



This is the poster title.  
It can be two lines if needed

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Introduction

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Here’s a list!

- item 1
- item 2
- etc

Model Equations: Spatial SIR Example

Blah blah blah

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

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

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

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 ( $\mu_i$ ), 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