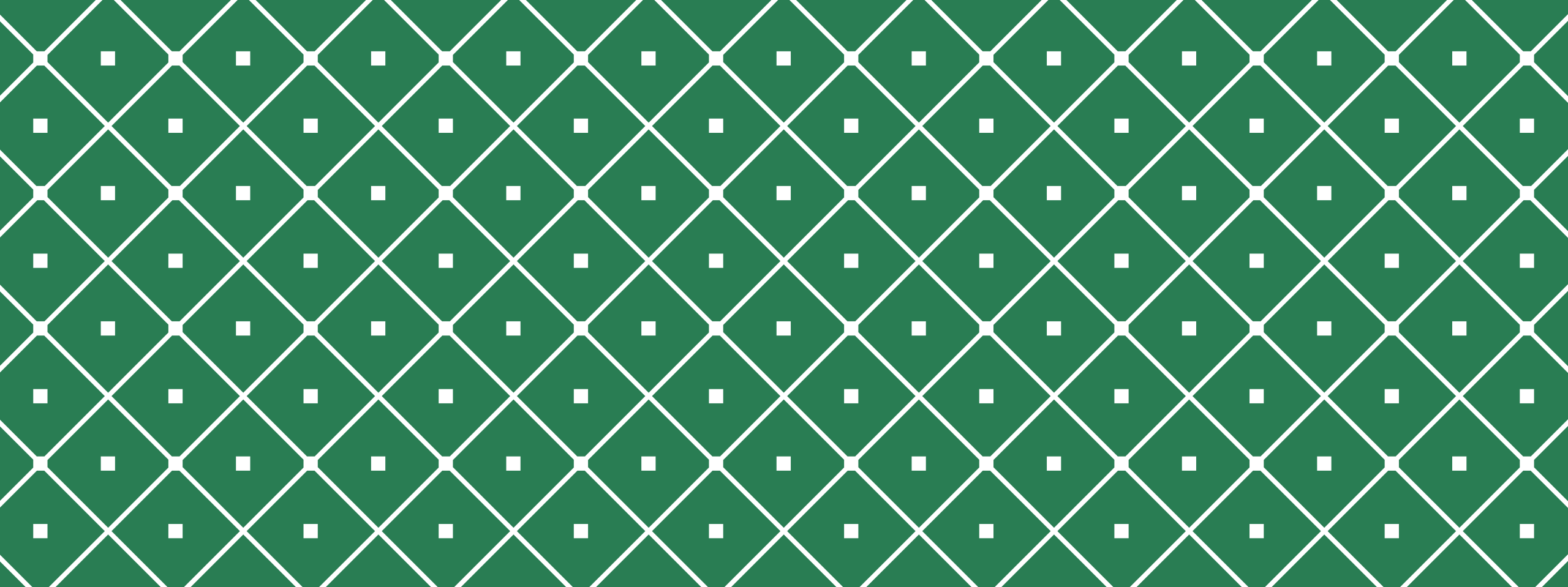


MODELLING INFECTIOUS DISEASES USING ~~GLOBAL STOCHASTIC~~ CELLULAR AUTOMATA

Mikler et al. 2005

BIO4134/8102

Martin Hanzel, Alanna Leale



HOW DOES DISEASE SPREAD DIFFER WITH SPATIAL STRUCTURE?

Classic SRI
Vs.
Simulation

SIMULATION VS. EQUATION MODELLING

PROS

- Incorporate spatial structure without complicated math
- Incorporate numerous variables/interactions (and track through time) with less math
- Enables stochasticity

CONS

- Predictions are difficult without actually running simulation
- Can't "see" how parameters are related and interact
- Too unrealistic or contrived (I beg to differ...)
- Stochasticity requires 1000+ runs → computing power!!!

