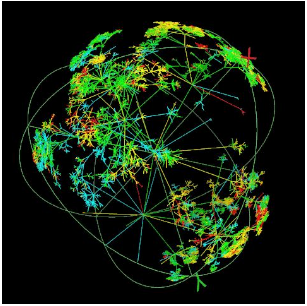
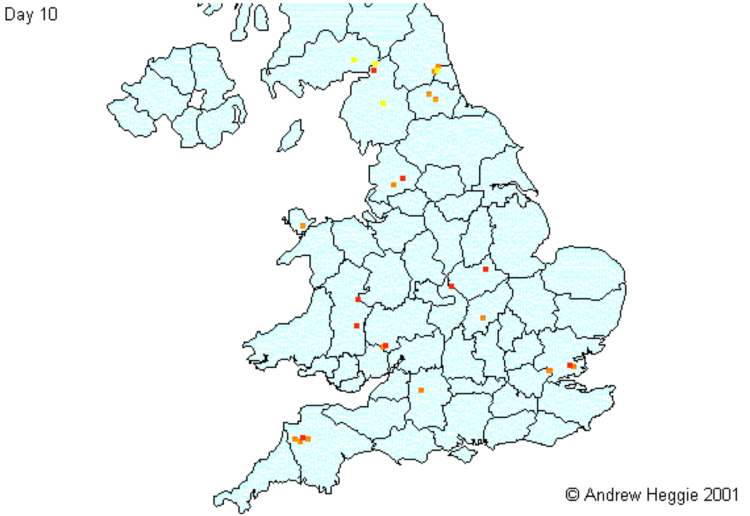
The structure of epidemic models

Denis Mollison



InFER, 28th March 2011



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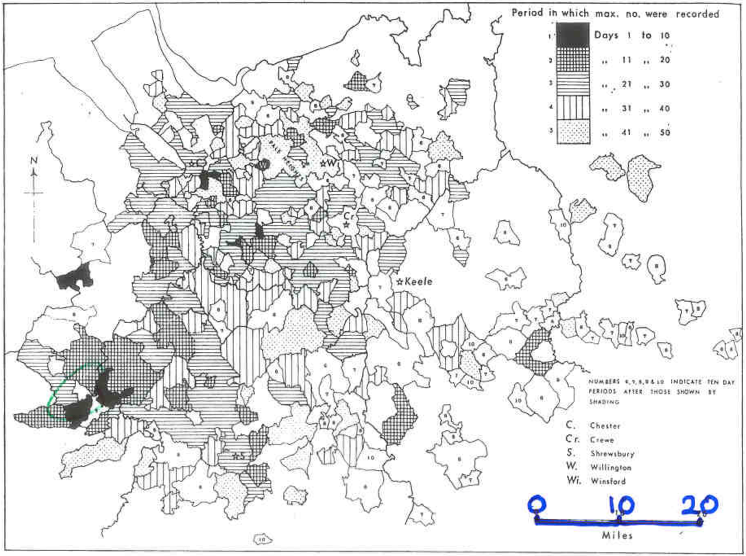
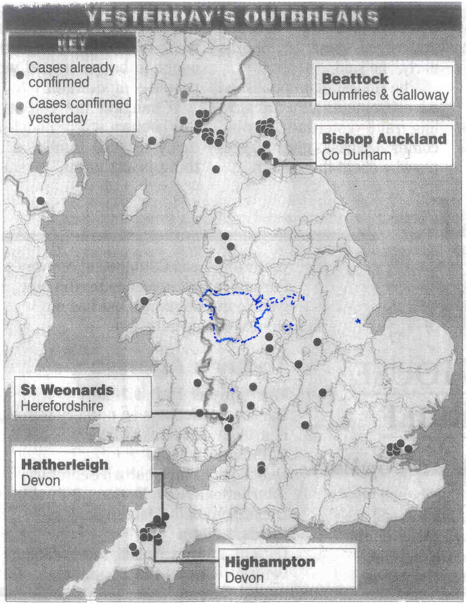
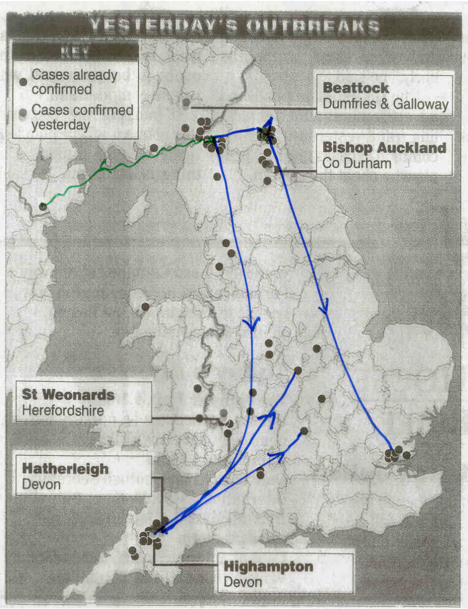


