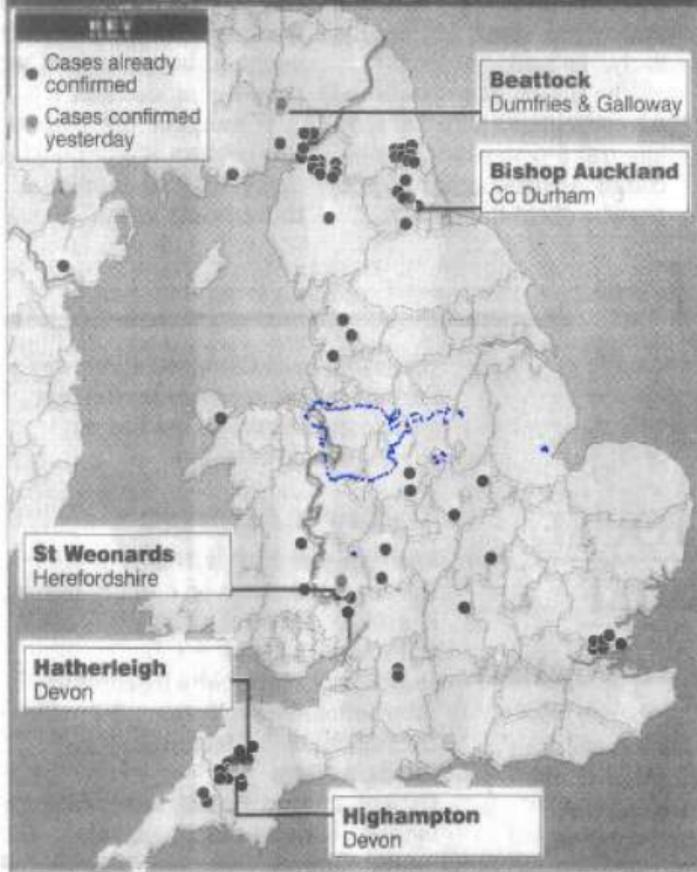
INTERESTS

- *Invasion* – threshold? R_0 ?
- *Spread* – velocity / duration? final size?
- *Persistence?* – pattern? control?

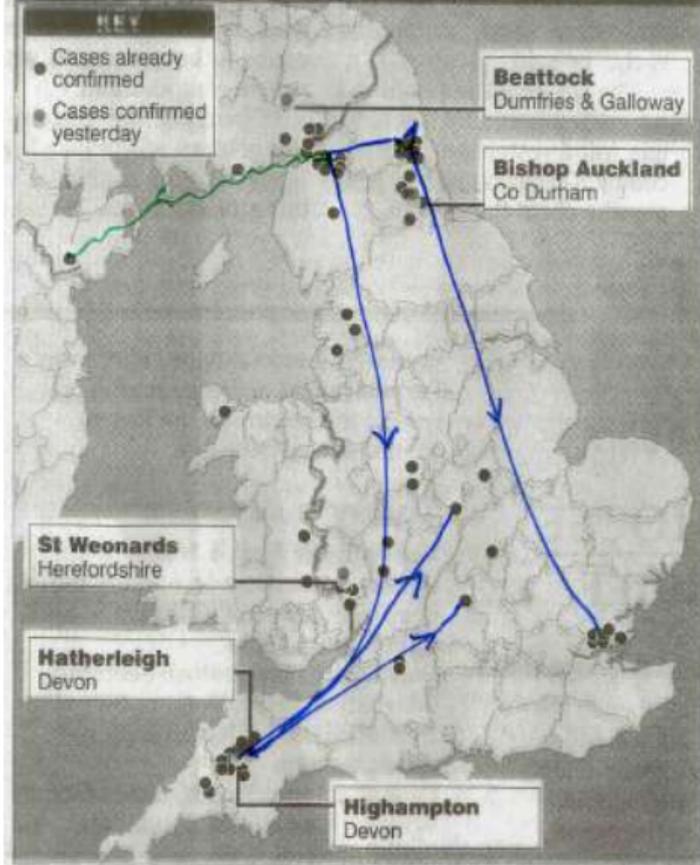
EXAMPLE Foot and mouth disease outbreaks in the UK, 1967-8 and 2001



