

Population and evolutionary dynamics bottom-upped from individuals

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Population and evolutionary biology viewed as dynamical systems

Differential/difference equations of p -state variables, e.g.,
population densities and strategies, etc.

Individual-based models that track i -state of individuals, e.g.,
body size, foraging ability, mobility, etc.

i -state configuration model (individuals as a discrete entity, mechanistic)

i -state distribution model (analytical)

Caswell 2000

Host-parasite interactions

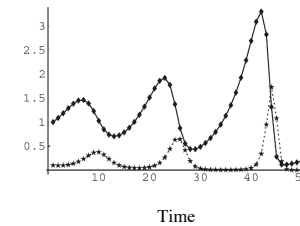
Population dynamics

$$H_{t+1} = Rf(H_t, P_t)H_t$$

Nicholson-Bailey random search

$$P_{t+1} = c(1 - f(H_t, P_t))H_t$$

$$f(H_t, P_t) = \exp[-aP_t]$$

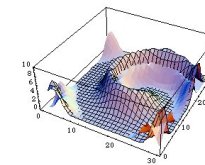
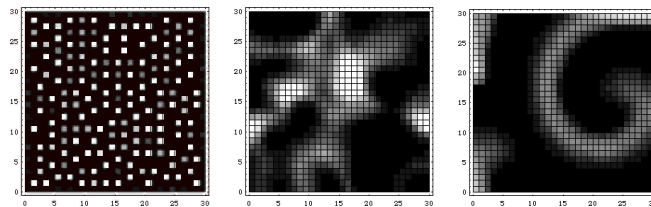


Spatial structure introduces patterns

Nicholson-Bailey model + spatial structure



Hassel et al. 1991



Dispersal can stabilize population dynamics

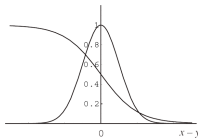
Nicholson-Bailey model + evolution of adaptive traits

Host resistance x and parasite virulence y as adaptive trait

$$H_{t+1}(x) = R \int f \times (1 - A(x, y)) \frac{P_t(y)}{\int P_t(y) dy} dy H_t(x)$$

$$P_{t+1}(y) = c \int (1 - f) H_t(x) A(x, y) dx$$

$A(x, y)$: success rate of parasitism



Evolutionary cycles of host resistance and parasite virulence

Sasaki and Godfray 1999, Takasu 2005

This talk

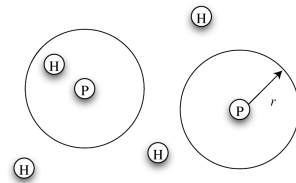
Focuses on

- 1) Population and evolutionary dynamics of host-parasite interactions
- 2) Population and evolutionary dynamics of conspecific parasitism

Aims to explore the link between i -state and p -state models

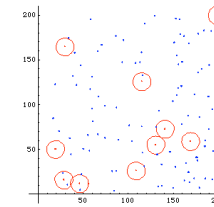
An individual-based model as a baseline

- 1) Individual is assigned a position in two dimensional space $A = L \times L$
- 2) A host that falls within a parasite's area of discovery a is parasitized and produces one parasite offspring
- 3) A host, if not parasitized, produces b offspring
- 4) Offspring disperse according to a certain rule

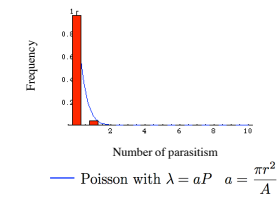
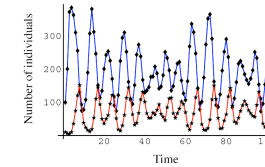


Example

Individuals are randomly distributed



Hosts and parasites with area of discovery



Analytical treatment

Let H_t and P_t be the number of hosts and parasites at t , respectively

$$H_{t+1} = \sum_{i=1}^{H_t} I_i \quad \begin{array}{ll} I_i = b & \text{if not parasitized} \\ I_i = 0 & \text{if parasitized} \end{array}$$

If parasites disperse randomly and independently, a host is parasitized by a parasite with probability

$$p = \frac{\pi r^2}{A}$$

$$E[I_i] = b \left(1 - \frac{\pi r^2}{A}\right)^{P_t}$$

$$\text{Var}[I_i] = b^2 \left(1 - \frac{\pi r^2}{A}\right)^{P_t} \left\{1 - \left(1 - \frac{\pi r^2}{A}\right)^{P_t}\right\}$$

Analytical treatment cont.

