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Spatial Epidemics & AL

Joana Margarida*

*CASA - UCL

Overview

- *Epidemic modelling*
- *Complexity*
- *AL epidemic models*
- *My model*

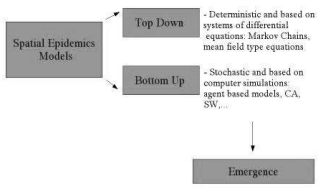
Epidemic Modelling

Spatial Epidemics - "Analysis of the spatial/geographical distribution of the incidence of a disease". (Lawson, A. B. , 2001)

Due to its nature, epidemics have interested scientists of the field of diffusion and spatial diffusion study.

Nowadays, with the emergence of AIDS as pandemic disease, the re-emergence of malaria and tuberculosis as global killers, Ebola, lyme disease and more recently SARS, the interest in epidemic diseases studies was renewed. (Cliff, A.; Hagget, P.; Smallman-Raynor, M., 1998)

Epidemic Modelling



Epidemic Modelling

Deterministic models:

SI model for microparasites. http://hilbert.dartmouth.edu/~m4w02/syl2.htm

Type of Epidemic	*Epidemic component*	*Mathematical symbol*	*Technology transfer equivalent*
Simple	Susceptible	S	Potential adopter
	Infective	I	adopter
general	Susceptible	S	Potential adopter
	Infective	I	adopter
	Removed	R	Rejector

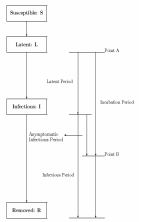
$$\frac{dS}{dt} = -rSI$$

$$\frac{dI}{dt} = rSI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

S - susceptible
I - infective
R - removed
r - infection rate
U - removal rate
r = r / U (threshold value)
$S_0 > r$

Epidemic Modelling



SLIR model (Chen, S., 2001)

$$\Delta S(t) = S(t+1) - S(t);$$

$$\Delta S(t) = -\beta(t)S(t)I(t);$$

$$\Delta L(t) = \beta(t)S(t)I(t) - \beta(t-\gamma)S(t-\gamma)I(t-\gamma);$$

$$\Delta I(t) = \beta(t-\gamma)S(t-\gamma)I(t-\gamma) - \beta(t-\gamma-\nu)S(t-\gamma-\nu)I(t-\gamma-\nu);$$

$$\Delta R(t) = \beta(t-\gamma-\nu)S(t-\gamma-\nu)I(t-\gamma-\nu)$$

β Infection force
γ Latent period
ν Infectious period

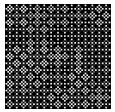
Epidemic Modelling

Some objections can be opposed to this kind of models:

- Diffusive or perfect mixing, and random motion are assumptions not always fulfilled, at least in human populations. (Mansila, R; Gutierrez, J.L.).
- These models tend to incorporate many parameters to explain reality, which increases their complexity and makes them computationally intensive and difficult to analyze!

Complexity

Contrary of what happens on top down approach, on complex systems approach it is considered that spatial extended systems (dynamical systems in which n spatial dimensions are added) are capable of non-trivial collective behaviour - unexpected behaviour which is observed in macroscopic quantities.
It is assumed that there are several levels of reality: at a microscopic level, interactions may be described by complicated potentials, but at a macroscopic level, the properties of the system are dominated by the aggregated effect of all microscopic interactions.



Human epidemics are strongly related to the dynamics of populations and to the network of social contacts, which is typically a complex system where emergence appears (Nowak, A.; Lewenstein, M.).

AL Epidemic Models

Epidemic models using artificial techniques try to capture the complexity of spatial epidemics.
Concerning the structure of the model, there have been essentially two approaches:

- The grid approach (cellular automata)
- the graph approach (small worlds)

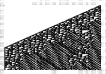
Some models combine this two approaches and even the compartmental models approach (Chen., S., 2001).

AL Epidemic Models

"Cellular Automata (CA) are discrete dynamical systems (in space and time) whose behaviour is completely specified in terms of a local relation" (Toffoli ET AL, 1991).

Some advantages of CA epidemic models:

- treat individuals in biological populations as discrete entities and allow to introduce local stochasticity.
- are very well suited for computer simulations, essentially due to its inherent parallelism and locality.