YESTERDAY'S OUTBREAKS



YESTERDAY'S OUTBREAKS



1967-8: spatial with jumps

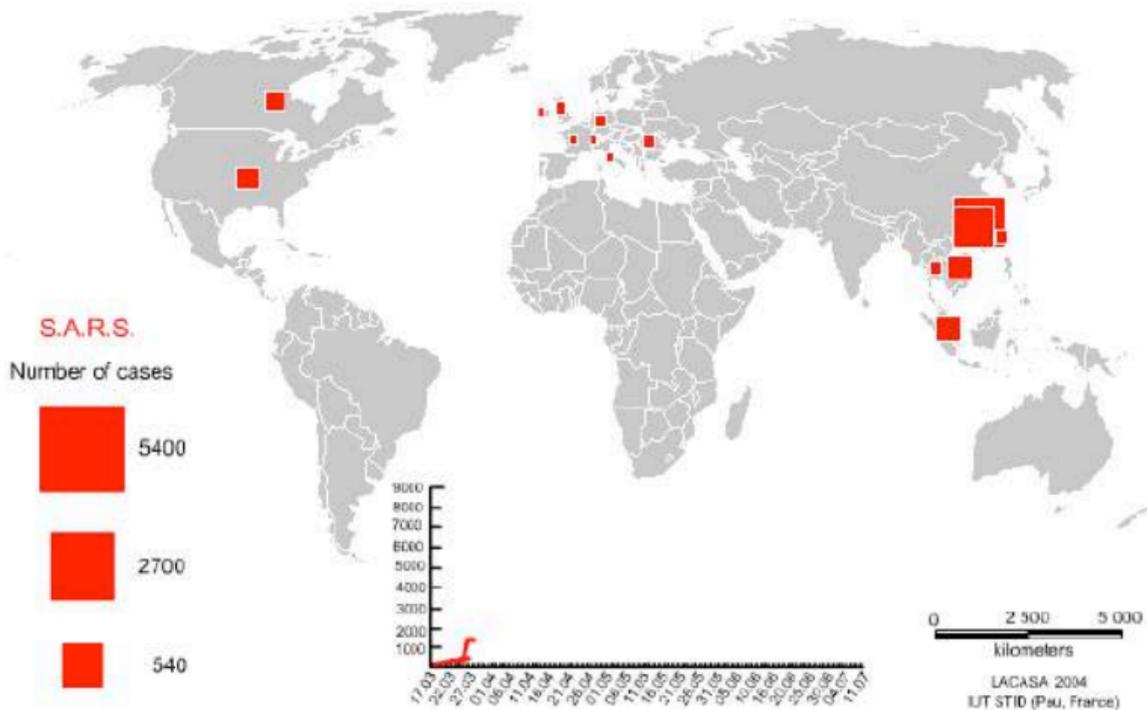
2001: two phases

- global
- spatial with jumps

2003: SARS



27 march 2003

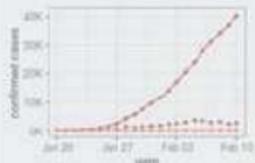


40548 cases

910 deaths

10 February 2020

26 countries affected



China: 40235 (2984 new)

Outside China: 312 (6 new)

Solid lines show cumulative case counts.

Dotted lines show new cases in past 24h.

Select mapping date

2020

10 Feb

20 Jan 20 Feb 03 Feb 17 Feb



2003-SARS

2009-H1N1 (swine flu)

2014-Ebola

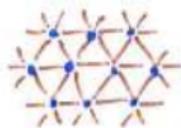
1 How can network models best be constructed to reflect spatial population structure?

e.g. regular lattices,
random geometric graphs,
'small world' models,
clustered graphs,
dynamic networks...

