Spatial (and other) models in mathematical biology

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Well-mixed populations: ODE's

Good model if pop sizes are large and everything is well mixed (e.g., chemostat). No spatial structure and randomness averages out.

- Single-species density: $u(t)$

$$\frac{du}{dt} = ru\Big(1 - \frac{u}{K}\Big) \quad \text{(logistic growth)}$$

- $r =$ intrinsic growth rate; $K =$ carrying capacity
- $u(t) \to K$, as $t \to \infty$

- Multi-species densities: $u_i(t), i = 1, 2, \ldots, n$

$$\frac{du_i}{dt} = u_i\Big(r_i + \sum_j a_{ij}u_j\Big) \quad \text{(Lotka-Volterra models)}$$

a_{ij}	a_{ji}	
$-$	$-$	*competitive*
$+$	$-$	*predator − prey*
$+$	$+$	*mutualistic*

Spatial dependence / local mixing: PDE's

- Intra- and inter-species interactions (as before)
- Fast *local movement*, but not global mixing

  (Ex: random motion of cells; diffusion of individuals in population)

Get some spatial structure (smoothed out and nonrandom)

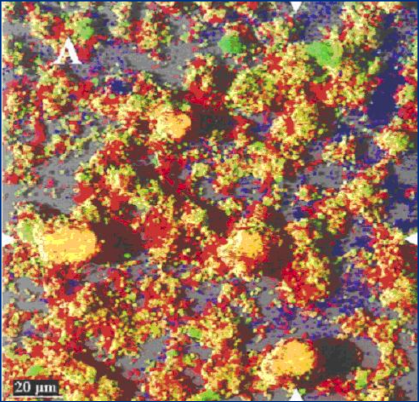
Single species

$u(x,t) =$ density at position x at time t

$$\frac{\partial u}{\partial t} = \Delta u + ru\Big(1 - \frac{u}{K}\Big) \quad \text{(diffusion + logistic growth)}$$

"Fisher's equation"

- spatial spread of advantageous allele or epidemic
- traveling wave front



Spatial biofilm structure; *P. putida* (red), *Acinetobacter* (purple), with transconjugants (green and yellow)

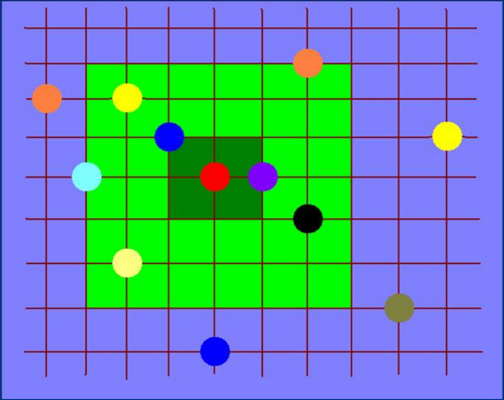
Interacting Particle Systems = CA models

- Explicitly model
    1. discrete (not smoothed out) spatial structure
    2. randomness
    3. local interactions
- Stochastic spatial simulator WinSSS (Grant Guan)

Basic set-up

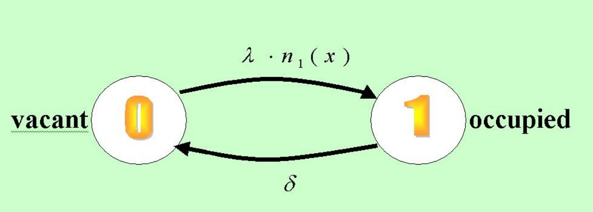
- Sites on grid or "checkerboard"
- Each site can be in several different states
- Specify local interactions: At what rate does a site in state i change to state j (based on what's in neighborhood)?

Picture of grid and neighborhoods



Ex. 1. Contact process

2 states: vacant = 0, occupied = 1



Ex 2: Epidemic model

3 states: Susceptible, Infective, Removed (dead)

Non-spatial (mass-action) model

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI + \cdots \\ \frac{dI}{dt} &= \beta SI - \delta I + \cdots\end{aligned}$$

* Spatial simulations *

some applications to microbiology

bacterial plasmids

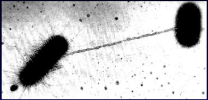
viruses (phage)

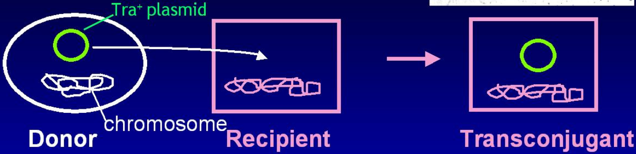
Plasmids (with Eva Top)

- Horizontal gene transfer in bacterial communities (antibiotic resistance)
- Extrachromosomal DNA can transfer quickly between members of same species and different species
- Rapid response to environmental selective pressure

Conjugation mechanisms

1. Self-transfer of Tra^+ plasmids





differential equations for liquid culture

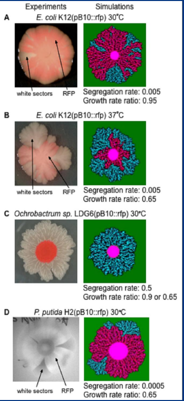
$$\frac{dR}{dt} = \psi_{_R} R + \psi_{_T} \tau T - \gamma_{_T} RT - u_{_R} R \quad \text{(recipients)}$$
$$\frac{dT}{dt} = \psi_{_T}(1-\tau)T + \gamma_{_T} RT - u_{_T} T \quad \text{(transconjugants)}$$

- ψ . . . growth rates (possibly depending on current density and nutrient concentration)
- γ . . . plasmid transfer (conjugation) rate
- τ . . . segregation probability
- u . . . death or washout rates

effects of spatial structure

- most bacteria live attached to surfaces (e.g., biofilms)
- contact is essential for plasmid transfer (conjugation)
- Is transfer of antibiotic resistance genes different from what is predicted by mass-action differential equations?
- Should antibiotic dosing regimens take this into account to slow down the spread of resistance (and the loss of effective antibiotics)?

Spatial patterns–experiment and simulation



Phage

- (Bacterio)phages are viruses that infect bacterial cells
- Great experimental system for studying evolution of viruses
- Effect of spatial structure
- (Opening for undergraduate researcher in my phage lab this semester–krone@uidaho.edu)

* Spatial simulations *