Period in which max. no. were recorded
1 Days 1 to 10
2 " 11 " 20
3 " 21 " 30
4 " 31 " 40
5 " 41 " 50
N
☆C.
☆W.
Cr.
☆Keele
☆S.
NUMBERS 6, 7, 8, 9 & 10 INDICATE TEN DAY PERIODS AFTER THOSE SHOWN BY SHADING
C. Chester
Cr. Crewe
S. Shrewsbury
W. Willington
Wi. Winsford
0 10 20
Miles


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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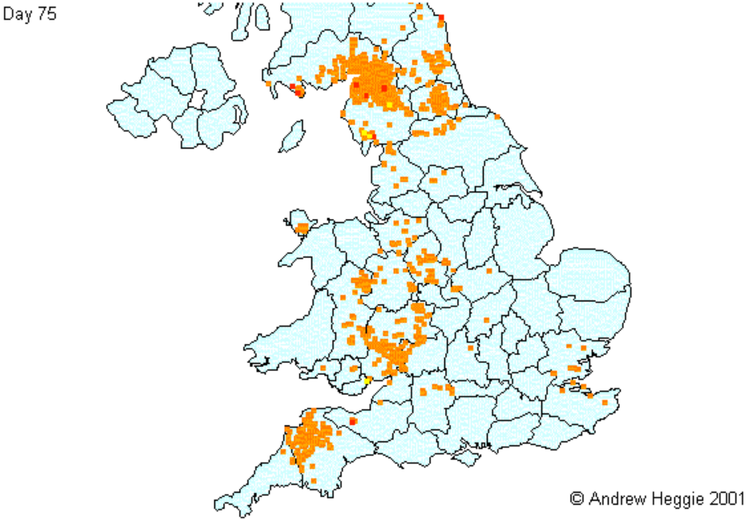

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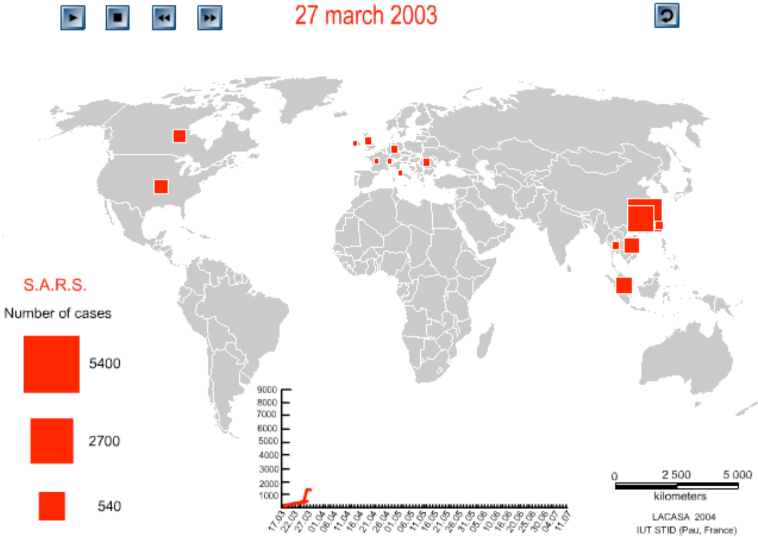

27 march 2003
S.A.R.S.
Number of cases
5400
2700
540
9000
8000
7000
6000
5000
4000
3000
2000
1000
17.03 22.03 27.03 01.04 06.04 11.04 16.04 21.04 26.04 01.05 06.05 11.05 16.05 21.05 26.05 31.05 05.06 10.06 16.06 20.06 25.06 30.06 04.07 11.07
0 2 500 5 000
kilometers
LACASA 2004
IUT STID (Pau, France)

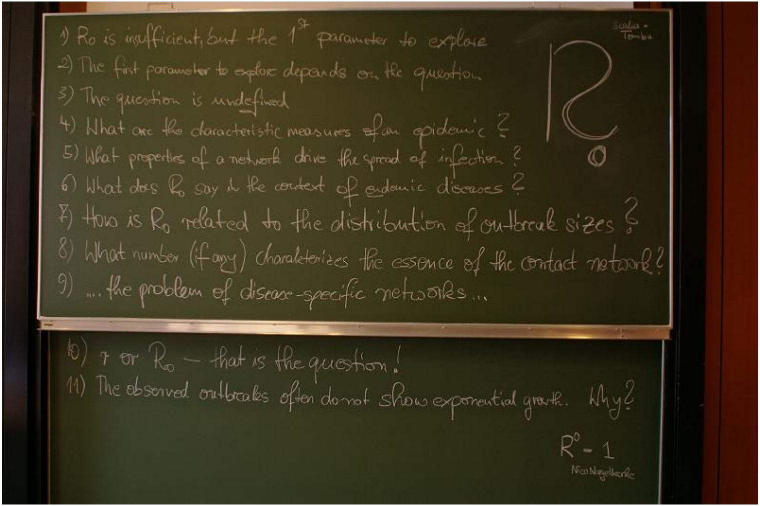
1 Building models

INTERESTS

- *Invasion* – threshold? R_0?