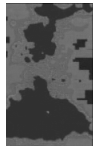


Wolfram's rule 130

AL Epidemic Models

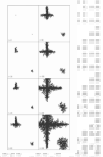
There are some examples of CA epidemic models in plant populations (A.C. Newton, G. Gibson & D. Cox).
As plants can not move, the pattern of infection is fully determined by local relations

In human populations, CA models also have to deal with the problem of movement of individuals, plus the interaction between individuals. There have been several approaches to this problem in recent studies.

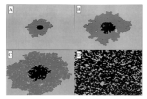


Map of red core severity, with blue areas denoting greater disease incidence (A.C. Newton, G. Gibson & D. Cox)

AL Epidemic Models



Epidemic model (Ching Fu., S.; Milne, G.)



Probabilistic CA model (Fuentes M. A., Kuperman, M. N., 1999)

- Interaction radius to define the neighborhood and probability transisiton rules: Fuentes M. A., Kuperman, M. N., 1999.
- Ching Fu, S.; Milne, G.

use neighborhood radius and motion radius to model contagious and movement, with probabilities associated to each one. In this model, a cell represents a equal sized area of the landscape containing individuals.

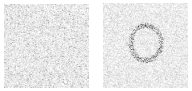
AL Epidemic Models

Lattice Gas Cellular Automata (LCGA):

LCGA - particular class of CA where the dynamics is performed in parallel over all the sites and can be decomposed in two stages: propagation: the particles jump to a nearest-neighbour site according to their direction; collision: the particles entering the same site at the same iteraction, interact, producing a new particle distribution. Examples: HPP, FHP (Chopard, B.; Droz, M; 1998)

▶ Fuks, H.; Lawniczak, T., 2002:

LGCA for reaction-diffusion systems (generic disease); hexagonal grid with a maximum density of individuals in each cell and random movement into adjacent cells.

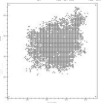


LGCA model with homogenic and barrier vaccination (Fuks, H.; Lawniczak, T., 2002.)

AL Epidemic Models

Site Exchange Cellular Automata (SE CA):

SE CA - CA networks whose rules consist of two subrules: contagious rule - is a local rule synchronously applied, based on Conway's " Game of life " (describes the behavior of the disease); transport rule: sequentially applied, describes the motion of individuals.



▶ Mansila, R; Gutierrez, J.L.:

In this model, movement is random, but the degree of mixing between individuals is controlled by a parameter (p).

Deterministic SE model (Mansila, R; Gutierrez, J.L.)

AL Epidemic Models

http://www.c3.lanl.gov/mega-math/gloss/graph/gr.html

Graphs - A graph G consists of a non empty set of elements (vertices) and a list of unordered pairs of these elements (edges). (Chen, S., 2001)

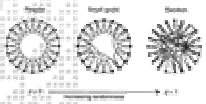
Graphs can be used to represent all kinds of networks, where vertices represent network elements (like people) and edges represent some kind of a predefined relationship between connected elements (like a transmission route).

The theory of Small worlds, also known as “six degrees of separation”, was developed by Duncan Watts and it refers to a particular kind of graphs between order and randomness (Watts, Duncan J., 2003).

AL Epidemic Models

Complex networks, such as social contacts, present some key characteristics:

- short average path length
- high level of clustering
- power law and exponential degree distributions



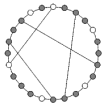
Small World Network (Chen, S., 2001)

The spread of a disease occurs by person-to-person contact, and the structure of networks of such contacts has a huge impact on the nature of epidemics.
There are some examples of SW epidemic models.

AL Epidemic Models

▶ Moore, C; Newman, M. E.J.:

CA probabilistic model: site and bond percolation.
The occupation probabilities of sites correspond to the susceptibility of individuals to the disease and the occupation probabilities of bonds correspond to the transmissibility of the disease.
The model is build on a SW network.

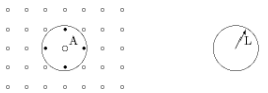


Small World network (Moore, C; Newman, M. E.J.)

