



Spatial Spread of Infectious Diseases

Part II

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Spatial Spread of Diseases

Population-based Approaches

Metapopulation Models

Lattice- or Grid-based Models

Continuous-space Models

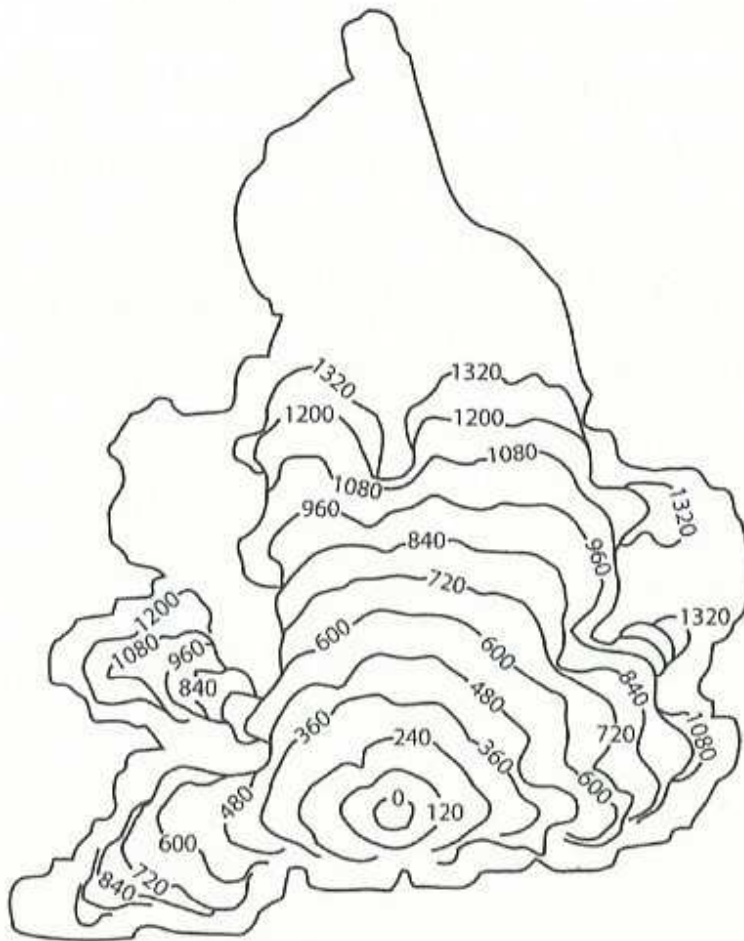
Continuous-Space Models

In lattice-based models, the resolution is limited by the scale of the grid cell.

However, space and population can be treated continuously, specifying a density of individuals at all locations.

This can be considered the limit of a lattice model as the grid size becomes infinitely finer.

Continuous-Space Models



Murray, JD; Stanley, EA; Brown, DL (1986). *On the Spatial spread of rabies among foxes.* Proceedings of the Royal Society of London

Continuous-Space Models

PDE formulation

Infectious individuals transmit the disease only at susceptibles at their current location

All individuals are free to move at random through the landscape

Continuous-Space Models

PDE formulation: SIR-type dynamics

$$\frac{\partial X}{\partial t} = \nu - \beta \frac{XY}{N} - \mu X + D_X \nabla^2 X$$

$$\frac{\partial Y}{\partial t} = \beta \frac{XY}{N} - \gamma Y - \mu Y + D_Y \nabla^2 Y$$

$$\frac{\partial Z}{\partial t} = \gamma Y - \mu Z + D_Z \nabla^2 Z$$

X , Y and Z are functions of space and time and represent local densities.

Continuous-Space Models

PDE formulation: SIR-type dynamics

In a 2-dimensional landscape, $X(x, y, t)$ and the diffusion term becomes

$$\nabla^2 X = \frac{\partial^2 X}{\partial x^2} + \frac{\partial^2 X}{\partial y^2}$$

Susceptible, infected and recovered individuals are assumed to diffuse at different rates D_X, D_Y, D_Z

Continuous-Space Models

PDE formulation: SIR-type dynamics

Ignoring the demography we have:

$$\frac{\partial X}{\partial t} = D_X \nabla^2 X$$

This has the solution:

$$X(x, y, t) \propto \frac{1}{2\pi D_X t} e^{-\frac{x^2 + y^2}{2D_X t}}$$

Bell-shaped Gaussian distribution with total density of individuals remaining constant.

