Challenges in representing spatial structure

Denis Mollison ICMS, 8th July 2016

Five challenges for spatial epidemic models

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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?

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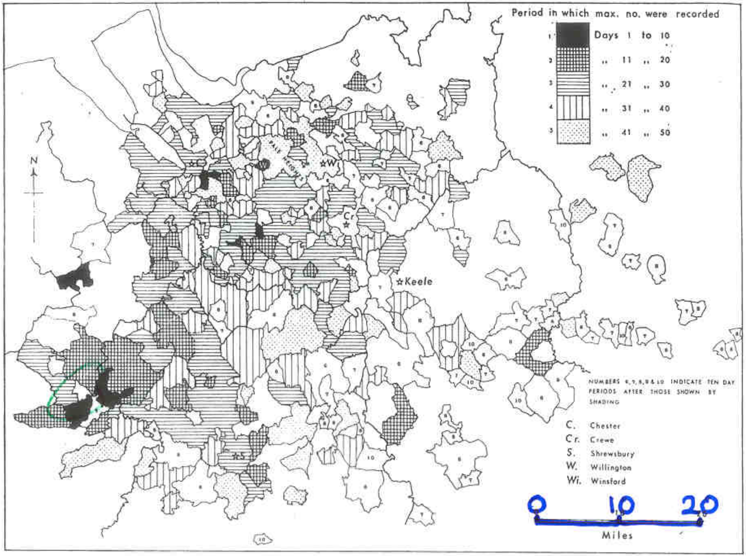
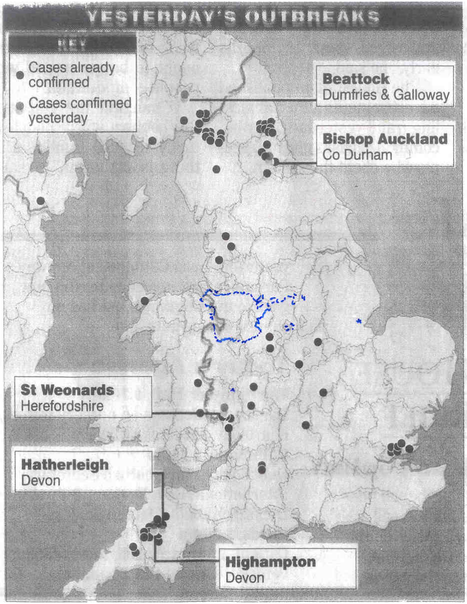
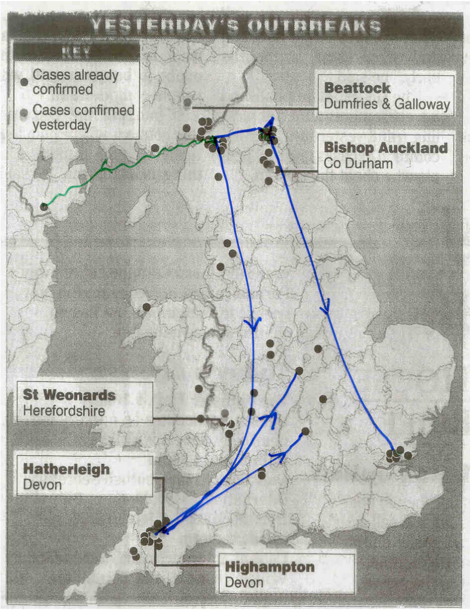
- *Spread* – velocity / duration? final size?
- *Persistence?* – pattern? control?