R_0

The ***basic reproductive ratio*** of an epidemic is the mean number of new infections made by an infected individual in a mostly susceptible population


1) Ro is insufficient, but the 1st parameter to explore
2) The first parameter to explore depends on the question
3) The question is undefined
4) What are the characteristic measures of an epidemic ?
5) What properties of a network drive the spread of infection ?
6) What does R0 say in the context of endemic diseases ?
7) How is R0 related to the distribution of outbreak sizes ?
8) What number (if any) charakterizes the essence of the contact network ?
9) ... the problem of disease-specific networks...
10) r or R0 – that is the question!
11) The observed outbreaks often do not show exponential growth. Why?
R0 - 1
Nico Nagelkerke
Scalia - Tomba

1 Building models

Interests

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

1 Building models

Interests

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

Types of model

- individual or continuous population?
- stochastic or deterministic?

Population space

- mean-field
- metapopulations
- spatial
- small-world

Equililibrium formulae

$\pi_i = \tau_i / L$

e.g.

$\pi_S = S/N = A/L$

for 'once-only' disease

Assuming homogeneous mixing,

$R_0 = \pi_S = S/N$,

so $R_0 = A/L$.

Ross (ca. 1911)

$R_0 = Mb^2cd$

where M is # mosquitoes/human

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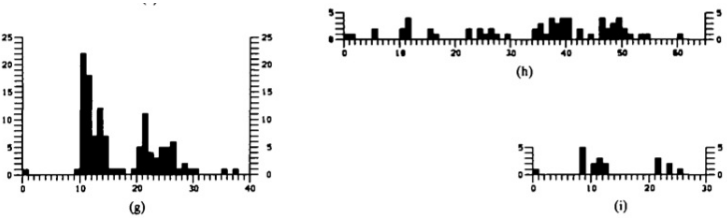
where M is # mosquitoes/human,

whence

$R_0 < 1$ iff $M < M_c$.

2. Simple network models



Three outbreaks of measles (Enko 1889)

In each generation,

Pr(escape infection)

$$= (1 - i)^{pN} \quad \text{(Enko 1889)}$$

$$= (1 - p)^{iN} \quad \text{(Reed-Frost)}$$

where $p = \mathrm{P(contact)}$, i = proportion infected

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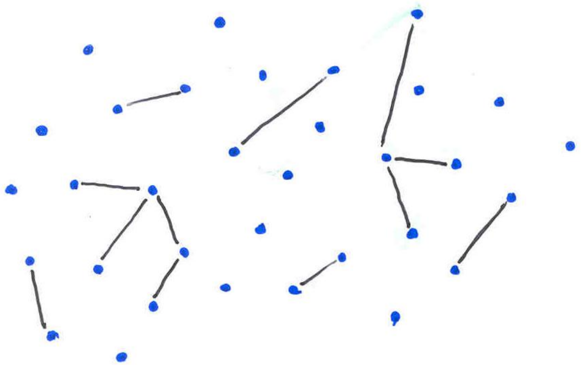
where $p = \text{P(contact)}$, $i = \text{proportion infected}$

$\rightarrow$

$$I_{n+1} \sim \text{Binomial}(S_n, (1 - (1 - p)^{I_n}))$$

Simple network model (random graph)



Here $R_0 \equiv Np$ is < 1

Results for simple random graph:

Giant component exists iff $R_0 > 1$.

Diameter of giant, $T \sim \log N$.

Final size (and probability of a large outbreak) are both given by the largest solution of

$$z = 1 - \exp(-R_0 z)$$

Deterministic (continuous population) equivalent,

a differential equation model ('SIR'):

$$\begin{aligned} \dot{S} &= -cSI \\ \dot{I} &= cSI - dI \\ \dot{R} &= dI \end{aligned}$$

Results for 'SIR':

Large outbreak *always* occurs if $R_0 \equiv c/d > 1$,
duration $T \sim \log N$,
and the final size z is given by

$$z = 1 - \exp(-R_0 z)$$

Stochastic structures

"UNNECESSARY DETAILS"

Example:

Simple birth and death process

(1) $r_{n,n+1} = an, \quad r_{n,n-1} = bn$

(2) Independent individuals, each with birth rate a and death rate b.

P(extinction) μ_n when initial pop. $= n$?