$$\frac{dS}{dt} = -\beta SI$$
$$\frac{dI}{dt} = +\beta SI - \gamma I$$

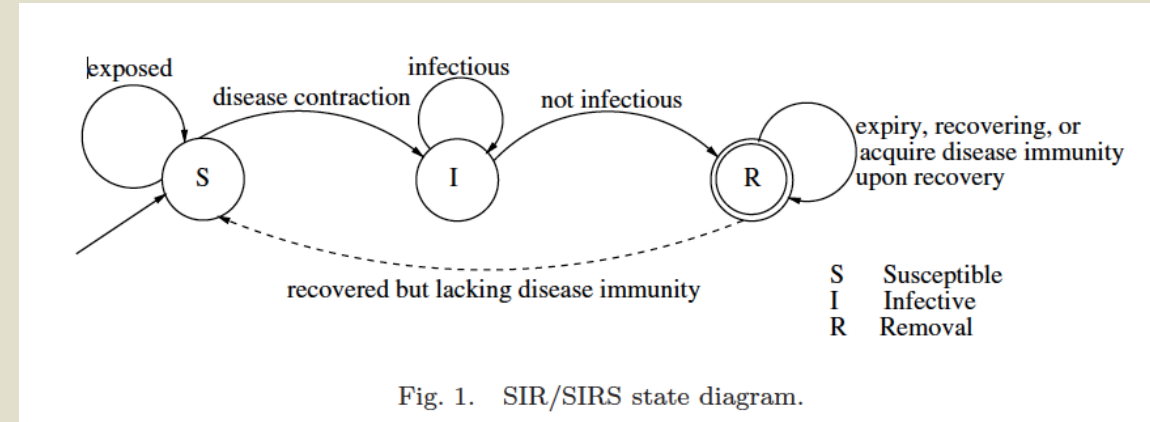
WHY DISEASE SIMULATION?

- Classic SIR models

- Assumes homogenous mixing (individuals interact equally)
- Spatial structure makes math too complicated!

- Cellular automata / simulation

- Interactions \sim geography, demography, environment...
- Improve epidemiology models \rightarrow better predict outbreaks



WHAT ARE CELLULAR AUTOMATA?

- Grid of cells

- Each has distinct state ($S_{i,j}$) – continuous / discrete
- Each has a neighbourhood of surrounding cells ($H_{i,j}$)

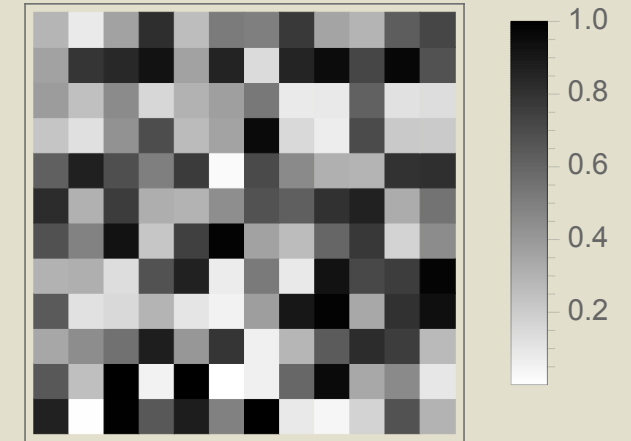
- Discrete time

- $S_{i,j}(t+1) = S_{i,j}(t) \sim S_{\text{neighb.}}(t)$

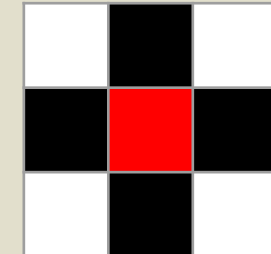
$$s_{i,j}(t) = f(H_{i,j}(t-1)).$$

- Model *simulation*

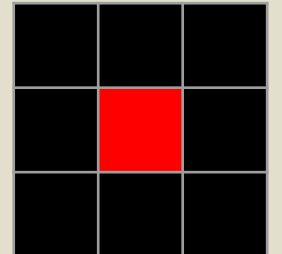
- Run one time step \rightarrow calculate S for every cell
- Repeat, repeat, repeat... (# iterations)



von Neumann
neighbourhood



Moore
neighbourhood



OUR MATHEMATICA MODEL

Initial States & Rules

- **SUSCEPTIBLE = 1** (if no infectious neighbours)
- **LATENT = 2** (1 time step)
- **INFECTIOUS = 3** (1 time step)
- **RECOVERED = 4** (permanent)

**you will add additional states (i.e., immune, latent1, latent2...)*

**you will change switch rules (i.e., return recovered to susceptible)*

IMPORTANT FUNCTIONS

Switch[exp, *form1*, *value1*, *form2*, *value2*...]

- Determines “*value*” ($S_{i,i}(t+1)$) based on “*form*” ($S_{i,i}(t)$)

If[condition, *t*, *f*]

- Turns susceptible \rightarrow infectious, based on neighbours

MemberQ[*list*, *form*]

- Does “*form*” ($S_{i,i} = \text{INFECTIOUS}$) exist in “*list*” of neighbour cells

***Think of it as “Contains[]”*

RandomReal[]

- Returns random value between 0 and 1 (used for probability)

***Hint: Use for %immune, % susceptible etc.*

THINGS TO NOT WORRY ABOUT...

- DiseaseLibrary.wl file
- mRunModel

****DiseaseLibrary.wl must be in same folder as xxx.nb*

THINGS YOU MAY WANT TO KNOW...

- vnNeighbours & mooreNeighbours
 - Makes list of the state of every neighbour cell
- mCellNextState