The Grand Unified Theory Of Copepods







Modeling copepod biodiversity and life-history using evolutionary computing



Motivating questions

o The Compupod Project

o Comments

Next steps





Modeling copepod biodiversity and life-history using evolutionary computing

Motivating questions

- Why are many arctic / subarctic systems dominated by single large Calanus species?
- Why do dominant Calanus congeners range in adult size by an order of magnitude? (e.g. finmarchicus vs hyperboreus)
- O How do temperature and seasonality structure the diversity
 of copepod communities?
- What influences the size structure of copepod communities?
- o Many others...





The Compupod Project

Broad approach

- O Build a first-principles mechanistic copepod ("compupod")
- Validation: test model against well-studied taxa
- Generalize formulation to population and community levels

Example: compuped development/growth





Mechanistic formulation

1)Temperature-dependent development rate

empirical: $D(T) = a(T - \alpha)^b$

- soft parameters a, b, α

mechanistic^(?): $D(T) = a \exp[-E(T - T_0)/(kTT_0)]$

(Arrhenius 1889)

(Belehradek 1935)

- soft parameters *a*, *E*







Mechanistic formulation

- 1)Temperature-dependent development rate
- 2)Ingestion
 - empirical: $I = I_{max} (1 exp(-aF))$

(Ivlev 1955)

- based on hunger

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mechanistic: I = Z F / (1 + h Z F) (Holling 1959)

- handling time, encounter rate are measurable
- follow allometric scaling (m^{3/4})



Mechanistic formulation

- 1)Temperature-dependent development rate
- 2)Ingestion
- 3)Allometric scaling
 - metabolism, foraging, etc. related to mass $(m^{3/4})$





Validation

Parameterize to 4 taxa (Maps et al 2011, in review)

- Calanus finmarchicus, C. glacialis, C. hyperboreus, Pseudocalanus spp.
- Tune parameters using genetic algorithm
- Validate using information from the literature not included in tuning





Validation



Good fits with lab data using genetic algorithm

Campbell et al. 2001

Validation

Good agreement with information from the literature

- O Temperature-dependent gut clearance rate
- Food-dependent egg production rate

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Allometric egg production rate



Population Level

For an individual compupod

- state variables: (stage, mass)

At the population level

- C(s,m) = concentration of compupods at stage=s, mass=m

$$\frac{\partial C_{i,j}}{\partial t} = -\frac{\partial (g_{i,j}(T,F)C_{i,j})}{\partial m} - \frac{\partial (d_{i,j}(T,F)C_{i,j})}{\partial s} - \mu_{i,j}(F) + \dots$$





Population Level



Gulf of Maine Research Institute O Discretize and compute like an advection problem

Q Use anti-diffusive
 scheme (e.g. MUSCL)
 to allow low resolution,
 high computational
 speed¹

¹Record & Pershing (2008)L&O-Methods 6:364-372

Population Level



- Simplified example of niche partitioning of 4 taxa
- o Using constant food, temperature, mortality, etc.

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Q Winner is taxon with highest lifetime egg production rate







Fig. 5.10. Schematic illustrating the morphological diversity of pelagic copepods. The morphologies of most pelagic copepods are all very similar in that they have well-developed sensory machineries and torpedo-shaped bodies and are, thus, efficient in detecting and escaping predators. This suggests that predation has been a very strong selective force in shaping the morphology of this successful group of zooplankton (Verity and Smetacek 1996).

Kiørboe 2008





What distinguishes one copepod species from others?

 $\frac{\partial C_{i,j}}{\partial t} = -\frac{\partial (g_{i,j}(T,F)C_{i,j})}{\partial m} - \frac{\partial (d_{i,j}(T,F)C_{i,j})}{\partial s} - \mu_{i,j}(F) + \dots$

Temperature-dependent development rate (D_0 , E_d) Search volume (V_0) Handling time (H_0)

Diapausing stage Broadcast vs sac spawning















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- Annual cycles change through time
- O Coexistence for long periods
- Changes in dominance
- \circ Some eventual exinction \rightarrow selection











Next steps

 \rightarrow

Parameterize other trade-offs

- broadcast vs sac spawning
- o diapausing stage
- foraging strategy
- o mixed diet
- Q ..

full paramosome

 $\begin{bmatrix} D_0, T_0, E, H_0, \alpha, \beta, \gamma, \dots \end{bmatrix}$ [9.3,0,0.9,.057,6,2.11,3,...] [8.9,0,0.7,0.35,7,2.11,3,...] [7.7,0,0.8,0.44,4,2.09,3,...]





Next steps

Selection experiments

- O Different food / temperature regimes
- O Different mortality regimes
- o Different time scales
- O Coupled ROMS ecosystem model
 O

 $\begin{bmatrix} D_0, T_0, E, H_0, \alpha, \beta, \gamma, \dots \end{bmatrix}$ [9.3,0,0.9,.057,6,2.11,3,...] [8.9,0,0.7,0.35,7,2.11,3,...] [7.7,0,0.8,0.44,4,2.09,3,...]





Goal: emergent, system-level properties