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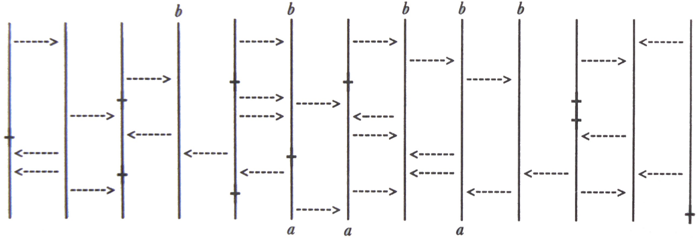
$\mu_n = \mu_1^n$

Coupling

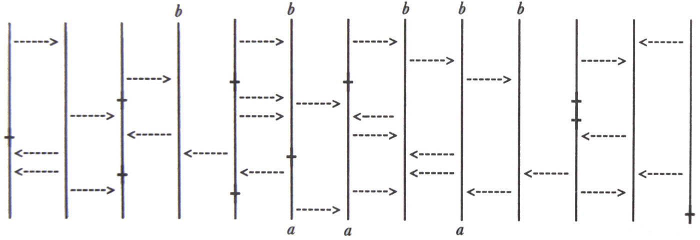
Example: the 'Contact Process' . . .



. . . is monotone with initial set

Coupling

Example: the 'Contact Process' . . .



. . . is monotone with initial set

. . . and with infection parameter

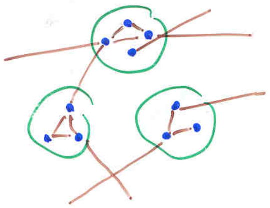
Thinking in the wrong order

Looking at simpler model first

...

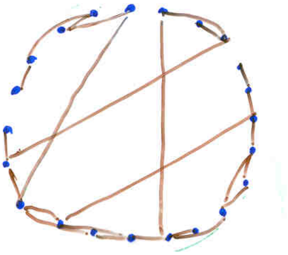
3 Metapopulation models

Consider a population with local and global contacts



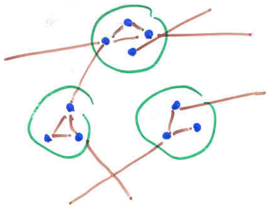
where the geography can be either mean-field . . .

. . . or spatial



('great circle' or 'small world' model)

Consider first the process including only global contacts, with reproductive ratio $R_0 = Nq$.



Relative to this 'global-only' process, local contacts have an amplifying effect.

Hence the overall reproductive ratio is

$$R_T = R_0 \mu$$

where μ is the mean size of a local outbreak.

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$$R_T = R_0 \mu$$

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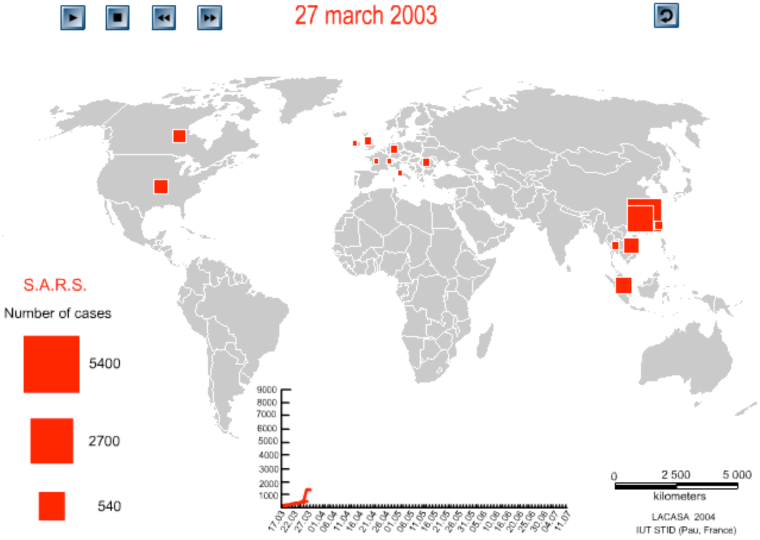
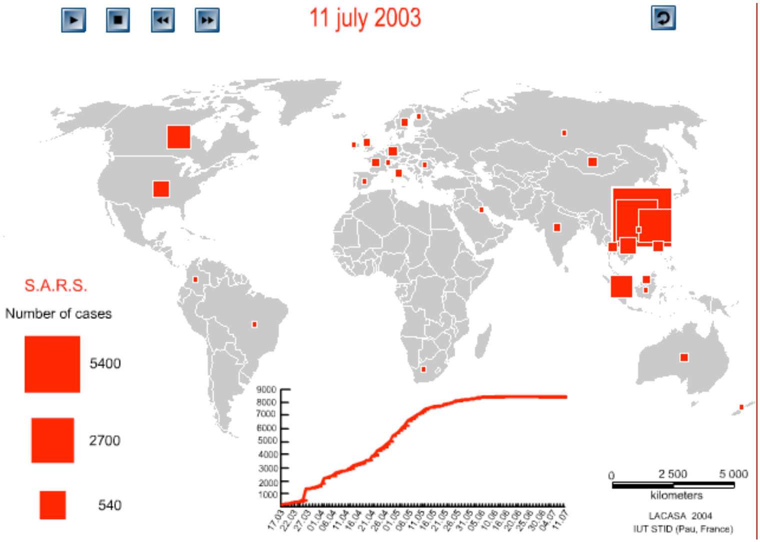
A key question for control is whether you can get local outbreaks below threshold (compare SARS and swine flu?)