fixed or variable degree distribution

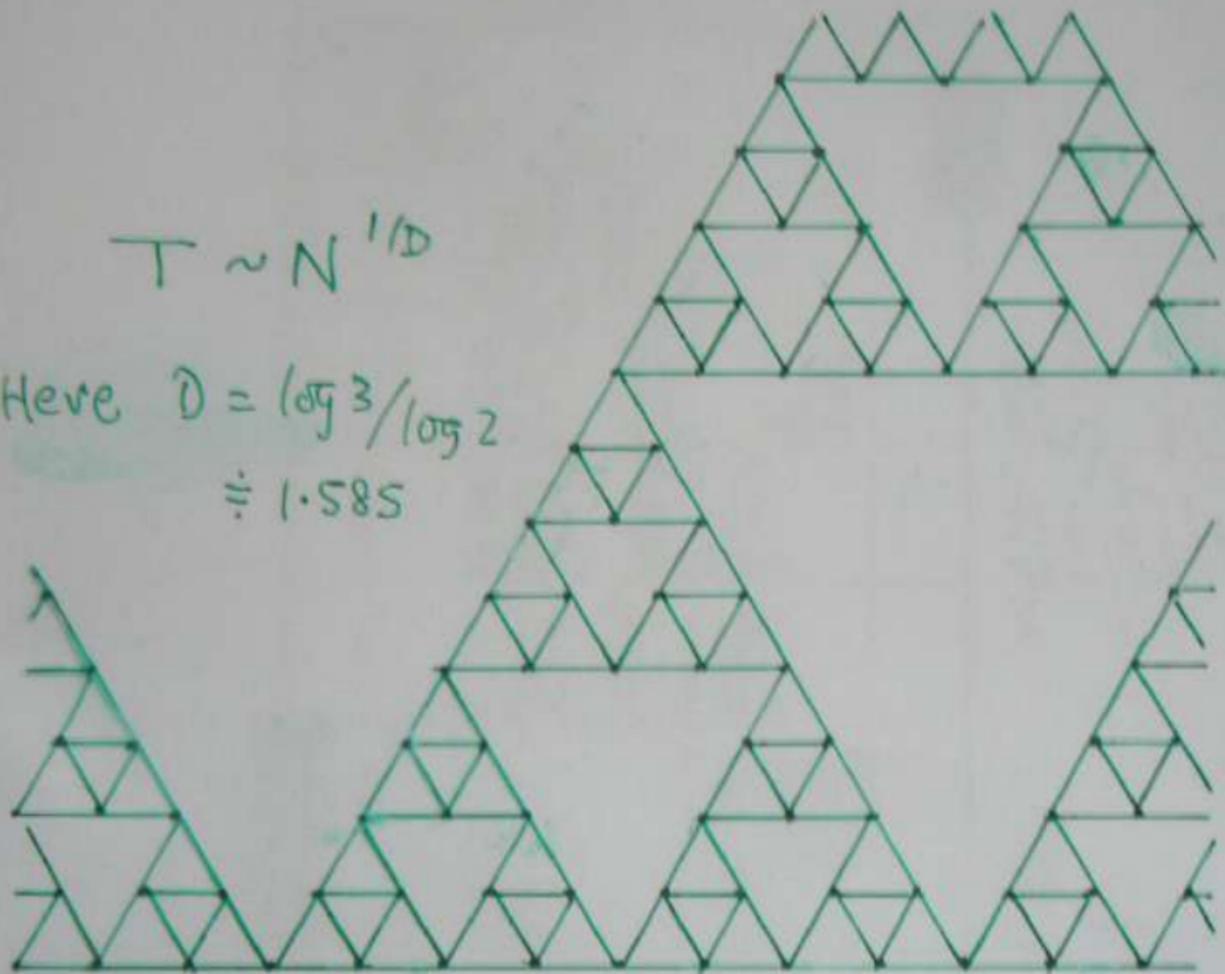
Example

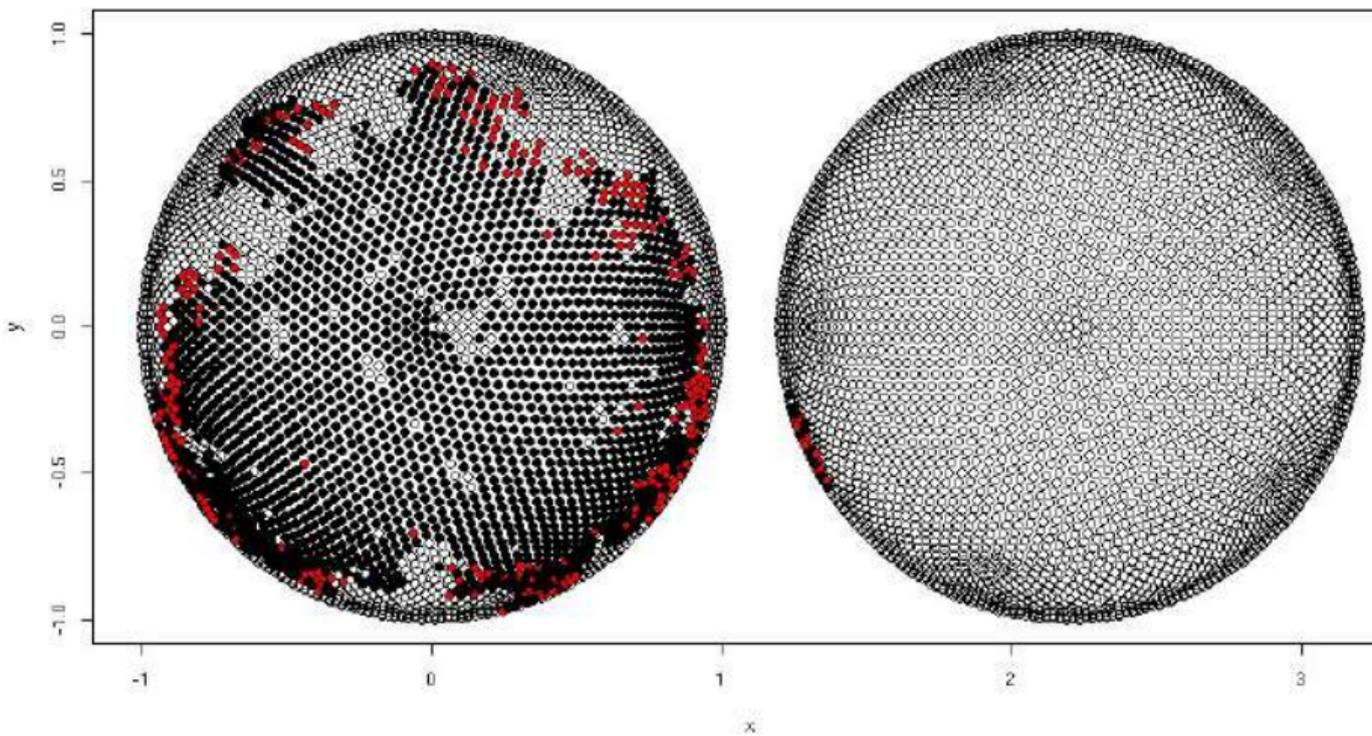
Regular lattice with only nearest-neighbour contacts