Continuous-Space Models

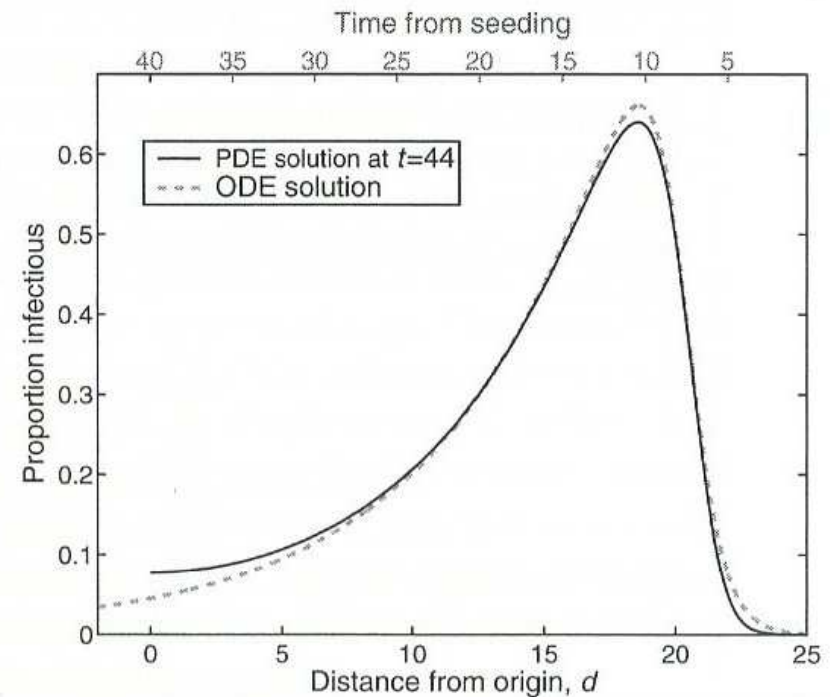
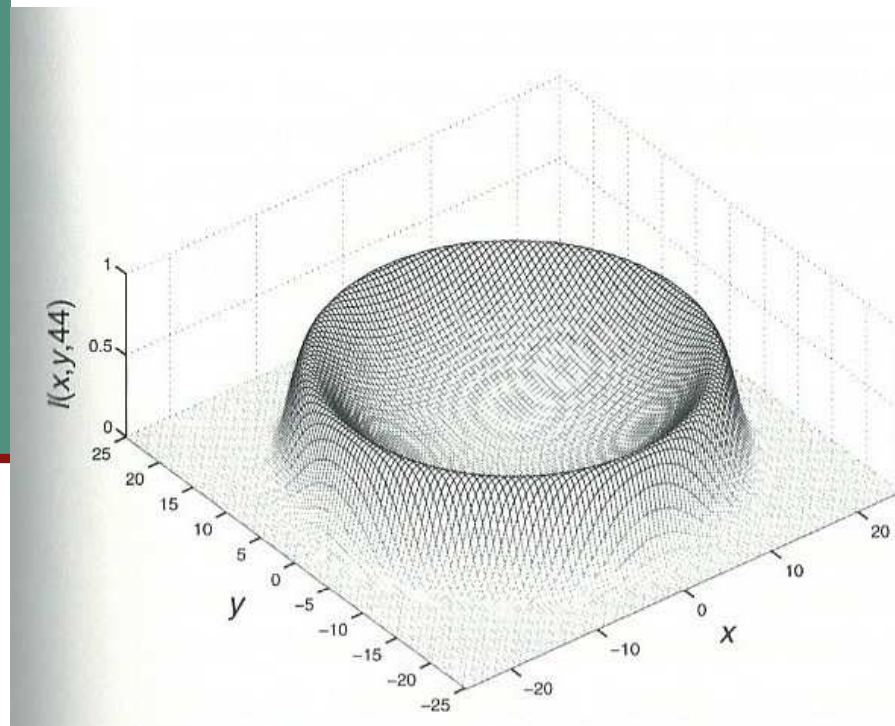
PDE formulation: SIR-type dynamics

Reaction-diffusion models assume local transmission of infection and rely on spatial diffusion of hosts to spread the infection.

For PDE models in 2 dimensions, infection spreads as a growing circular wave of near constant velocity

Continuous-Space Models

PDE formulation: SIR-type dynamics



Continuous-Space Models

IDE formulation

IDE models focus on longer-range transmission from static individuals

Continuous-Space Models

IDE formulation of a SIR-type model

$$\frac{dX(x,t)}{dt} = \nu(x) - \lambda(x,t)X(x,t) - \mu(x)X(x,t)$$

$$\frac{dY(x,t)}{dt} = \lambda(x,t)X(x,t) - \gamma(x)Y(x,t) - \mu(x)Y(x,t)$$

$$\text{with } \lambda(x,t) = \beta \int Y(y,t)K(x-y)dy$$

Here x is a point in a one-, two-, or more dimensional space

Continuous-Space Models

IDE formulation of a SIR-type model

$\lambda(x, t)$ models the transmission of infection from all points y in space to the point x .

The kernel K defines how infectivity decreases with distance.

Continuous-Space Models

IDE formulation

$$\lambda(x, t) = \beta \int Y(y, t) K(x - y) dy$$

models transmission as a density-dependent process.

There are other ways to define how the transmission operates

Continuous-Space Models

IDE formulation

$$\lambda(x, t) = \beta \int \frac{Y(y, t)}{N(y, t)} K(x - y) dy$$

The local proportion infectious individuals at each point is important.

This may represent at each point y interactions that take place sequentially, so that transmission is based on the point frequency

Continuous-Space Models

IDE formulation

$$\lambda(x, t) = \beta \frac{\int Y(y, t) K(x - y) dy}{\int N(y, t) K(x - y) dy}$$

The averaged proportion infectious is important

This may represent simultaneous interaction with individuals from a range of points

Continuous-Space Models

IDE formulation

Suppose that demographic and epidemiological parameters are invariant across space and that space is infinite and two-dimensional.

Rescale the parameters such that the population density at each point is one:

$$N = 1$$

Continuous-Space Models

IDE formulation

$$R_0 = \beta \int_{\mathbb{R}^2} K(y) dy = 2\pi \beta \int_0^\infty r K(r) dr$$

For $R_0 < \infty$ it is necessary that

$$K(r) < r^{-2} \text{ for } r \rightarrow \infty$$

Otherwise the integral is infinite

Continuous-Space Models

IDE formulation

The average dispersal distance is

$$D = \frac{\beta \int_{\mathfrak{R}^2} \|y\| K(y) dy}{\beta \int_{\mathfrak{R}^2} K(y) dy} = \frac{2\pi\beta}{R_0} \int_0^\infty r^2 K(r) dr$$

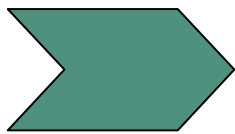
Finite D requires that the “tail” of $K(r)$ decays faster than r^{-3}

Continuous-Space Models

IDE formulation

If $K(r)$ decreases faster than r^{-4} then the variance of D is finite:

$$\text{var}(D) = \frac{2\pi\beta}{R_0} \int_0^\infty r^3 K(r) dr - D^2$$

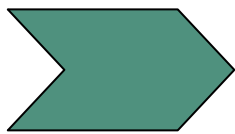


A wave of infection that moves at constant speed

Continuous-Space Models

IDE formulation

If $\text{var}(D)$ is infinite but D is finite, then the wave front accelerates indefinitely.