http://www.cybergeo.eu/index12803.html



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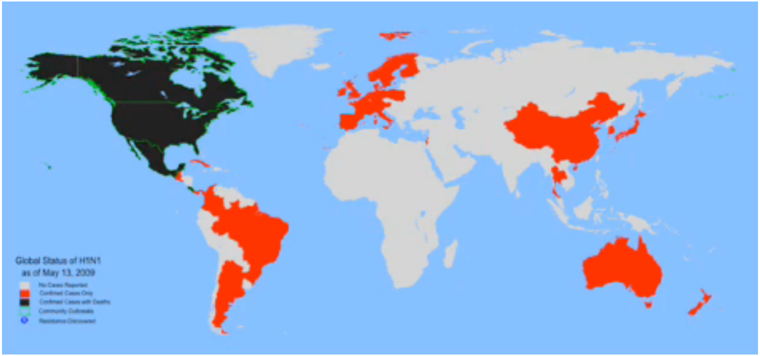
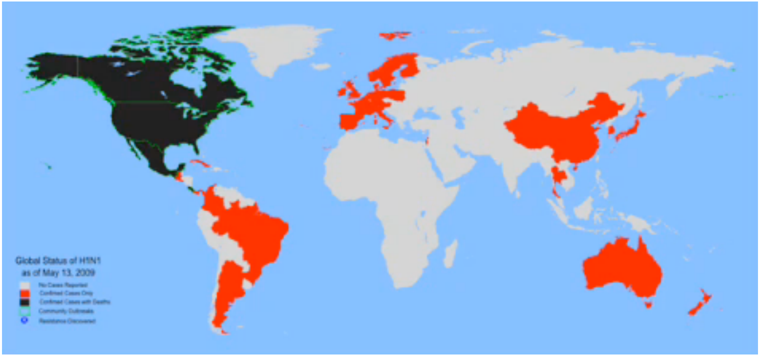
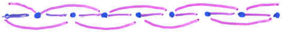
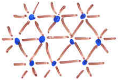

Global Status of H1N1
as of May 13, 2009
No Cases Reported
Confirmed Cases Only
Confirmed Cases with Deaths
Community Outbreaks
Resistance Discovered



“swine flu map youtube”