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


Period in which max. no. were recorded
Days 1 to 10
" 11 " 20
" 21 " 30
" 31 " 40
" 41 " 50
N
☆Keele
NUMBERS 6, 7, 8, 9 & 10 INDICATE TEN DAY PERIODS AFTER THOSE SHOWN BY SHADING
C. Chester
Cr. Crewe
S. Shrewsbury
W. Willington
Wi. Winsford
0 10 20
Miles


YESTERDAY'S OUTBREAKS
KEY
Cases already confirmed
Cases confirmed yesterday
Beattock
Dumfries & Galloway
Bishop Auckland
Co Durham
St Weonards
Herefordshire
Hatherleigh
Devon
Highampton
Devon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1967-8: spatial with jumps

2001: two phases

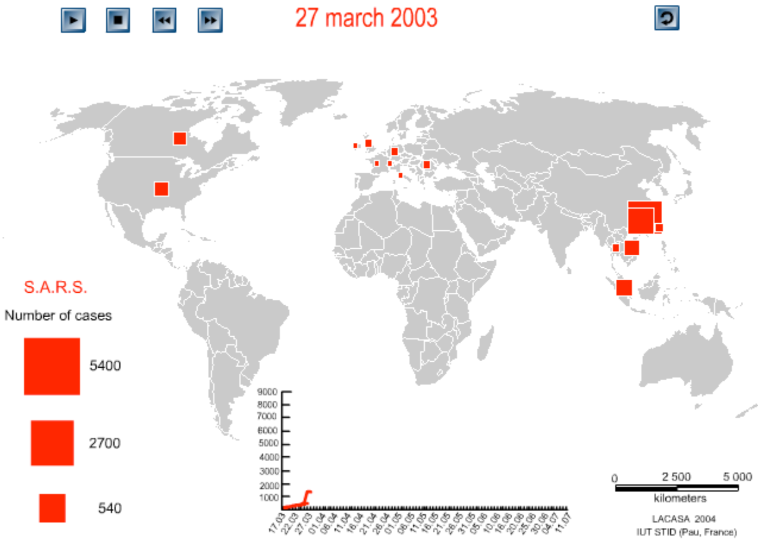
- global
- spatial with jumps

1967-8: spatial with jumps

2001: two phases

- global
- spatial with jumps

2003: SARS


27 march 2003
S.A.R.S.
Number of cases
5400
2700
540
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
2 500
5 000
kilometers
LACASA 2004
IUT STID (Pau, France)

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

e.g. regular lattices,

random geometric graphs,

'small world' models,

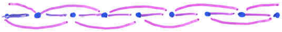
clustered graphs,

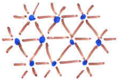
dynamic networks...