AL Epidemic Models

▶ Chen, S (2001):

Foot and Mouth Disease; Two levels: individuals inside the farms, combine compartmental models (mean field assumption) and lattice based methods; agents between farms: SW method.
Individuals move randomly inside the farm, between the neighborhoods.
Virus transmission routes could be local (neighbor farms) or long-distance (countrywide movement).
A variable P (0 to 1) controlled this movement from neighborhood to totally random (de



Definition of the local neighbours of a farm (Chen, S., 2001)

AL Epidemic Models

▶" Modeling Global Epidemics "*:
CA model of the propagation of diseases in the world, where each cell represents the people living in the area. It was assumed that people living in highly populated areas are interacting with more people and that people living in parts of the world with more developed infrastructure tend to travel over large distances (structured diffusion).

$$\frac{I_{cont} \cdot W_{1x,y} \cdot W_{2x} \cdot W_{2y} \cdot N_0 \cdot C_0}{area_{cell}}$$

I_{cont} - number of people that are contagious in the source-cell X.
S- number of people that are susceptible in the target-cell Y.
$w_{1x,y}$- weight between 0 and 1. It is proportional to the fraction of time a person living in the target-cell X in average spends in the source- cell Y during a time step.
w_{2x} and w_{2y} - weight depending on the infrastructure in the source and target-cell respectively.
N_0 and C_0 number of interactions and contagiousness.
$Area_{cell}$- area of the cell in km^2.
Weight ($W_{1x,y}$) parameter – several travelling possibilities are considered: stay in home cell, neighbour cell, Gaussian travelling (Gaussian distribution centred at the persons home site), SW network.

*http://www.dd.chalmers.se/~f97kahe/epidemicsim/epidemicsim.htm

Model

Targets:

-create an individual based model where each cell actually represents an individual, so that locality is not lost by an aggregation effect.
-create a realistic motion model that considers different kinds of movements, that are not totally random, but present a structure, emulating what happens in human populations.
-create a realistic model of the disease, considering latent periods and extra parameters such as age or infrastructure qualities.
-create a coupled GIS-CA model that can put together the visualization and analysis capabilities of GIS with a fast CA model.
SE CA
two phases: (i) mixing and (ii) contagious; assuming there is no virus transmission while the individual is moving.

Model

Mixing Phase:

Let Z be the set of integer numbers and be the lattice

where represents their subclass (susceptible, infective, removed...) and i,j the position on the matrix.

is a function that satisfies the following conditions:

Let be the image of the element under the application of

if

for every

if

Model

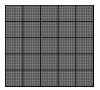
Transport Rules:

The contains a subset of Lattice units

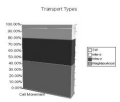
The probabilistic rules applied to every

consider four types of movement:

- neighborhood
- intra
- inter
- SW

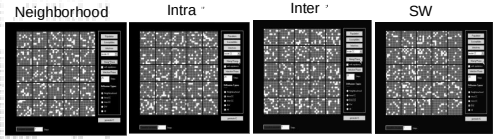


Lattice with units (Blue) and slots (grey)



Model

Neighborhood Intra Inter SW



All

Model

Contagious Phase:

For now, it is used a SIR model, with Moore neighborhood:

The contagious rule is deterministic and totalistic.

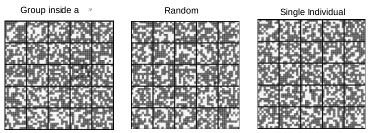
The states of a cell can be expressed as s=I,S,R
Let 1 be an infected site and 0 a non infected site.
The transition of a cell to I, is given by

If => $\begin{cases} 1 & \text{if } \sum_{i=i-1}^{i+1} \sum_{j=j-1}^{j+1} \geq 1 \\ 0 & otherwise \end{cases}$

The transition of I to R is given by

Model

Initial conditions (distribution of infected individuals):



Model

Questions and future developments:

- Transport rules need to be tested concerning the proportions of each type of movement.
- Contagious rules need to be more sophisticated and should fit the characteristics of the specific disease.
- The application to a case study will imply the preparation of the data and of the model in a way that it can be as realistic as possible.
- This task may enforce the use of GIS and the technical implementation of the model as to consider its efficiency.

- **Structure of the model: Graph X CA?**
- **Any suggestions or questions are welcome!**

CASA
http://casoco.casa.ucl.ac.uk/~joana/upgrade/main.htm
j.simoes@ucl.ac.uk

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