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Author Primary¹, C. O. Author²

¹Department of Mathematics & Statistics - University of Nevada, Reno (UNR); ²Mathematics - University of X



Introduction

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Here’s a list!

- ▶ item 1
- ▶ item 2
- ▶ etc

Model Equations: Spatial SIR Example

Blah blah blah

$$\begin{aligned} \frac{dS_i}{dt} &= \overbrace{-m\mathcal{E}_iS_i + m\Phi_i(\vec{S})}^{\text{Movement}} \overbrace{-\mu\vec{S}_i - \beta\vec{S}_iI_i}^{\text{Loss \& Disease}} \\ \frac{dI_i}{dt} &= -m\mathcal{E}_iI_i + m\Phi_i(\vec{I}) - \mu I_i + \beta S_iI_i - \gamma I_i \\ \frac{dR_i}{dt} &= -m\mathcal{E}_iR_i + m\Phi_i(\vec{R}) - \mu R_i + \gamma I_i \end{aligned}$$

Movement rates depend on habitat (patch) quality $r_i \equiv (G_i - G_{min})/\mu$. Individual rates of growth, $G_i \equiv G(T_i, DO_i, i)$, and mortality, $\mu_i \equiv \mu(T_i, DO_i, i)$, are calculated from temperature (T) and dissolved oxygen (DO) data using a bioenergetics model for rainbow smelt. We assume

$$\mathcal{E}_i = \exp(-hr_i), \qquad \Phi_i(\vec{X}) = \frac{e^{hr_i}}{\sum_j e^{hr_j}} \left(\sum_j \mathcal{E}_j X_j \right)$$

where \mathcal{E}_i determines the emmigration rate from patch i , and those emmigrants are distributed among the other patches according to $\Phi_i(\vec{X})$, where \vec{X} is either \vec{S} , \vec{I} or \vec{R} . Total fish biomass in patch i (c_i) changes with growth (G_i), death (μ_i), and movement according to

$$\frac{dc_i}{dt} = -m\mathcal{E}_i c_i + m\Phi_i(\vec{c}) + G_i c_i - \mu_i c_i.$$

Preliminary Results & Conclusions

- ▶ Climate-driven warming & hypoxia negatively impact survival & individual body weight – an key determinant of fecundity.
- ▶ Hypoxia-induced aggregation increased disease transmission & epizootic size. Stress & body condition effects less pronounced.
- ▶ Additional research is needed to clarify environmental dependencies, differences arising from different host and parasite natural histories, host bioenergetics and parasitism, & the importance of different transmission routes between hosts.

etc.

References