Gaussian and exponential kernel distributions always lead to a traveling infectious wave front moving at a constant speed.

Power-law kernels can give rise to a wide variety of behavior.

Continuous-Space Models

IDE formulation

The shape of the tail of the transmission kernel (which defines the long-range transmission) determines the eventual spatial pattern of invasion, from wavelike spread, to scattered local foci, to highly probable extremely long-range jumps.

However, the precise shape of the kernel is difficult to estimate from data.

Continuous-Space Models

Usually, PDE and IDE models do not have exact analytical solutions, so numerical simulations are required

Computations require the discretization of space into a fine-resolution grid of subpopulations, breaking the continuous space assumption.



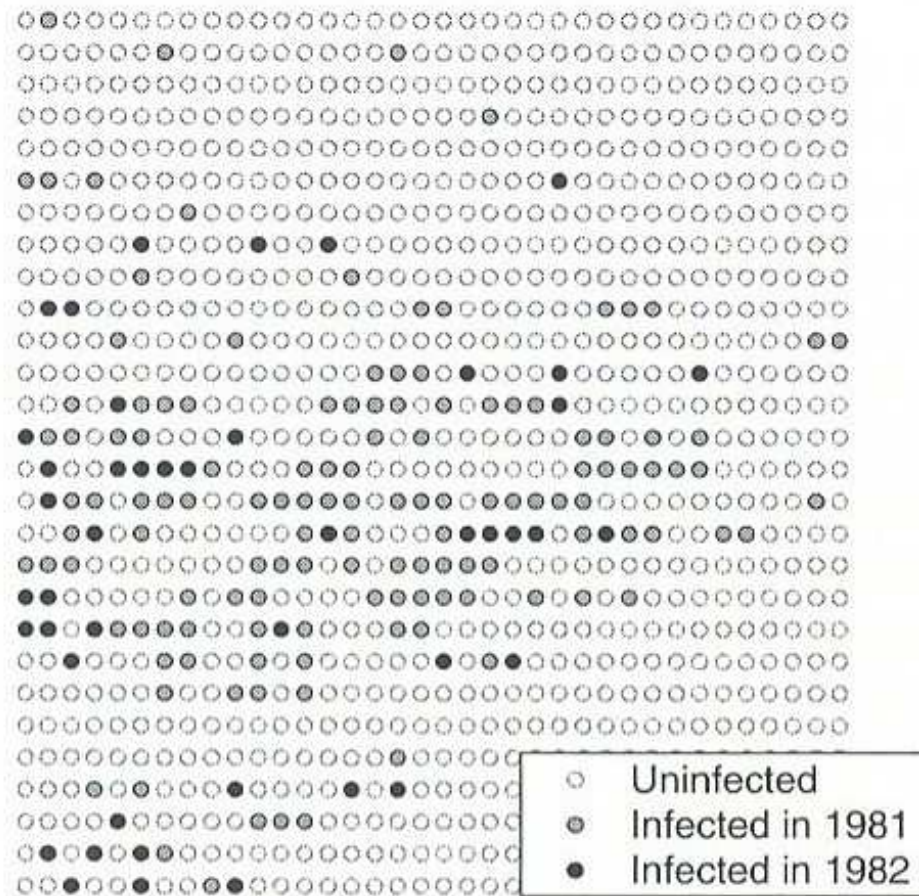
Individual-based Models

Individual-Based Models

Individual-based models account for the spatial interaction between individual hosts distributed on a spatial landscape. They can include a wide variety of complex (more biologically realistic) behavior that often features a spatial component.

This often leads to a large number of parameters that can be difficult to determine from available data.

Individual-Based Models



Marcus, R., Svetlana, F., Talpaz, H., Salomon, R., and Bar-Joseph, M. (1984) On the spatial distribution of citrus tristeza virus disease. *Phytoparasitica* 12 45–52.

Individual-Based Models

Individual-based models have properties in common with continuous space models and stochastic metapopulation models:

- ▶ a transmission kernel captures the spatial spread of infection
- ▶ a stochastic, individual-based nature of the population processes



Slower rate of spatial spread

Individual-Based Models

Consider a general stochastic individual-based model:

- each host is capable of localized movement
- transmission is distance dependent

Probabilistic events:

transmission, recovery, birth, death, and movement.

Individual-Based Models

Transmission

Rate of transmission to susceptible i is

$$\lambda_i = \beta \sum_{j \in \text{infectious}} K(d_{ij})$$

d_{ij} is distance from i to infectious j

K_T is the transmission kernel

Individual-Based Models

Recovery

Usually assumed independent of the environment:

$$\gamma_j = \gamma \text{ constant}$$

Individual-Based Models

Birth

- Individual may find a mate
- Fecundity is a function of the individual's fitness



Two additional kernels may be required

Individual-Based Models

Death

In many situations the death rate of an individual will be a function of the local density, which in turn is a measure of the local competitive effects.



May require another kernel to calculate the strength of competition

Individual-Based Models

Movement

Individuals move through the environment.

The simplest assumption is that individuals randomly and spontaneously move as prescribed by a local movement kernel.

For many species individual movement may be more complex.

Individual-Based Models

Difficulties

Large numbers of parameters.

Errors and biases in the definition of kernels that affect the epidemiological dynamics.

Increasing number of interactions as the population increases:

For a population of N individuals the number of S-I combinations is proportional to N^2 and time for simulation is proportional to N^3

Individual-Based Models

Networks

Are especially useful when each individual is in direct contact with only a small proportion of the population

The advantage of network models is their ability to capture complex individual-level structure in a simple framework

Useful for understanding the transmission of infection in human populations due to either social or sexual contacts

Individual-Based Models

Networks

Connections within a network can be specified through a matrix containing all the interaction strengths ρ_{ij}

For simplicity, connections can be defined only as 0 (not connected) or 1 (connected).