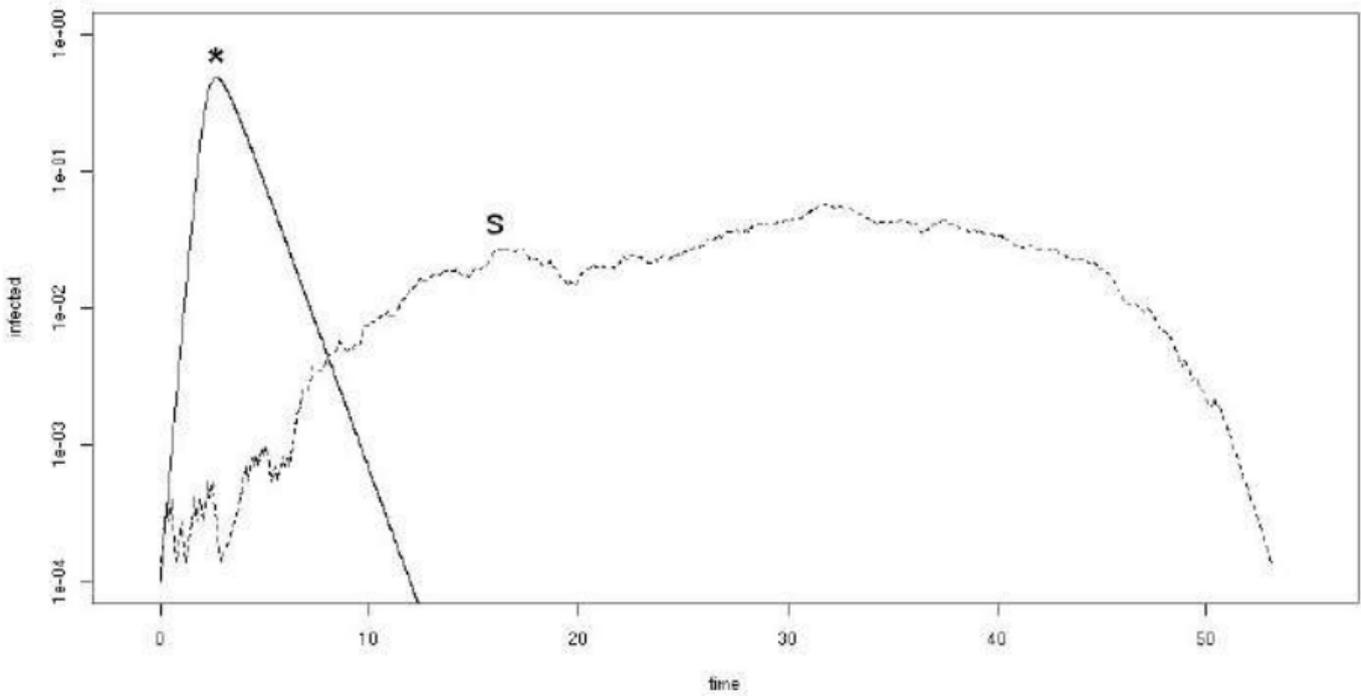


$$T \sim N^{1/D}$$

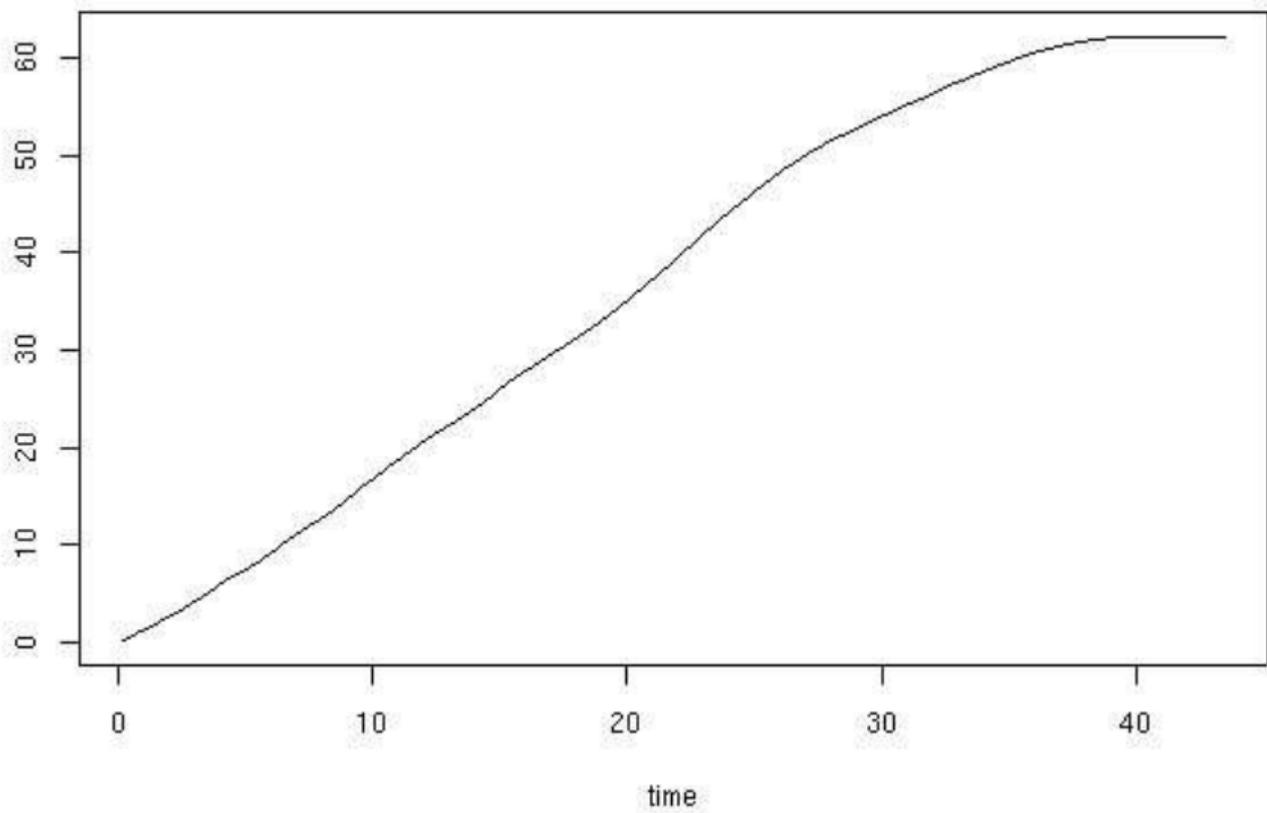
Here $D = \log 3 / \log 2$
 ≈ 1.585







distance



contact/dispersal distribution: nearest-
neighbour \rightarrow Normal/Exp \rightarrow power law

individuals static or mobile?

(diffusion as historic example)

gravity model? $n_1 n_2 / r^2$

Example: Calculation of velocities

Provided the dispersal distribution falls off at least exponentially, deterministic models do provide reasonable approximations.

Many nonlinear spatial deterministic models have been studied, especially diffusion equations (KPP, Fisher, Skellam, ...)

Breakthrough in late 1980s: the approach of Diekmann (and others) shows how linear theory can find velocities for a wide range of nonlinear models.

All you need is the *reproduction and dispersal* kernel K that describes the space-time distribution of the infections made by an individual in a mostly susceptible population.

Can think of K as a space-time version of R_0

Three advantages of the R&D kernel approach:

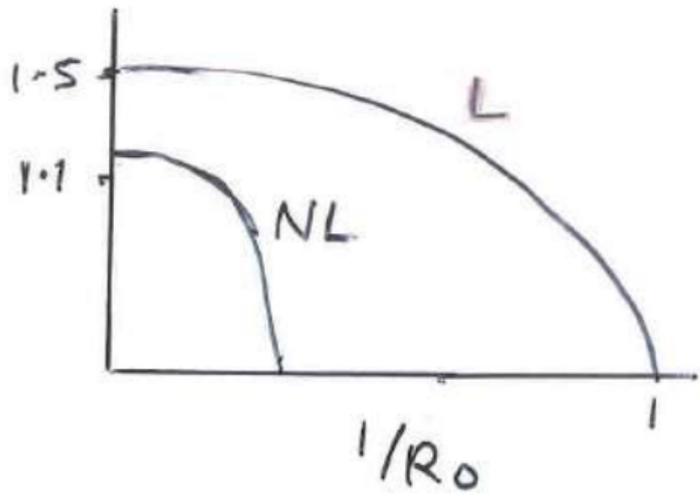
- Much easier to calculate
- Not restricted to DEs and diffusion equations
- Can look at the broad dependence of the velocity on basic components
(*e.g.* is it $\sim \log(R_0)$, $\sim \sqrt{R_0}$ or $\sim R_0$?)

.. but note

These calculated velocities are somewhat larger than those of the more realistic individual stochastic models -

