Discrete population models and dispersal: Part II

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Sequels were never good.

Highlights Part I:

1. The **response** of total population to increasing dispersal is **monotonic** or **unimodal**.
2. That is **general**: unaffected by asymmetry or considering continuous time.

What does make a sequel good?

A twist!

Highlight Part II:

1. There are **models** with more than four different **responses** of total population to increasing dispersal.

Work in collaboration

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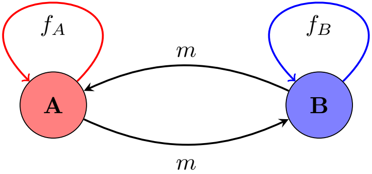
J. Theoret. Biol. 2024 and **J. Math. Biol.** (submitted)

Coupled dynamical systems



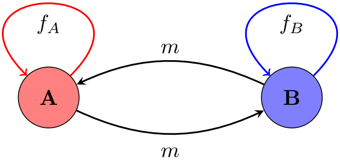
Dispersal model

$$\begin{cases} x_{t+1} = (1-m) f_A(x_t) + m\, f_B(y_t), \\ y_{t+1} = m\, f_A(x_t) + (1-m) f_B(y_t), \end{cases}$$

with $t \in \mathbb{N}$,

- x, y the population sizes in A and B,
- $m \in [0, 0.5]$ the dispersal rate.

Does local dynamics affect number of responses?



Beverton-Holt maps (monotone, simple dynamics / contest)

$$f_i(x) := \frac{r_i x}{1 + x/M_i}$$

Ricker maps (unimodal, rich dynamics / scramble)

$$f_i(x) := r_i x \mathrm{e}^{-x/M_i}$$

Quadratic maps (unimodal, rich dynamics / scramble)

$$f_i(x) := r_i x(1 - x/M_i)$$

with $r_i > 0$ and $M_i > 0$ for $i \in \{A, B\}$.

Is H well defined?

Dispersal is beneficial/detrimental depending on the sign of function

$$\mathbf{H(m) := x(m) + y(m) - (K_A + K_B)},$$

with K_A and K_B the attractors of f_A and f_B when isolated.

1. Ricker: $r_i \in (1, \mathrm{e}^2)$ and $m \in [0, 0.5]$
   Bajo and Ruiz-Herrera. Math. Biosciences (2017).

   Positive equilibrium is a strong attractor in the sense of Liz and Ruiz-Herrera, J. Diff. Equations (2013).

   (Jiménez-López provided them the proof of a key result).
2. Quadratic: $r_i \in (1, 3)$ and $m \in [0, 0.5]$.

Shift points

Lemma

Assume $K_A \neq K_B$. The zeros of H are

$$\left\{ \frac{x - f_A(x)}{K_A + K_B - 2f_A(x)} \middle| \psi(x) = 0 \right\} \cap [0, 0.5],$$

where $\psi \colon [0, K_A + K_B] \to \mathbb{R}$ is given by

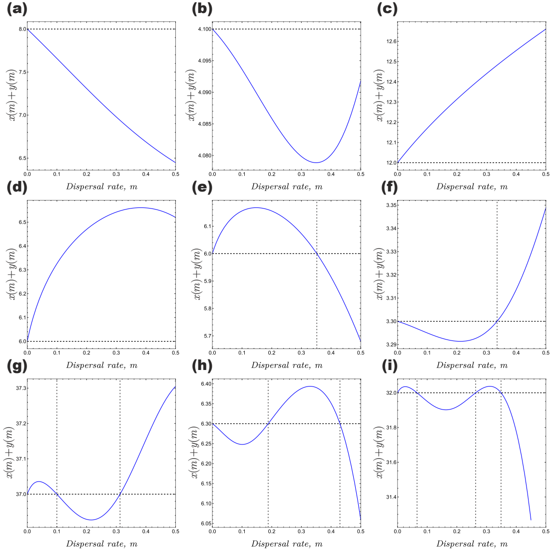
$$\psi(x) := f_A(x) + f_B(K_A + K_B - x) - K_A - K_B.$$

Proposition (Ricker)

Assume $0 < r_A, r_B \leq e^2$ and $K_A \neq K_B$. Then, ψ (equivalently, H) has at most four zeros.

Ricker

New scenarios!



Relevance. No characterization as in B-H.