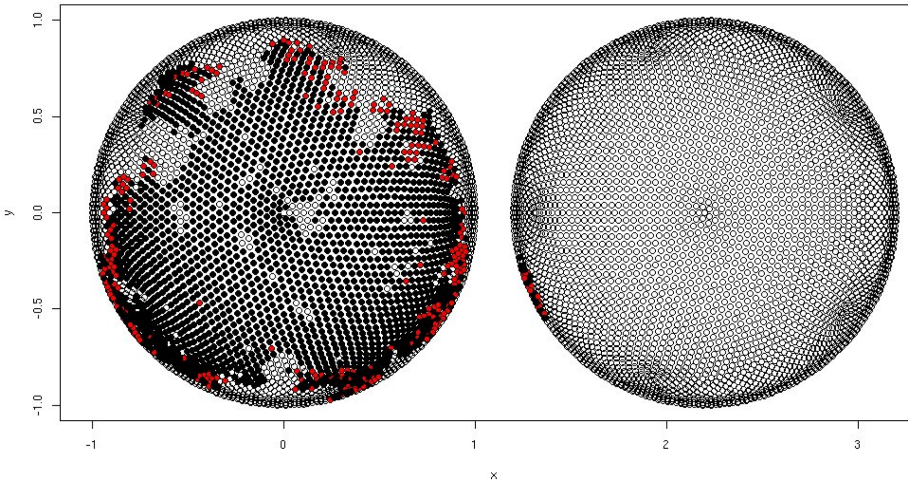
4 Spatial models



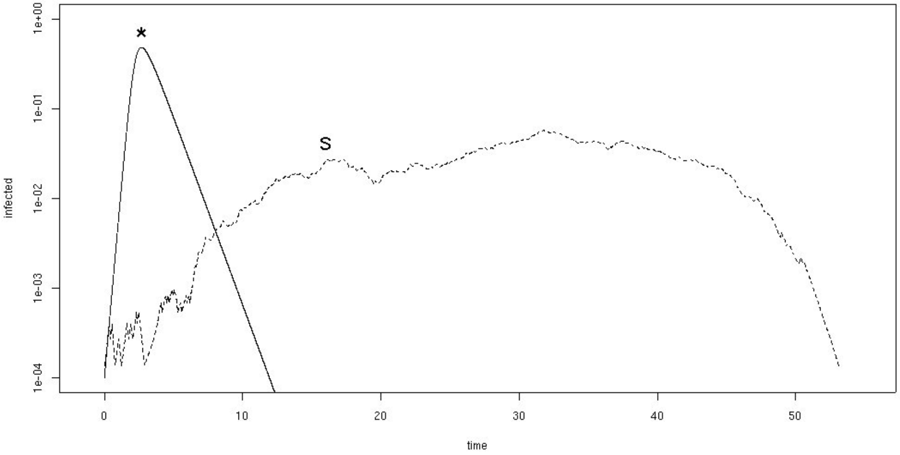


Nearest-neighbour

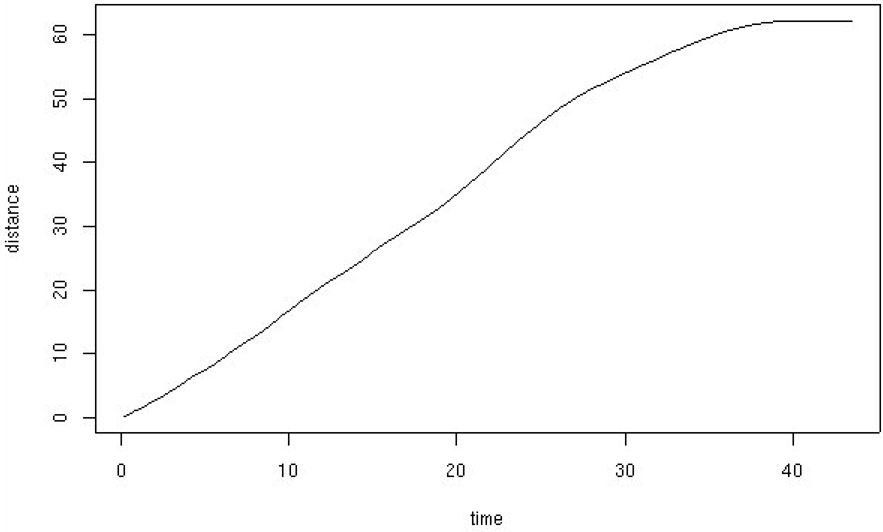
...or more general dispersal distribution



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



*
S
1e+00
1e-01
1e-02
1e-03
1e-04
infected
0
10
20
30
40
50
time



distance
0
10
20
30
40
50
60
0
10
20
30
40
time

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 -

.. but note

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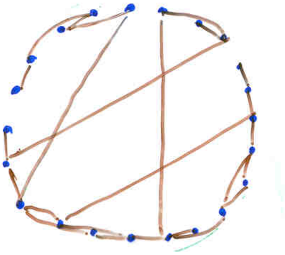
The problem is treating the population as continuous (atto-foxes) rather than determinism *per se*

5 Small worlds



Threshold: $R_T = R_0\mu > 1$ (as for metapopulation model)

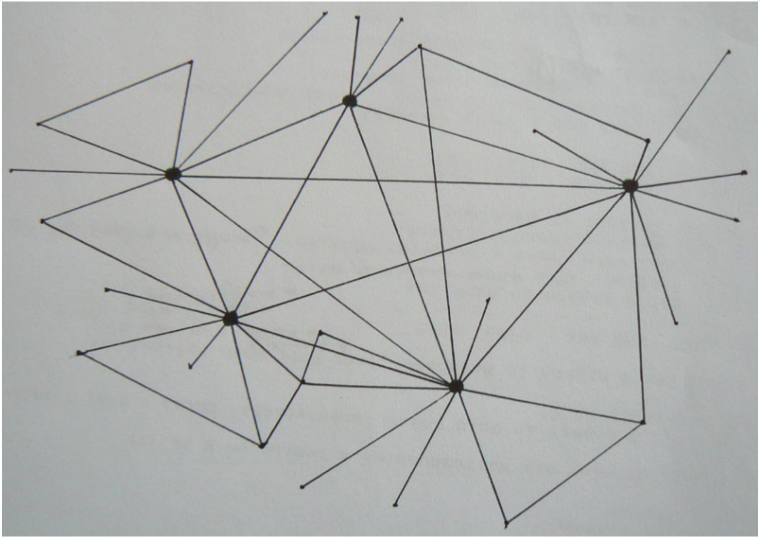
T reduces from $\sim N$ to $\sim \log N$ as the number of global links increases

'Small world' phenomenon:

The proportion of global links required to reduce T to $\sim \log N$ is surprisingly small.

‘Scale-free’ models:

A related study is of models with very high variability in the number of contacts per individual.



$T = 3$

NOTE When considering different degree distributions

(a) the epidemic is run *on* a fixed network.

(b) links from/to an individual are not independent

NOTE When considering different degree distributions

(a) the epidemic is run *on* a fixed network.

(b) links from/to an individual are not independent.

Compare SRG / Reed-Frost where:

(a) doesn't matter

(b) they are independent.