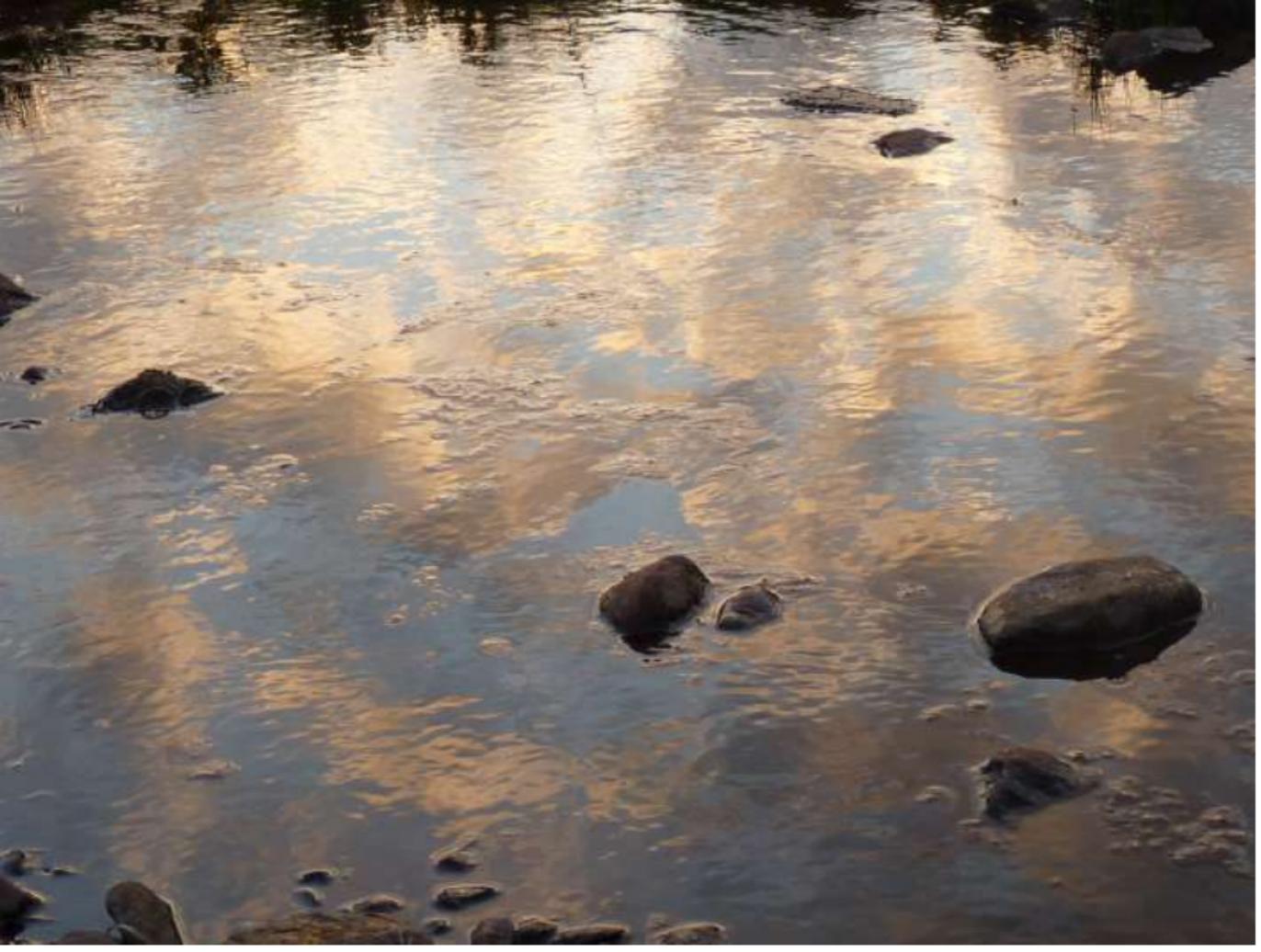
2-D

vel. ↑



velocities of ne-ne SIR

The problem is treating the population as continuous (atto-foxes) rather than determinism *per se*



Example 2: Pair approximations

Does local correlation capture spatial structure?

Recall the deterministic SIR:

$$\begin{aligned}\dot{S} &= -\beta SI \\ \dot{I} &= \beta SI - \gamma I \\ \dot{R} &= \gamma I\end{aligned}$$

More accurately

$$\dot{S} = -\beta[SI]$$

$$\dot{I} = \beta[SI] - \gamma I$$

$$\dot{R} = \gamma I$$

$$[\dot{S}S] = -2\beta[SSI]$$

$$[\dot{S}I] = \beta([SSI] - [SI] - [ISI]) - \gamma[SI]$$

$$[\dot{S}R] = \dots$$

$$[\dot{I}I] = \dots$$

For closure, use

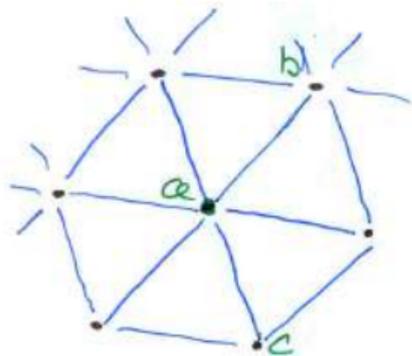
$$[ABC] \approx \left(1 - \frac{1}{n}\right) \frac{[AB][BC]}{[B]} \\ \times \left(1 - \phi + \phi \frac{[AC]}{[A][C]}\right)$$

where

$$\phi = P(ac|ab \ \& \ bc)$$

(Keeling 1999)

EXAMPLE hexagonal lattices (HBFs)