Ruling out an scenario

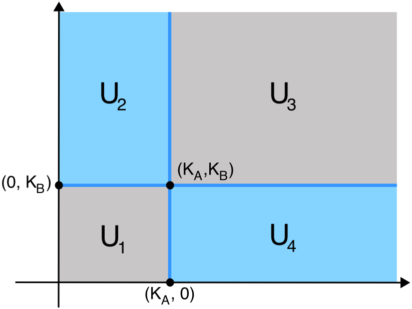
Proposition.

Assume H is well defined in $[0, 0.5]$. Then, the response scenario Detrimental/Beneficial/Detrimental/Beneficial is not possible.

Proof. Assume that H has four zeros in the interval $[0, 0.5\mathbf{)}$.
To rule out the scenario in the statement, we prove $\boldsymbol{H(0.5) < 0}$.
For given $m \in [0, 0.5)$, $(x(m), y(m))$ belongs to the set

$$C = \left\{(x, y) \in \mathbb{R}^2_+ \mid f_A(x) - x + f_B(y) - y = 0\right\}.$$

C is a simple curve of class one joining the points $(K_A, 0)$ and $(0, K_B)$, and passing through (K_A, K_B).



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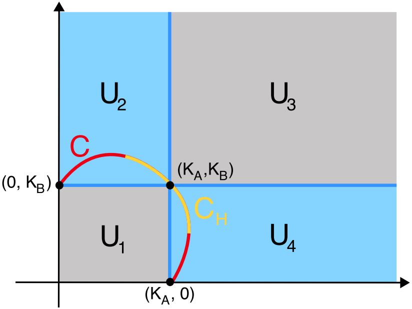


Consider the segment of C parametrized by the dispersal rate

$$C_H = \{(x(m), y(m)) \mid m \in [0, 0.5)\}.$$

Consider

$$L = \left\{(x, y) \in \mathbb{R}^2 \mid x + y = K_A + K_B\right\}.$$

By hypothesis,

$$L \cap (C \setminus C_H) = \emptyset.$$

Since $x + y < K_A + K_B$ for both $(K_A, 0) \notin C_H$ and $(0, K_B) \notin C_H$, then the inequality holds for all points in $C \setminus C_H$. Given that $(x(0.5), y(0.5)) \in C \setminus C_H$, we have

$$x(0.5) + y(0.5) < K_A + K_B \Longrightarrow H(0.5) < 0$$

$\square$

Why the differences between B-H and Ricker?

Scramble/Contest?

Unimodal/Monotone?

Why the differences between B-H and Ricker?

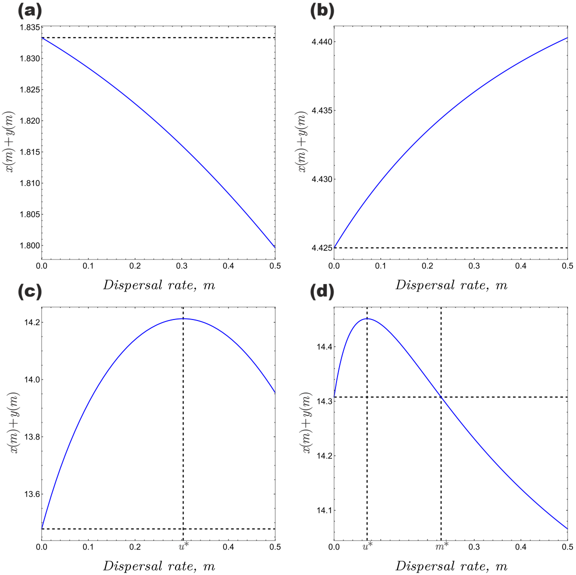
Scramble/Contest?

Unimodal/Monotone?

No

Quadratic

Similar results to B-H



Convexity

BH and the quadratic map are concave downward in their whole domains, but Ricker has an inflection point.

Shift points are obtained by transforming the zeros of

$$\psi(x) = f_A(x) + f_B(K_A + K_B - x) - (K_A + K_B)$$

by the map $x \mapsto m = \frac{x - f_A(x)}{K_A + K_B - 2f_A(x)}$.

If $f_A'' < 0$ and $f_B'' < 0$, then $\psi'' < 0$ and ψ can have at most two zeros.

More patches

Coupling n maps

$$x_i(t+1) = \sum_{j=1}^{n} d_{ij} f_j(x_j(t)), \quad i \in \{1, \ldots, n\},$$

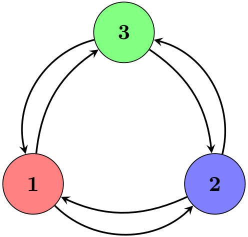
$0 \leq d_{ji} \leq 1$ give the fraction that moves from i to j. We assume no cost to dispersal, i.e., $\sum_{i=1}^{n} d_{ij} = 1$ for all $j \in \{1, \ldots, n\}$.