If each host reproduces independently,

$$\frac{H_{t+1} - H_t \mu}{\sqrt{H_t \sigma^2}} \approx N(0, 1) \quad \text{for } H_t \gg 1 \quad \begin{array}{l} \mu = E[I_i] \\ \sigma^2 = \text{Var}[I_i] \end{array}$$

$$x_t = \frac{H_t}{A} \quad y_t = \frac{P_t}{A}$$

$$\begin{aligned} x_{t+1} &\approx x_t b \left(1 - \frac{\pi r^2}{A}\right)^{A y_t} + b \sqrt{\frac{x_t}{A} \left(1 - \frac{\pi r^2}{A}\right)^{A y_t} \left\{1 - \left(1 - \frac{\pi r^2}{A}\right)^{A y_t}\right\}} \epsilon_t \\ &= x_t b e^{-a y_t} \quad A \rightarrow \infty \end{aligned}$$

Analytical treatment cont. 2

$$P_{t+1} = \sum_{i=1}^{H_t} J_i \quad J_i = (b - I_i)/b$$

$$y_{t+1} \approx x_t \left\{1 - \left(1 - \frac{\pi r^2}{A}\right)^{A y_t}\right\} + b \sqrt{\frac{x_t}{A} \left(1 - \frac{\pi r^2}{A}\right)^{A y_t} \left\{1 - \left(1 - \frac{\pi r^2}{A}\right)^{A y_t}\right\}} \epsilon_t$$

$$= x_t (1 - e^{-a y_t}) \quad A \rightarrow \infty$$

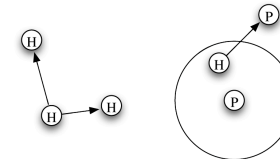
These stochastic difference equations would describe the IBM for random dispersal

Non-random dispersal

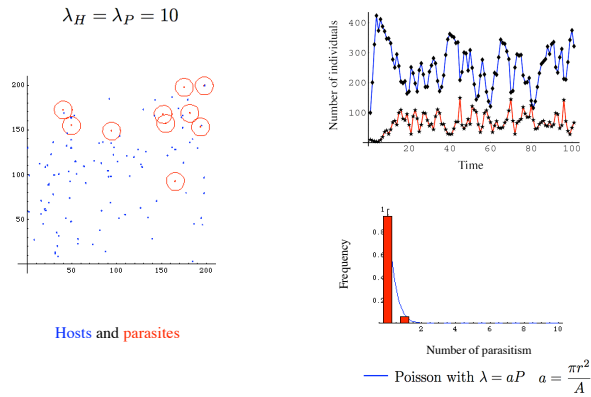
Offspring are distributed in the neighborhood of parents

Dispersal distance x is a random variable

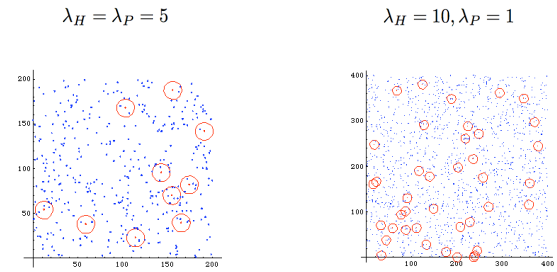
$$\text{Dispersal distance } x \quad \lambda^{-1} \exp[-\lambda^{-1} x]$$



Non-random dispersal 1

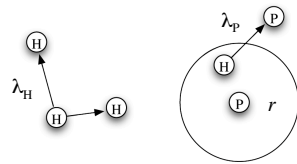


Non-random dispersal 2



Evolution of parameters as adaptive traits

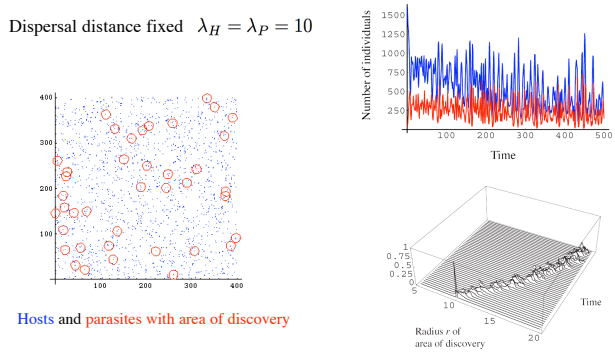
The radius of area of discovery, r
 Average dispersal distance, λ_H and λ_P