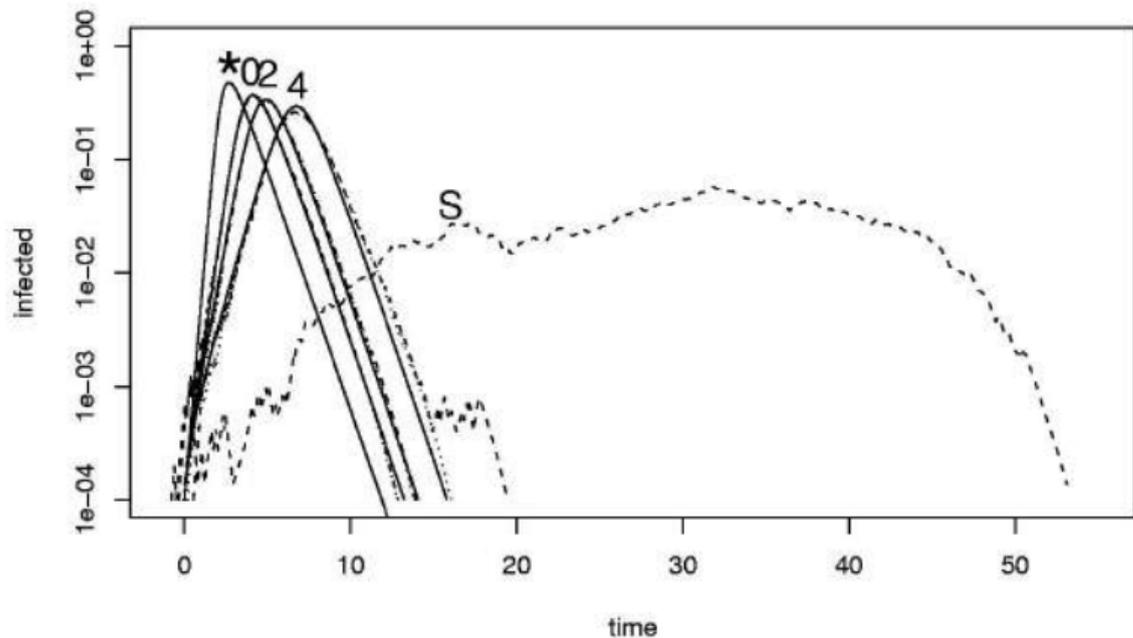
$$\phi = 6/15 = 0.4$$

So does $G(6, 0.4)$ have $T \sim \sqrt{N}$?

where $G(\star, \phi)$ is the random graph with degree distribution \star and clustering parameter ϕ

SIR (dashed line) and its pair approximation (solid line), for $\phi = 0, 0.2, 0.4$.

Also, spatial SIR ('S') and ordinary deterministic SIR ('*').



We conclude that local structure is a poor guide to global structure:

the pair approx is good for ‘typical’ $G(n, \phi)$ graphs, but such graphs are mean-field –

with $T \sim \log N$

– not spatial

Yet there *are* spatial examples of $G(n, \phi)$ –
HBFs – with $T \sim \sqrt{N}$

The resolution of this paradox is that the non-mean-field cases are of negligible probability –

HBFs, even as small as $N = 150$,
are *Adams-improbable*.

‘We are now cruising at a level of $2^{25,000}$ to 1 against and falling, and we will be restoring normality just as soon as we are sure what is normal anyway.’

(Adams 1979)

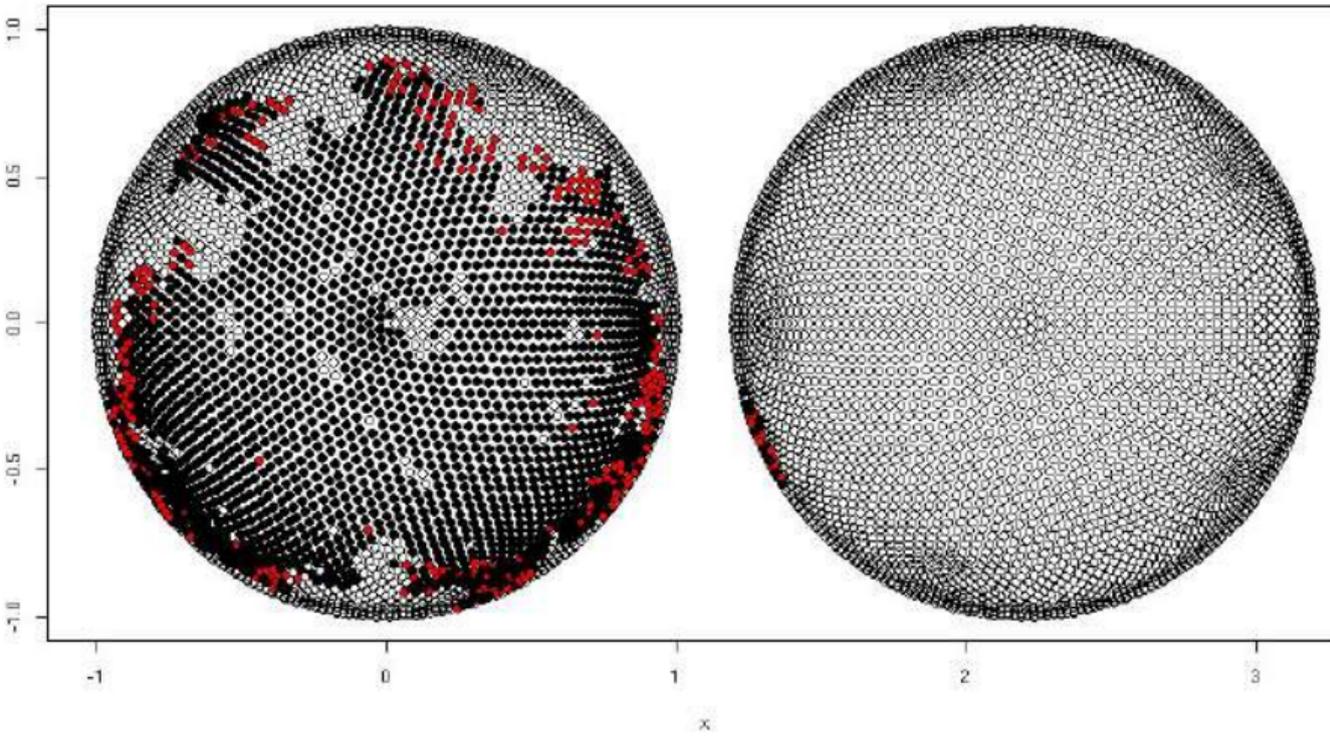
2 How do we define a threshold parameter for spatial models?