With matrix notation

$$X(t+1) = D\,F(X(t))^T,$$

$D = (d_{ij})$, $X(t) = (x_1(t), \ldots, x_n(t))$, $F(X(t)) = (f_1(x_1(t)), \ldots, f_n(x_n(t)))$.

1. Do the response scenarios depend on the number of patches within the metapopulation?
2. Revisiting previous results about the effect of increasing connectivity.



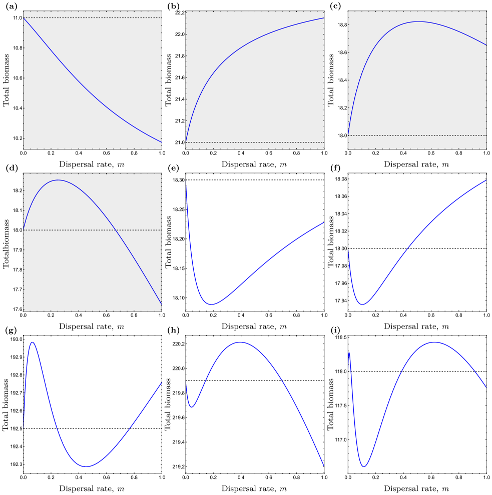
Assumption

The probability of using a path i depends on the number n_i of colonization routes leaving it: each path has the same probability of being used.

$$D = \begin{pmatrix} 1-m & \frac{m}{2} & \frac{m}{2} \\ \frac{m}{2} & 1-m & \frac{m}{2} \\ \frac{m}{2} & \frac{m}{2} & 1-m \end{pmatrix}$$

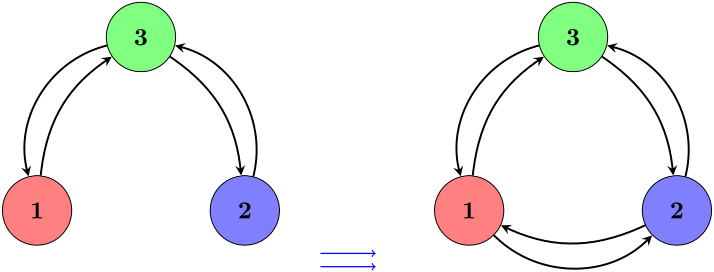
New scenarios!

A 3-patch ring topology under the previous assumption and with B-H local dynamics presents the same responses of the 2-patch Ricker case.

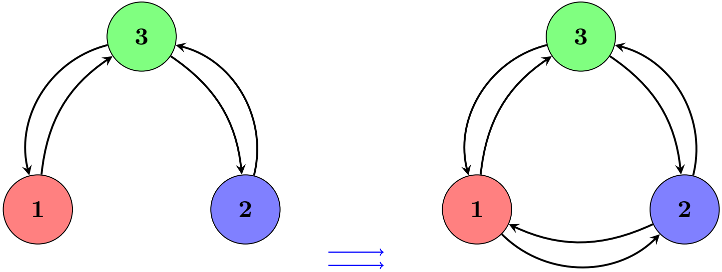


Effect of increasing connectivity

Change a chain to a ring



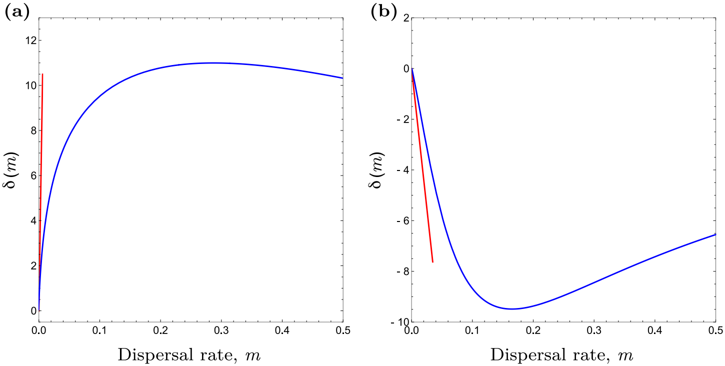
Ruiz-Herrera, A. Metapopulation dynamics and total biomass: Understanding the effects of diffusion in complex networks, Theor. Popul. Biol. (2018).