fixed or variable degree distribution

Example

Regular lattice with only nearest-neighbour contacts

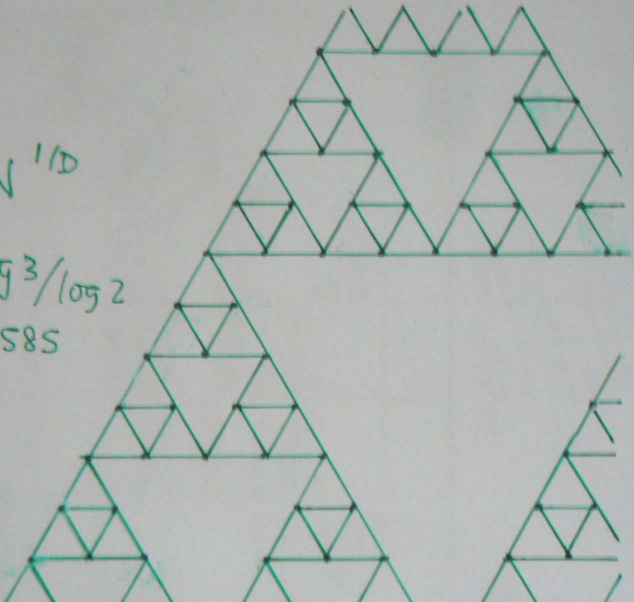


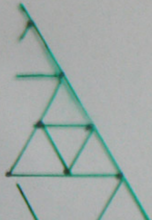


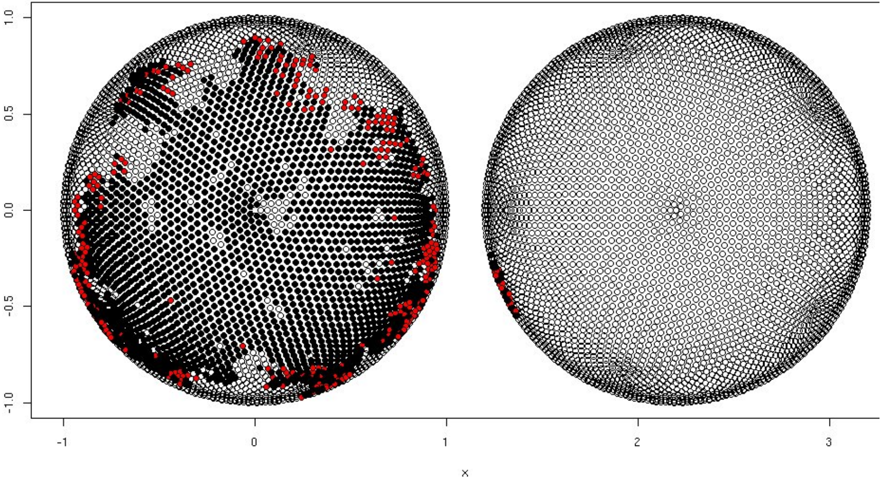
$T \sim N^{1/D}$

Here $D = \log 3 / \log 2$

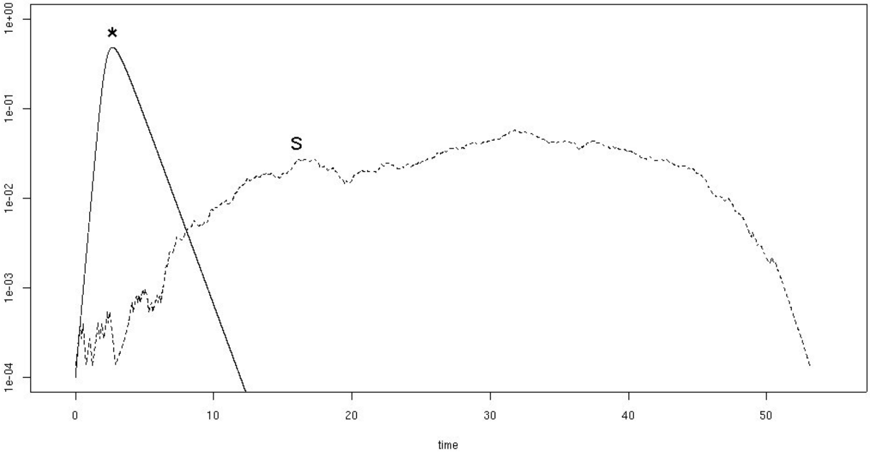
$\fallingdotseq 1.585$







1.0
0.5
0.0
-0.5
-1.0
-1
0
1
2
3
x


1e+00
1e-01
1e-02
1e-03
1e-04
*
S
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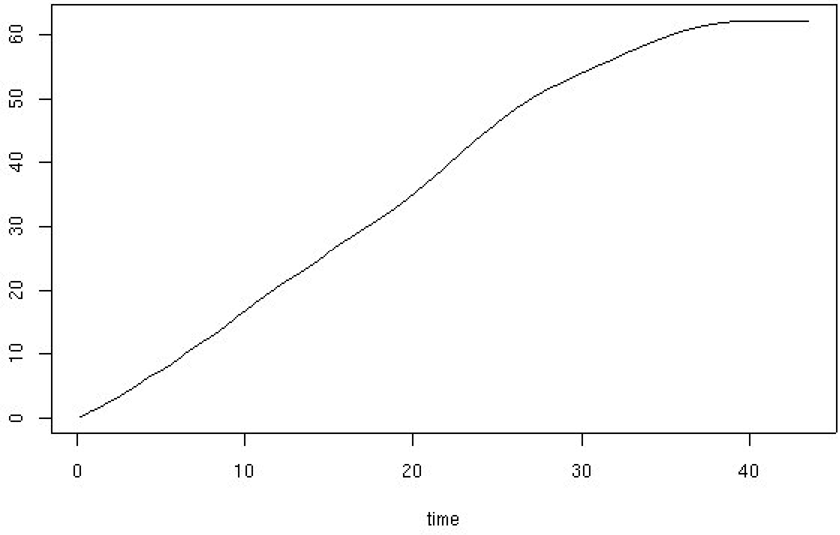
20
30
40
50
time