The contact matrix is usually symmetric.

Individual-Based Models

Networks

A matrix G can be used to completely specify the network, indexing all possible transmission links between individuals

Networks provide a robust means to consider the individual nature of disease transmission.

Individual-Based Models

Random Networks

- ignore the actual spatial position of individuals
- connections are formed at random

In one of the analytically tractable versions of the random network, each individual has the same number of contacts

It is characterized by a lack of heterogeneity in the number of contacts and a lack of clustering

Individual-Based Models

Random Networks

These models show that the initial growth rate of a disease in a network $\tau(\bar{n} - 2)$ is reduced compared to the random-mixing equivalent $\tau\bar{n} = \beta$

where τ is the transmission rate across a contact and n is the average number of contacts.

Individual-Based Models

Spatial Networks

They are flexible and related to the individual-based models.

The probability of any two individuals being connected depending on the distance between them is often calculated using a kernel.

Spatial networks generally show a reasonably high degree of heterogeneity, with the number of neighbors often being approximately Poisson distributed.

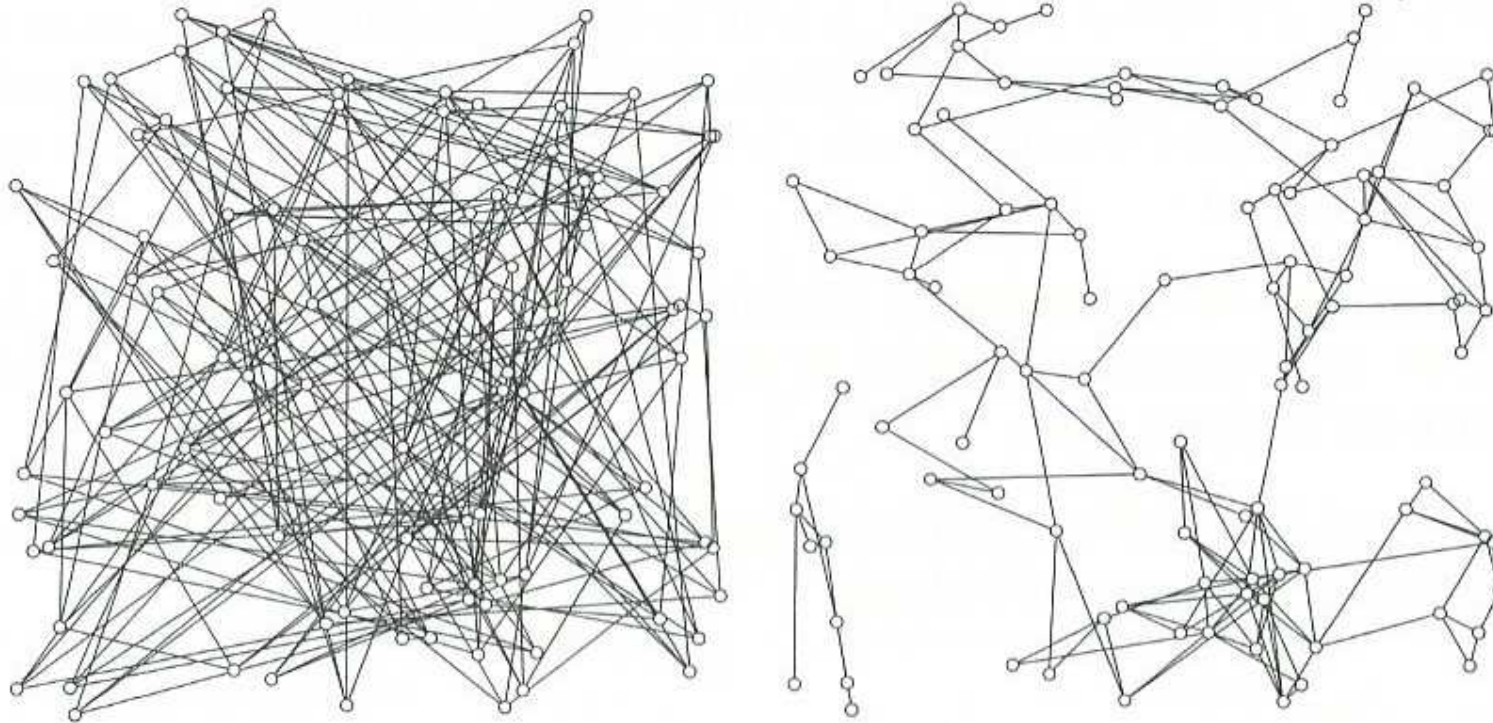
Individual-Based Models

Spatial Networks

When the connection kernel preferentially links nearby individuals, the spatial wavelike spread of infection that characterizes lattice models is observed.