Usual ' $R_0 > 1$ ' depends on having a Branching Process approximation

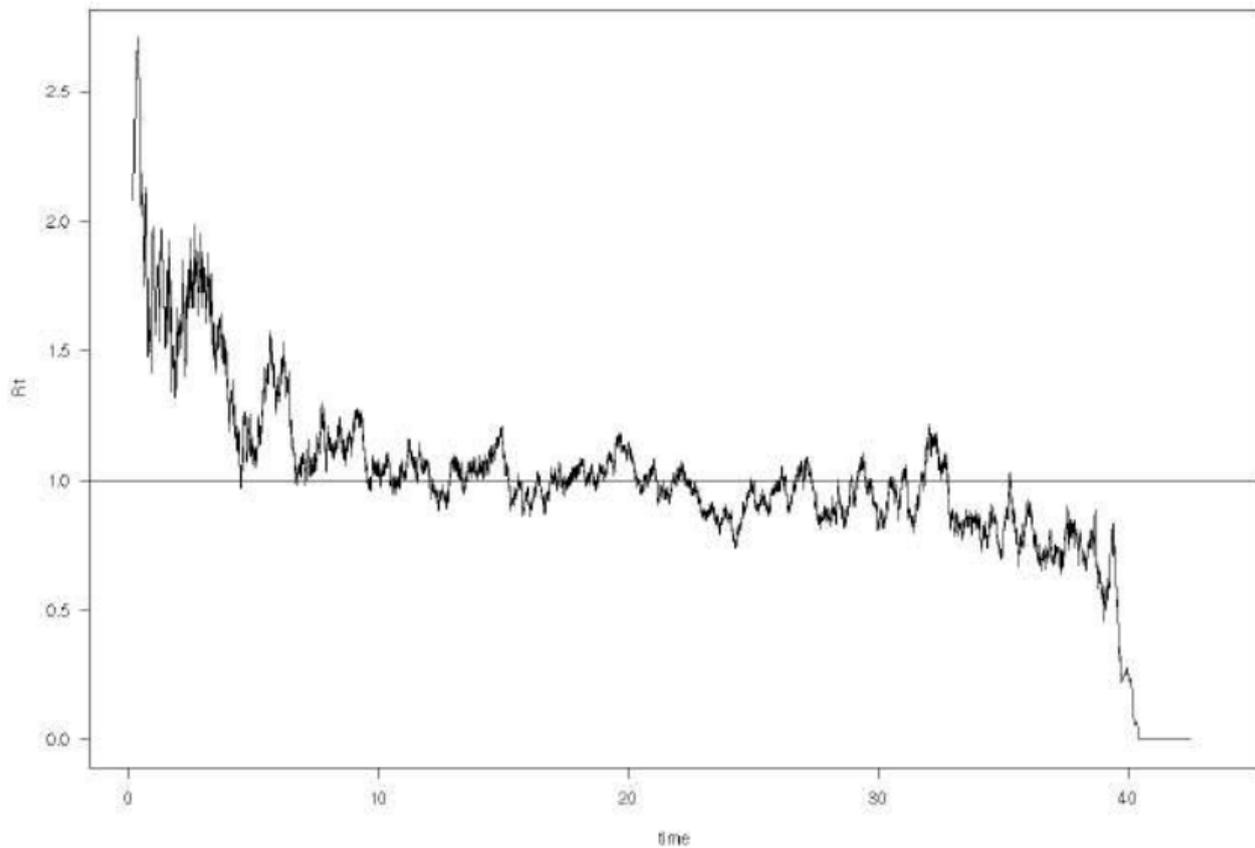
If we define R_0 as expected number of contacts, critical value is > 1 , *e.g.* 2-2.4 for ne-ne lattice

[could use adjusted $R_0 (= R_0/R_{0_{crit}})$]

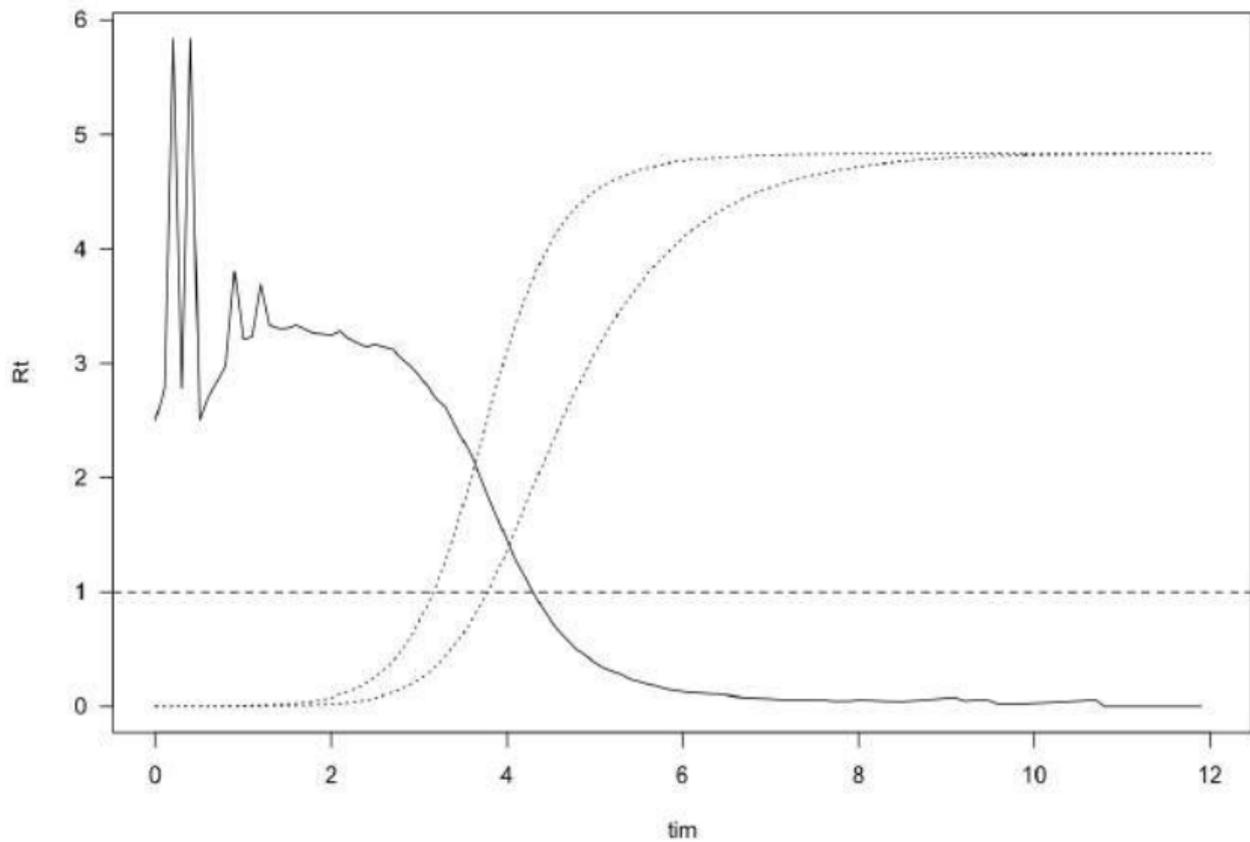
idea of next-generation operator \rightarrow steady state ?