TIMOR SEA
INDIAN OCEAN
CORAL SEA
SOUTH PACIFIC OCEAN
TASMAN SEA
GREAT BARRIER REEF
Gulf of Carpentaria
Great Australian Bight
Bass Strait
DARWIN
GOVE (Nhulunbuy)
HORN ISLAND
WEIPA
CAPE YORK PENINSULA
KUNUNURRA
KIMBERLEY
BROOME
CANNING BASIN
PORT HEDLAND
KARRATHA
PILBARA
PARABURDOO
NEWMAN
GREAT SANDY DESERT
WESTERN AUSTRALIA
ALICE SPRINGS
AYERS ROCK/ ULURU
CAIRNS
TOWNSVILLE
MT ISA
PROSERPINE
HAMILTON ISLAND
MACKAY
QUEENSLAND
LONGREACH
BARCALDINE
EMERALD
BLACKWATER
ROCKHAMPTON
GLADSTONE
BLACKALL
BUNDABERG
HERVEY BAY
CHARLEVILLE
ROMA
MAROOCHYDORE (SUNSHINE COAST)
BRISBANE
GOLD COAST
BALLINA
NORFOLK ISLAND
LORD HOWE ISLAND
MOREE
NARRABRI
ARMIDALE
COFFS HARBOUR
TAMWORTH
PORT MACQUARIE
DUBBO
NEW SOUTH WALES
NEWCASTLE
SYDNEY
WOLLONGONG
CANBERRA
WAGGA WAGGA
ALBURY
MILDURA
VICTORIA
MELBOURNE
MELBOURNE (AVALON)
ADELAIDE
KALGOORLIE
NULLARBOR PLAIN
PERTH
DEVONPORT
LAUNCESTON
HOBART
TASMANIA
Sector times and distances may vary according to seasonal weather, flying conditions, aircraft type and route variations. Routes shown are indicative only.
Location of The Qantas Clubs or associated lounges
Qantas routes
Jetstar routes
QantasLink routes
Routes operated by other airlines for Qantas
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National Capital
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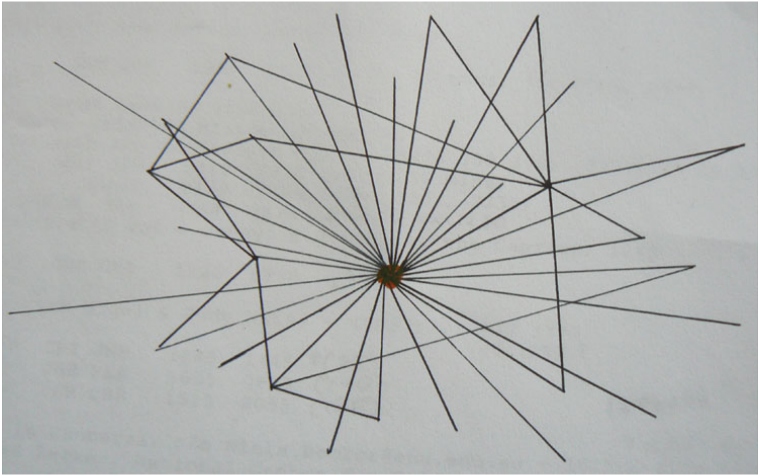
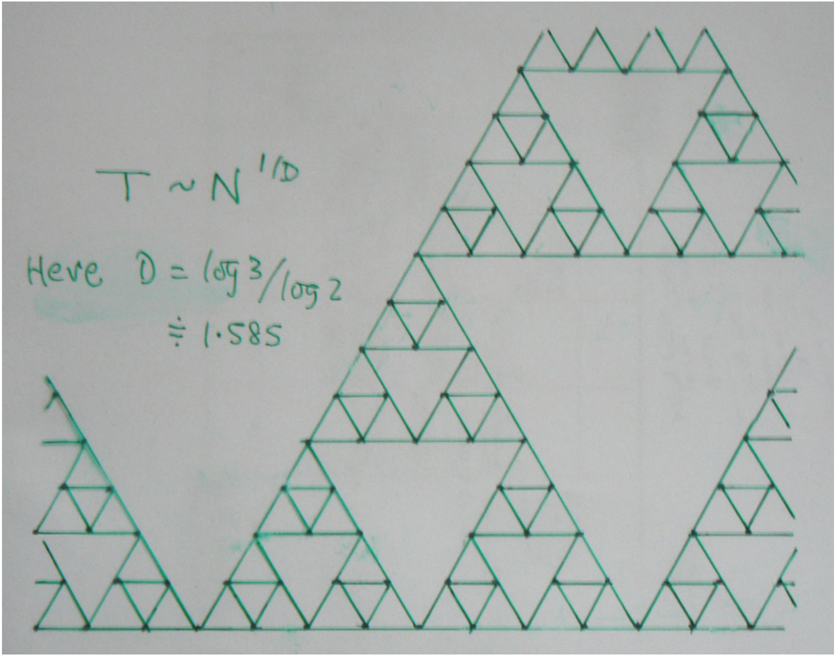