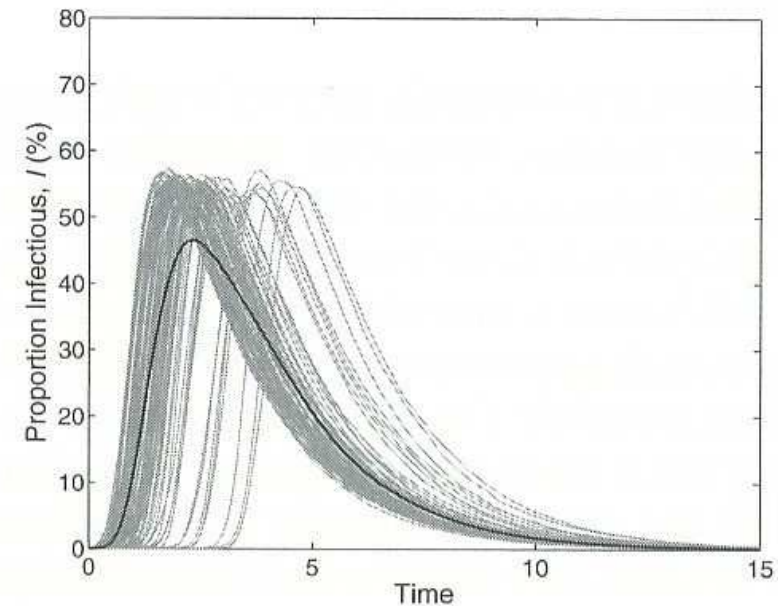
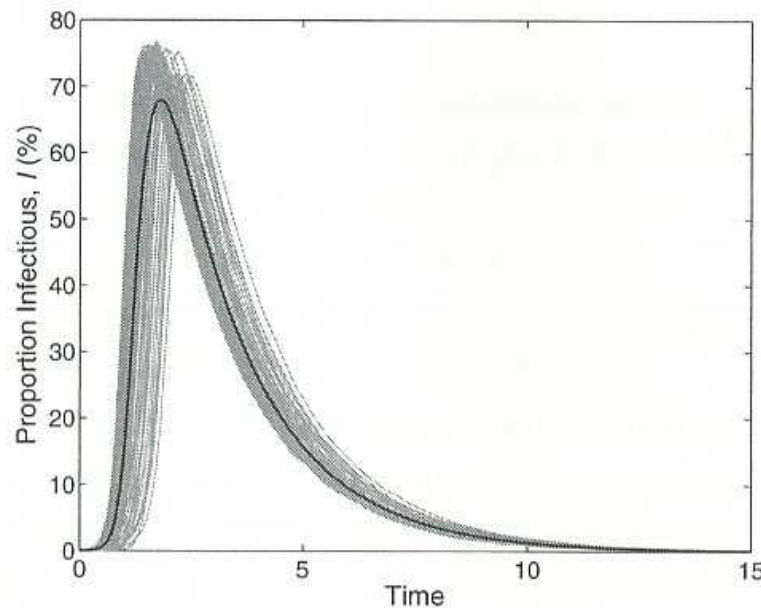
Individual-Based Models

Random and Spatial Networks



Individual-Based Models

Random and Spatial Networks



100 epidemic curves with 10,000 individuals

Individual-Based Models

Lattices

Lattices are associated with a regular grid of contacts and each individual has a fixed number of contacts (usually either 4 or 8).

Contacts are localized in space, hence lattices possess stronger clustering than random networks.

Individual-Based Models

Lattices

The average path length is very long because the only way to transverse the lattice from one side to the other is by steps of a single grid size.

Individual-Based Models

Small World Networks

They are based upon a lattice structure, with a small number of “long-range” connections added.

Locally, small world networks look very much like lattices.

Transmission of infection is predominantly localized so that the strong saturation effects and wave like spread observed in the lattice models still occur

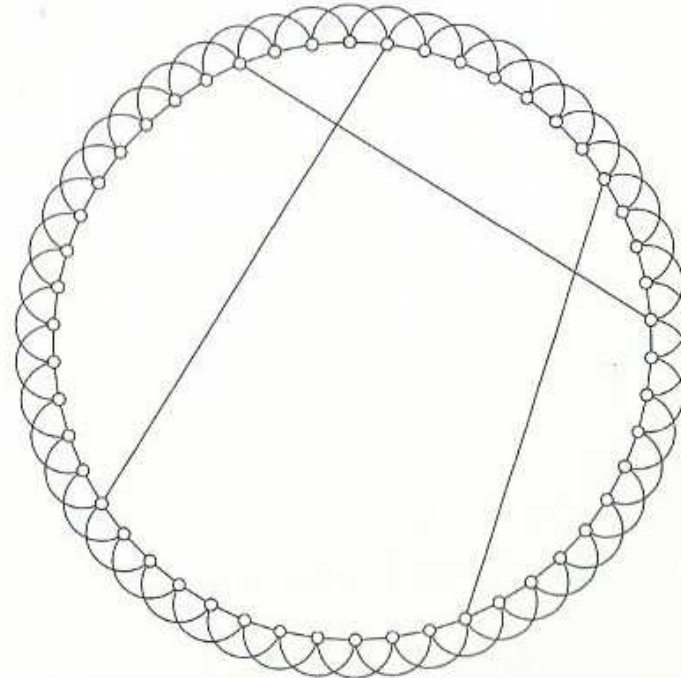
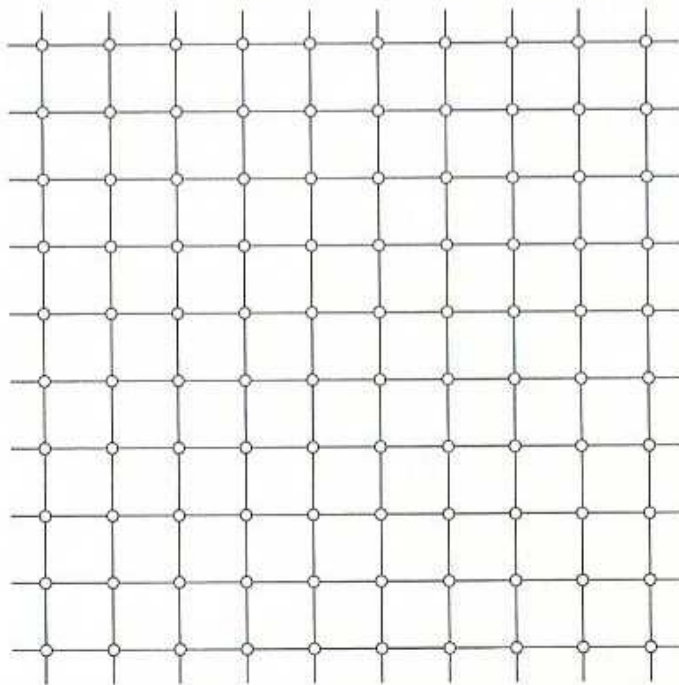
Individual-Based Models

Small World Networks

The few long-range connections provide shortcuts across the network, vastly reducing the average path length and allowing a spreading infection to jump to new susceptible areas.