Rt for spatial epidemic



Rt for random graph



3 How should we analyse models with long distance interactions?

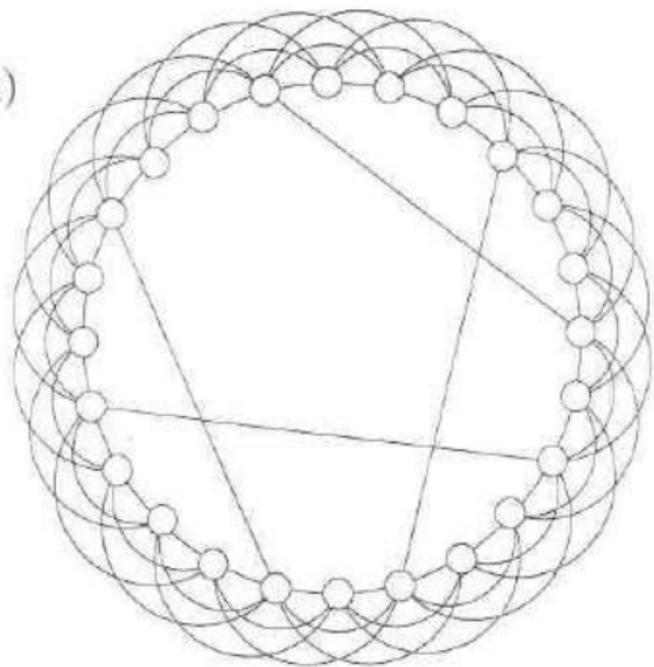
key statistic is duration T

($\log N$ in non-spatial, \sqrt{N} in 2-D ne-ne)

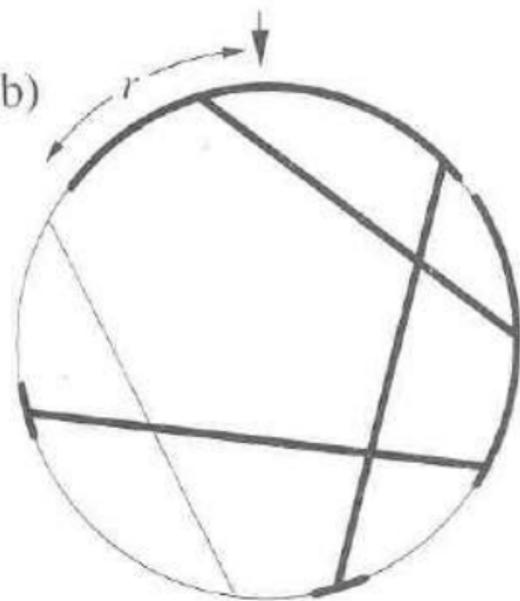
intermediate models:

e.g. great circle / small world, where T reduces from $\sim N$ to $\sim \log N$ as the number of global links increases

(a)



(b)



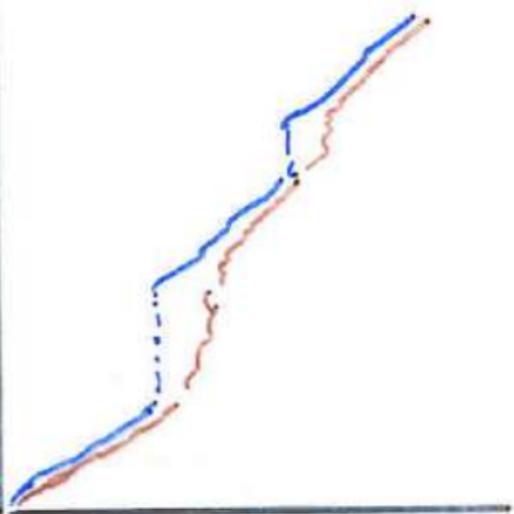
For what contact/dispersal distributions is velocity finite?

Relates closely to how number of k-step neighbours scales with k

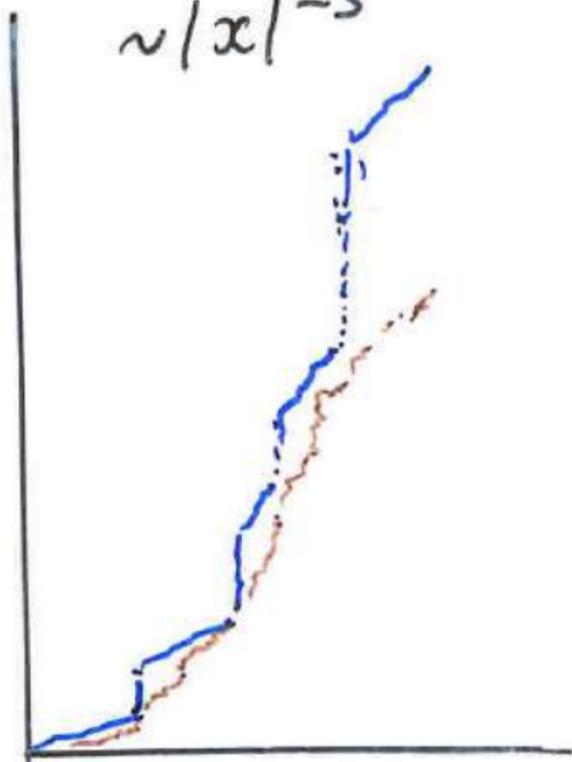
In 2-D, finite iff tail bounded by x^{-4}
(Biskup 2009)

Deijfen et al (2013) extend to weighted case

$$\beta(x) \sim |x|^{-4}$$



$$\sim |x|^{-3}$$



4 On what scale is intervention most effective?

Models need to be on the same scale as used for interventions?

1. ring-culling/vacc
2. targeting long-dist contacts
3. contact tracing

Examples: F&M / SARS

- F&M: targeting long-dist contacts, then ring-culling
- SARS: targeting long-dist contacts, then contact tracing

Some discussion points

What features of spatial structure or contact networks matter?

- Local structure is a poor guide to global structure
- Many networks of interest are ‘improbable’
- Patterns of spread and persistence can depend critically on stochastic behaviour of individuals
- Difficult to study too many features simultaneously (Euler’s elephant)

Small worlds?

Need a small diameter network of differently skilled researchers