$T = 2$


$T \sim N^{1/D}$
Here $D = \log 3 / \log 2$
$\doteqdot 1.585$

Footnotes

The structuralist ethic

Only trust a model if you can take it apart and put it together again

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The structuralist ethic

Only trust a model if you can take it apart and put it together again

Limits of prediction

Footnotes

THE STRUCTURALIST ETHIC

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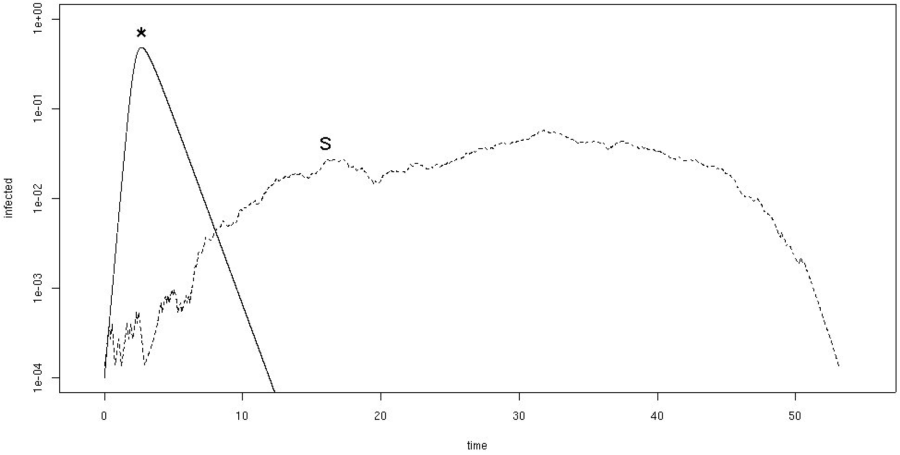
LIMITS OF PREDICTION

Avian flu in humans currently has an R_0 of ~ 0.02.

6 Pair approximations

Pair approximations try to use local correlations to capture spatial structure.



1e+00
1e-01
1e-02
1e-03
1e-04
infected
*
S
0
10
20
30
40
50
time

Reconsider the deterministic SIR:

$$\begin{aligned}\dot{S} &= -cSI \\ \dot{I} &= cSI - dI \\ \dot{R} &= dI\end{aligned}$$

More accurately

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

More accurately

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

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

For closure, use

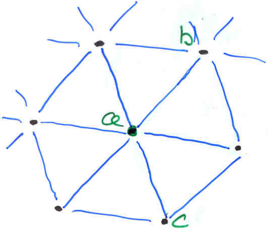
$$[ABC] \approx (1 - \frac{1}{n})\frac{[AB][BC]}{[B]} \times (1 - \phi + \phi\frac{[AC]}{[A][C]})$$

where the clustering parameter ϕ is

$$P(ac|ab \,\&\, bc)$$

(Keeling 1999)

EXAMPLE hexagonal lattices (HBFs)



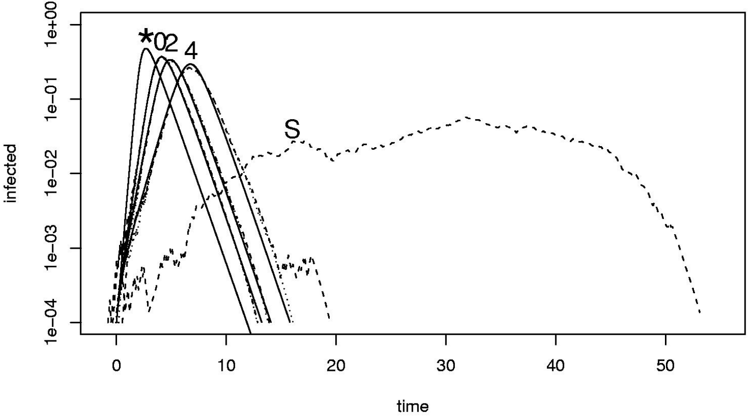
$\phi = 6/15 = 0.4$

We have seen that the SIR on this graph has $T \sim \sqrt{N}$.

How about the pair approximation SIR with $\phi = 0.4$?

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

Also, spatial SIR ('S') and ordinary deterministic SIR ('$\star$').



The pair approximation with $\phi = 0.4$ does fit well for epidemics on ‘typical’ graphs of degree 6 and clustering parameter 0.4 ...

...but **not** for the spatial (hexagonal) SIR.

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…but **not** for the spatial (hexagonal) SIR.

Is there a paradox here?

Just because a graph has degree 6
and clustering parameter 0.4,
it doesn't have to be hexagonal.

Just because a graph has degree 6
and clustering parameter 0.4,
it doesn't have to be hexagonal.

In fact that's very very unlikely – we might say
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)

1 References

Adams, D (1979) *The Hitchhiker's Guide to the Galaxy*, Pan Books.

For other references see

`http.ma.hw.ac.uk/∼denis/`