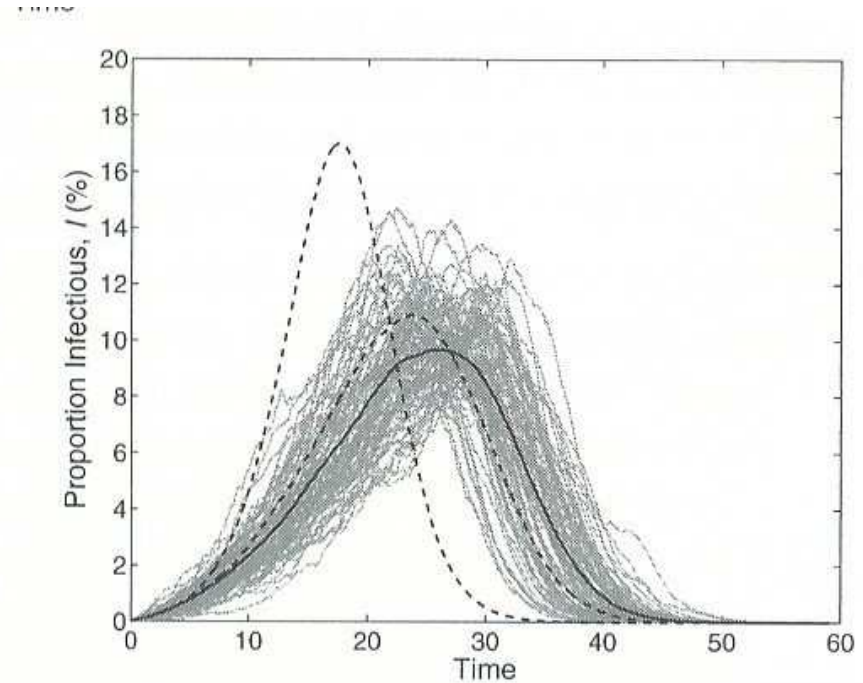
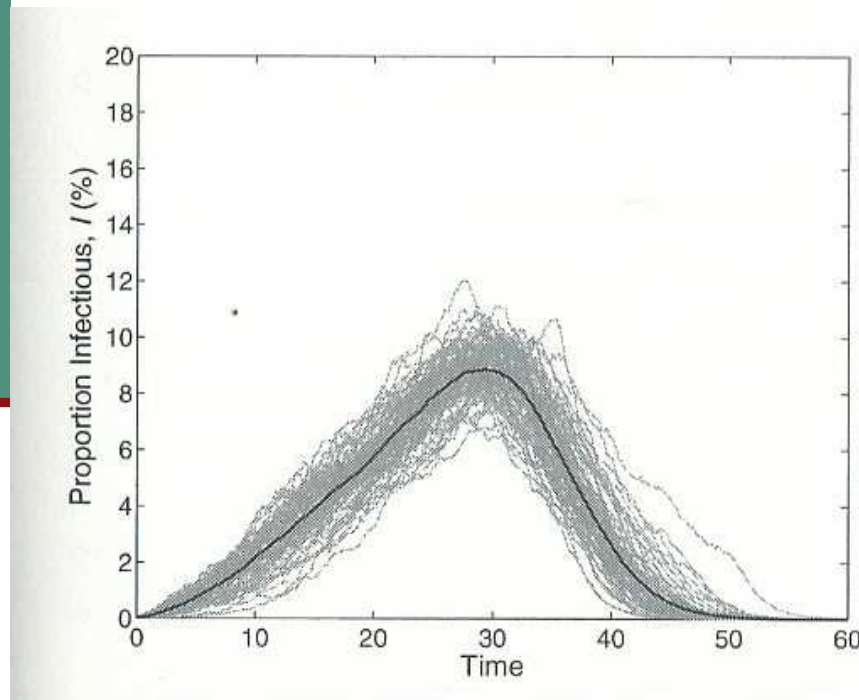
Individual-Based Models

Lattices and Small World Networks



Individual-Based Models

Lattices and Small World Networks



100 epidemic curves with 10,000 individuals

Individual-Based Models

Scale-free Networks

In most of networks that have been studied, the number of contacts per individual is very heterogeneous, with most individuals having a relatively small number and a few have many contacts

Since the most connected individuals are likely to be disproportionately important in disease transmission, networks that incorporate these heterogeneities are vital tools.

Individual-Based Models

Scale-free Networks

These networks are generally created dynamically, adding new individuals to a network one at a time, mimicking the natural formation of social contacts.

A new individual that is added to the population connects preferentially with individuals that already have a large number of contacts.