0
10
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60
0
10
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30
40
time

2 How should we model contact structure in spatially heterogeneous populations?

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

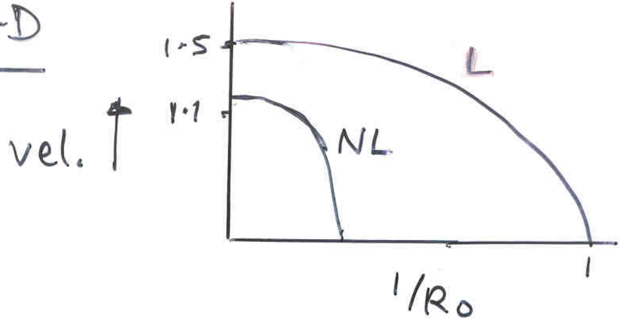
Three advantages of the R&D kernel approach:

- 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



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?

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Does local correlation capture spatial structure?

Recall the deterministic SIR:

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

More accurately

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

$$\begin{aligned}
[\dot{SS}] &= -2\beta[SSI] \\
[\dot{SI}] &= \beta([SSI] - [SI] - [ISI]) - \gamma[SI] \\
[\dot{SR}] &= \cdots \\
[\dot{II}] &= \cdots
\end{aligned}$$

For closure, use

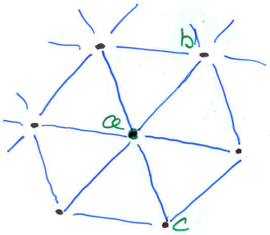
$$[ABC] \approx (1 - \frac{1}{n})\frac{[AB][BC]}{[B]} \times (1 - \phi + \phi\frac{[AC]}{[A][C]})$$

where

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

(Keeling 1999)

EXAMPLE hexagonal lattices (HBFs)



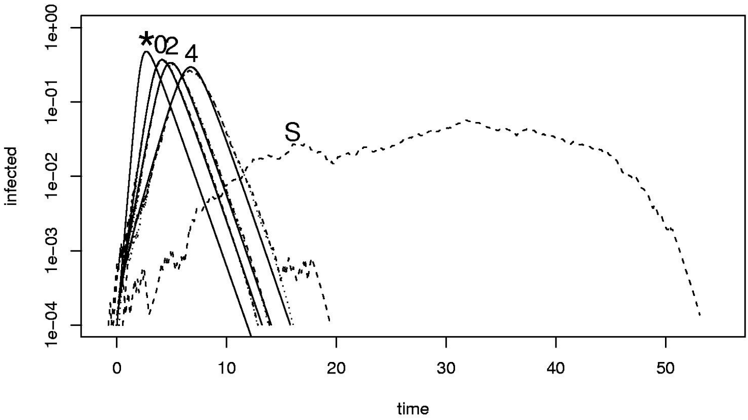
$\phi = 6/15 = 0.4$

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 ('$\star$').



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)

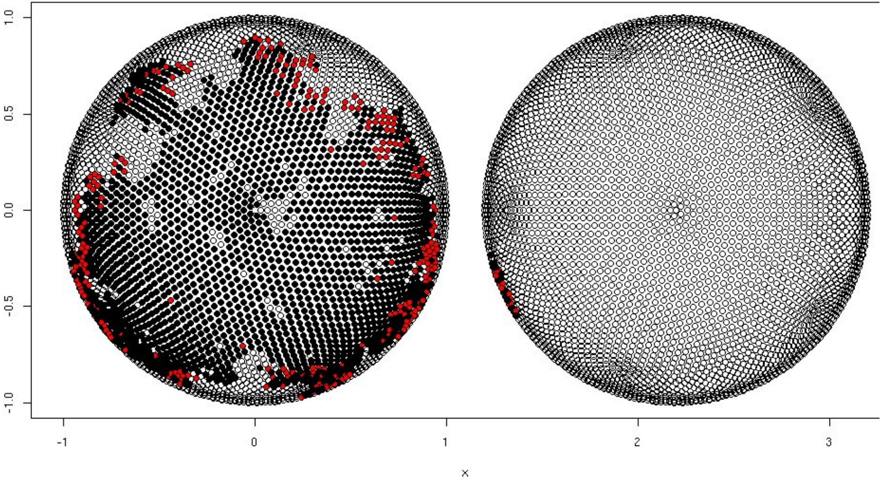
3 How do we define a threshold parameter for spatial models?