Individual is assigned a set of strategies, λ_H for hosts and r and λ_P for parasites
 These strategies are either asexually or sexually inherited

Evolution of the area of discovery

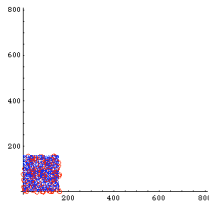
Radius r of area of discovery can evolve
 Dispersal distance fixed $\lambda_H = \lambda_P = 10$



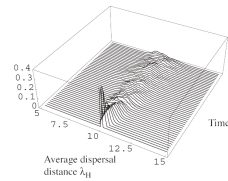
Evolution of the dispersal distance 1

Radius r of area of discovery fixed $r = 10$

Dispersal distance of hosts λ_H can evolve ($\lambda_p = 10$)



Hosts and parasites with area of discovery

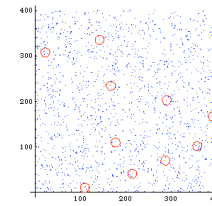


λ_H seems neutral

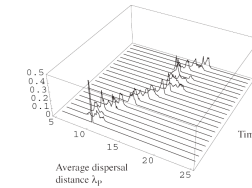
Evolution of the dispersal distance 2

Radius r of area of discovery fixed $r = 10$

Dispersal distance of parasites λ_p can evolve ($\lambda_H = 10$)



Hosts and parasites with area of discovery

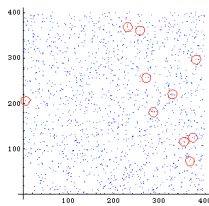


λ_p evolves to be larger

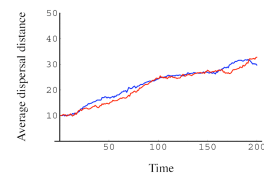
Evolution of the dispersal distance 3

Radius r of area of discovery fixed $r = 10$

Dispersal distance of both hosts λ_H and parasites λ_p can evolve



Hosts and parasites with area of discovery



λ_H and λ_p evolve to be larger

A way to go

The individual-based model (i -state configuration) suggests

Parameters describing hosts and parasites evolve interdependently

The interdependency not fully explored

Can the simulation results be validated by some analytical way?

Derivation of i -state distribution model from the rules of IBM

Comparison with corresponding p -state model

Population and evolutionary dynamics viewed in terms of individuals would provide a rich array of researches in mathematical biology

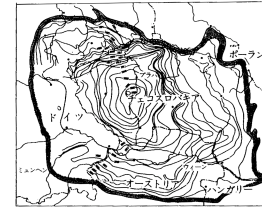
Models of dispersal

Individuals moves and disperse within and between generations

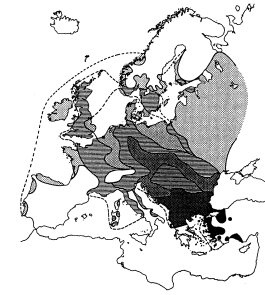
Species	Speed of range expansion (km/yr)
Weedy plant	9.4-32.9
Gypsy moth	9.6
Muskrat	0.9-25.4
Collared dove	43.7
European starling	200
Crab	55
Barnacle	30
Snail	34
Mussel	115

Individual dispersal + reproduction ---> range expansion

Examples



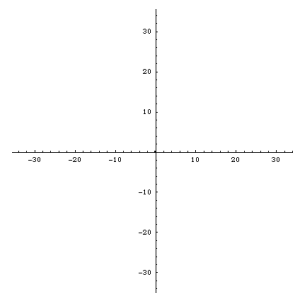
Muskrat



Collared dove

Individual-based model

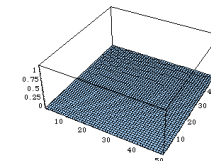
Individuals move randomly
(Random walk)



Reaction diffusion model

Population density n at position (x, y) at time t obeys the following equation

$$\frac{\partial n}{\partial t} = D \left(\frac{\partial^2 n}{\partial x^2} + \frac{\partial^2 n}{\partial y^2} \right) + f(n)$$



And others

Stratified diffusion model