Individual-Based Models

Scale-free Networks

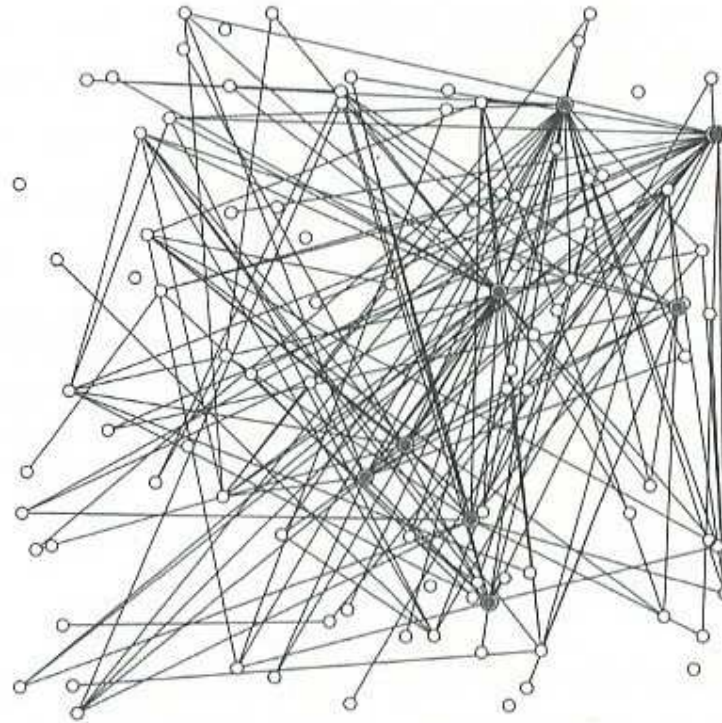
The resultant network has a power-law distribution for the probability of having a given number of contacts:

$$P(\text{contacts} > n) \approx n^{-\alpha}$$

This type of heterogeneities are likely to be present in the social contacts that permit the spread of infection

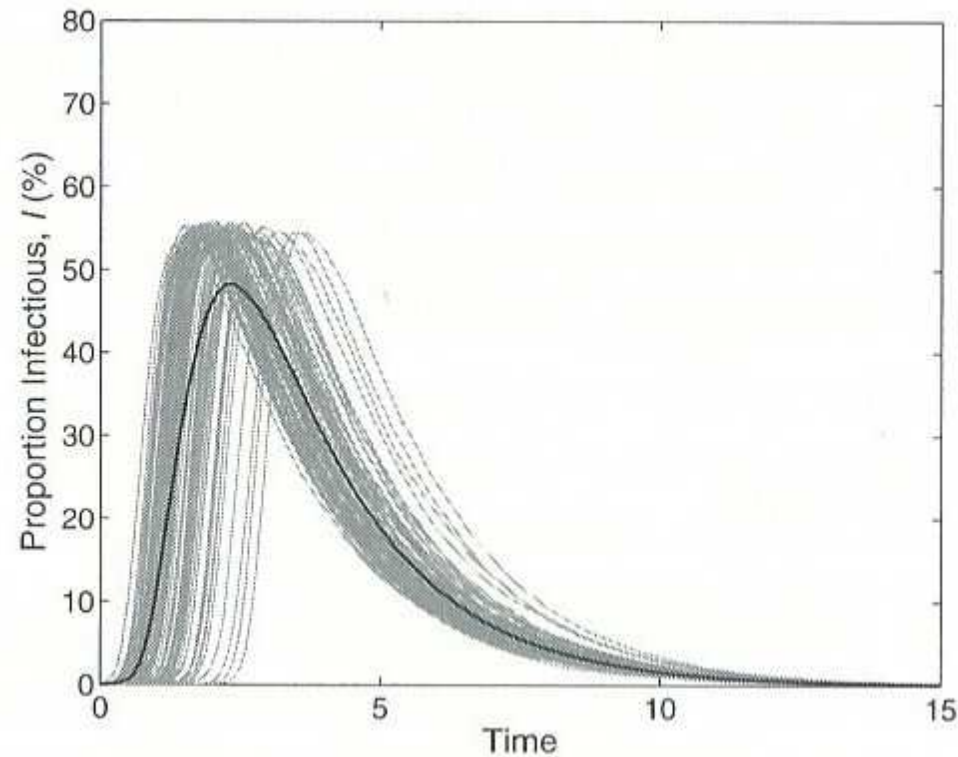
Individual-Based Models

Scale-free Networks



Individual-Based Models

Scale-free Networks



100 epidemic curves with 10,000 individuals

Individual-Based Models

Networks

Many different types of network structure are possible.

They differ in the amount of heterogeneity, clustering, and average path length, thus reflecting the different transmission routes.

Individual-Based Models

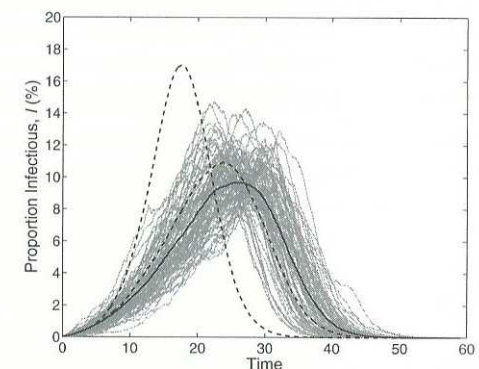
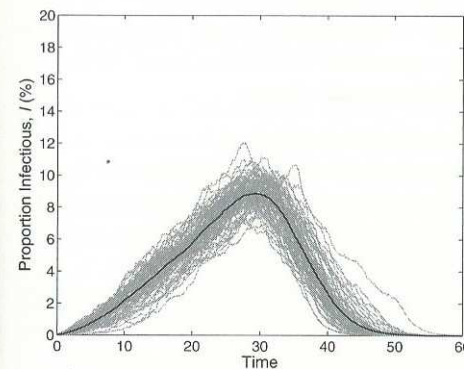
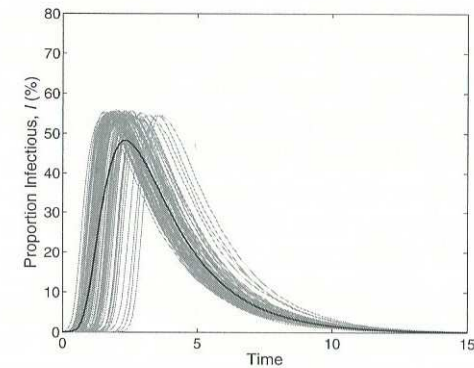
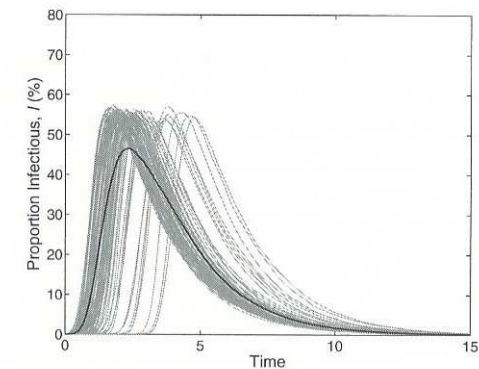
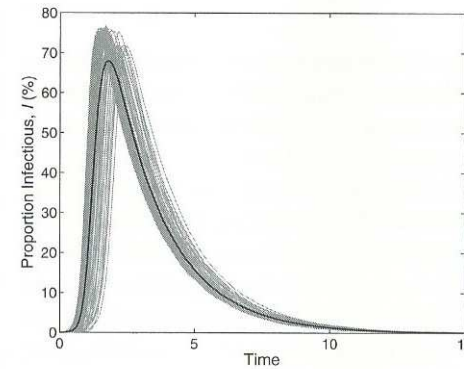
Networks