Usual '$R0 > 1$' depends on having a Branching Process approximation

If we define $R0$ as expected number of contacts,
critical value is > 1, *e.g.* 2-2.4 for ne-ne lattice

[could use adjusted $R0$ ($= R0/R0_{crit}$)]

idea of next-generation operator $\rightarrow$ steady state ?


1.0
0.5
0.0
-0.5
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3
x

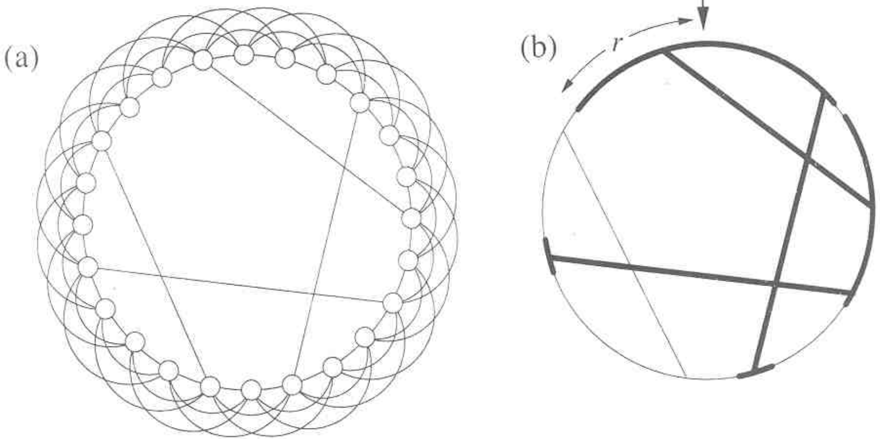
4 How should we analyse models with long distance interactions?

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

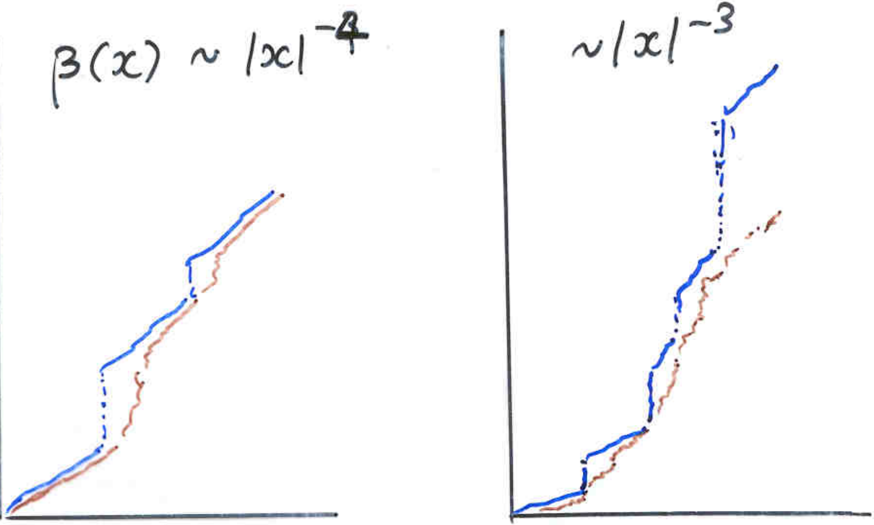

(a)
(b)
r

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


$\beta(x) \sim |x|^{-4}$
$\sim |x|^{-3}$

5 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