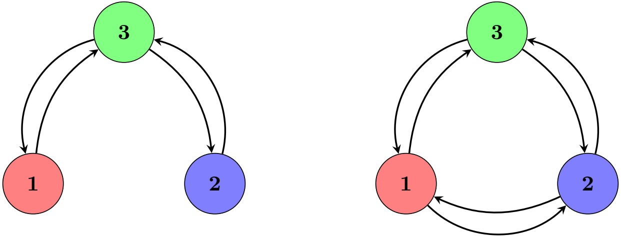


$$D_c = \begin{pmatrix} 1-\frac{m}{2} & 0 & \frac{m}{2} \\ 0 & 1-\frac{m}{2} & \frac{m}{2} \\ \frac{m}{2} & \frac{m}{2} & 1-m \end{pmatrix} \qquad D_r = \begin{pmatrix} 1-m & \frac{m}{2} & \frac{m}{2} \\ \frac{m}{2} & 1-m & \frac{m}{2} \\ \frac{m}{2} & \frac{m}{2} & 1-m \end{pmatrix}$$

$$\delta'(0) = H_c'(0) - H_r'(0) > 0$$

R-H affirms that connecting source patches that were initially disconnected is always beneficial. However, this becomes false when more biologically realistic maps allowing for different intraspecific competition strengths in the subpopulations are considered.





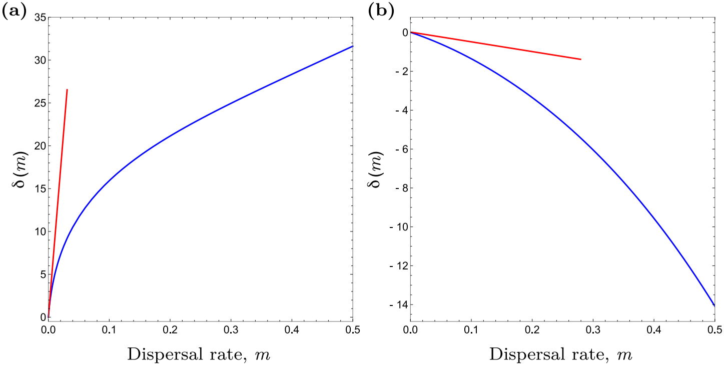
Assumption B

Dispersal depends on the probability to remain in a patch with independence of the number of connections of it with other patches.

$$D_c = \begin{pmatrix} 1-m & 0 & \frac{m}{2} \\ 0 & 1-m & \frac{m}{2} \\ m & m & 1-m \end{pmatrix} \qquad D_r = \begin{pmatrix} 1-m & \frac{m}{2} & \frac{m}{2} \\ \frac{m}{2} & 1-m & \frac{m}{2} \\ \frac{m}{2} & \frac{m}{2} & 1-m \end{pmatrix}$$

Under Assumption B

Connecting source patches that were initially disconnected, even with the same intraspecific competition strengths in the subpopulations!, can be beneficial or detrimental.



Thank you!

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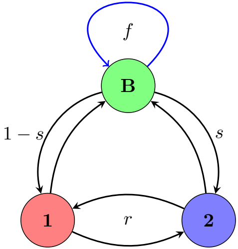
A final twist

Some species have breeding areas where move for reproduction.
Consider a population using three patches: one is the breeding site and the other two (labelled 1 and 2) are feeding sites.
Model the following basic processes:

- Adults produce Juveniles, denoted J, in the breeding site;
- Juveniles become Adults and move to patch 1 or 2, denoted A_1 and A_2;
- Adults in patch 1 or 2 remain in that patch or move to the other.



$$\left.\begin{aligned} J(t+1) &= f\big(A_1(t)+A_2(t)\big), \\ A_1(t+1) &= (1-s)J(t)+(1-r)\lambda A_1(t)+r\mu A_2(t), \\ A_2(t+1) &= sJ(t)+r\lambda A_1(t)+(1-r)\mu A_2(t), \end{aligned}\right\} \qquad (1)$$

where $r, s, \lambda, \mu \in [0,1]$ are constants and $f : \mathbb{R}_+ \to \mathbb{R}_+$.
Remark: System (1) extends the Allen-Clark model ($\lambda = \mu$)

$$z(t+1) = \alpha z(t) + \beta f(z(t-1)).$$

Symbol	**Interpretation (each per time-step)**
f	recruitment function of new Juveniles
r_i	proportion of Adults who move from site i to $3-i$
s	proportion of Juveniles who move to patch 2
λ	survival probability of Adults in site 1
μ	survival probability of Adults in site 2