In general, networks display slower epidemic dynamics compared to randomly mixed models.

Hence, networks that are most like the random-mixing models—with short-average path length (*Small-World*, *Random*, and *Scale-free*) and little clustering (*Random* and *Scale-Free*)—show the fastest epidemic growth rates for a given average number of contacts per individual.

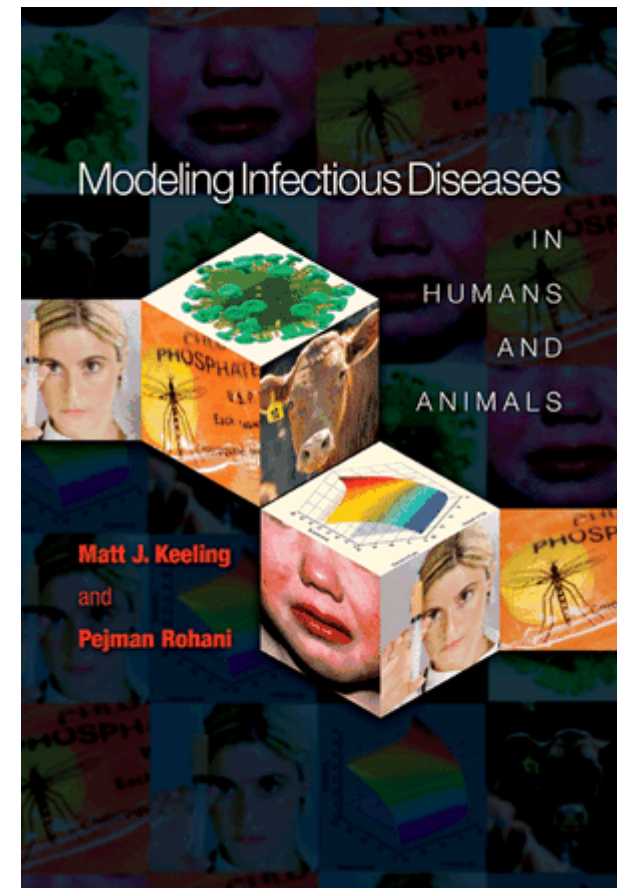
Individual-Based Models

Networks



Books

Matt J. Keeling & Pejman Rohani
**Modeling Infectious Diseases
in Humans and Animals**
Princeton University Press
2008

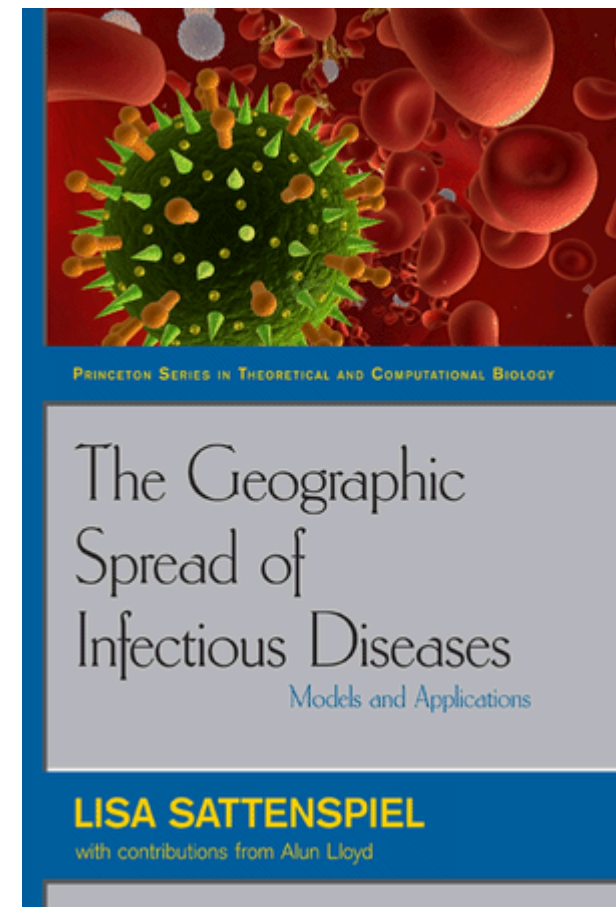


Books

Lisa Sattenspiel
with contributions from Alun
Lloyd

The Geographic Spread of Infectious Diseases: Models and Applications

Princeton Series in
Theoretical and
Computational Biology
2009



Questions and

감사합니다 Natick
Danke Ευχαριστίες Dalu
Thank You Köszönöm
Grazie Tack Obrigado
Спасибо Dank Gracias
谢谢 Merci Seé
ありがとう